

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 05:20:10 ; Search time 58.31 Seconds
(without alignments)
1919.809 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254
Sequence: 1 MICORFCVLLHWEFTYIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4784.5	76.5	1162	2	PC4184
2	4766.5	76.2	1162	2	PC4184
3	3793	60.6	900	2	S68438
4	3785	60.5	900	2	S68440
5	3785	60.5	894	2	S68437
6	3729	59.6	895	2	S74225
7	3340	53.4	805	2	S68441
8	366	5.9	917	2	I49699
9	345.5	5.5	918	2	A36337
10	339.5	5.4	918	2	A44257
11	313	5.0	837	2	A34898
12	294.5	4.7	1097	2	S17308
13	288.5	4.6	863	2	C38252
14	284	4.5	783	2	JH0329
15	281.5	4.5	1092	2	JX0312
16	277	4.4	771	2	B38252
17	251.5	4.0	2302	2	T14328
18	220	3.5	830	2	I50455
19	209.5	3.3	831	2	JQ1655
20	191.5	3.1	6805	2	S20901
21	188	3.0	26926	1	I38344
22	182.5	2.9	1471	2	T19506
23	177	2.8	2481	2	A43908
24	174	2.8	1375	2	T13822
25	172	2.8	1896	2	T08851
26	170	2.7	1332	2	T43027
27	169.5	2.7	1443	2	I50600
28	166.5	2.7	1443	1	TDFPLK
29	166	2.7	3488	2	T34418

30	165	2.6	630	2	I51086	prolactin receptor
31	165	2.6	1526	2	T13823	frizzled gene prot
32	160	2.6	1197	2	T30581	neural cell adhesi
33	159	2.5	2340	2	I48310	kinase-related pro
34	158	2.5	1825	2	C68400	protein H19M22.1 l
35	158	2.5	1825	2	T32828	hypothetical prote
36	158	2.5	2338	2	T73957	kinase-related pro
37	156	2.5	1000	2	I46521	leukemia-6 rece
38	154.5	2.5	2286	1	FNHU	fibronectin precu
39	153.5	2.5	440	2	JL0144	interleukin-6 rece
40	153.5	2.5	460	2	JL0145	interleukin-6 rece
41	153.5	2.5	610	2	A36116	prolactin receptor
42	150.5	2.4	310	2	A29884	prolactin receptor
43	150.5	2.4	412	2	A41070	prolactin receptor
44	150.5	2.4	5005	2	F82884	hypothetical prote
45	148.5	2.4	610	2	A34631	lactogen receptor

ALIGNMENTS

RESULT 1
PC4184
leptin receptor, OB-Rb - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Aug-1996 #sequence_revision 13-Mar-1997 #ext_change 01-Dec-2000
C:Accession: J04895; J04896; J04897; PC4184; J04797
R:Takeya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Ta
Blochem. Biophys. Res. Commun. 225, 75-83, 1996
A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifi
A:Reference number: J04895; M01D:96532408
A:Accession: J04895
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1162 <TA2>
A:Cross-references: DDBJ:D85558; NID:q1526441; PIDN:BA12831.1; PID:q1013515; PID:g15
A:Accession: J04896
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <TA2>
A:Cross-references: DDBJ:D85557
A:Accession: J04897
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796, 'G', '1157-1158, 'TVLLN' <TA3>
A:Cross-references: DDBJ:D85559
R:Takeya, K.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Blochem. Biophys. Res. Commun. 224, 597-604, 1996
A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)
A:Reference number: PC4184; M01D:96295531
A:Accession: PC4184
A:Molecule type: mRNA
A:Residues: 840-1162 <TID>
A:Cross-references: DDBJ:D84550
R:Takeya, K.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 222, 19-26, 1996
A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker f
A:Reference number: J04797; M01D:96212906
A:Accession: J04797
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <TID>
A:Cross-references: DDBJ:D84125; NID:q1374707; PIDN:BA12230.1; PID:q1374708
A:Experimental source: adipose cell
C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa
C:Genetics:
A:Gene: fa
C:Keywords: appetite; transmembrane protein
F:440-860/Domain: transmembrane #status predicted <TM>
F:661-1162/Domain: intracellular #status predicted <IN>

Query Match 76.5%; Score 4784.5; DB 2: length 1162;
Best Local Similarity 75.6%; Pred. No. 6.5e-303;

Matches 882; Conservative 118; Mismatches 161; Indels 5; Gaps 5;

QY 1 MICOKFCVLLHMEFIYVITAFNLSTYPTPMRKLSCMPNSTYDYFLPAGLSKNTNS 60
 Db 1 MTCOKFYVLLHMEFLVITAFNLALNLAAPTSPMRKFLPCAPSTTDDSLSPAGVNNNSL 60

QY 61 NGHEFVAEPEKFNSSGTHFNLSKTTTHCCFRSDORNCISLADNIGKTFVSTVNSLVF 120
 Db 61 KGASEALVEAKFNSTGIYVELSKTIFHCFCGNGONCSALNGTNGEKTALASVVKPLVF 120

QY 121 QOIDAMNNIOCMKLGDKLFTCYVESLFKNLFRNRYNKVHLVLPVLEDSPLVPQKS 180
 Db 121 ROLGVNMDICMKMGDLTLETCHEMPLKMPFKYDSKHLHLYDLPVLDLPLPKDS 180

QY 181 FOMVHCNSVHECCCLVPPYPAKNDLTLLMCLKITSGGVIFOSPLMSVOPINMKVDPDP 240
 Db 181 FOMVHCNSVHECCCLVPPYPAKNDLTLLMCLKITSGGVIFOSPLMSVOPINMKVDPDP 240

QY 241 LGHMEITDDGNLKISWSSPPLVPPLQOVKYSNSTYIREDKIVSATSLVDSILP 300
 Db 240 LGHMEITDDGNLKISWSSPPLVPPLQOVKYLENS-TIVRAAEIVSDTSLVDSILP 298

QY 301 GSSYEVOVGRKRLDGCINSDMSTPRVFTTQDYIYFPPKILTVSGNSVSHCIYKKNKI 360
 Db 299 GSSYEVOVGRKRLDGCINSDMSTPRVFTTQDYIYFPPKILTVSGNSVSHCIYKKNKI 358

QY 361 VPSKEIYVMMNLAERKIPQSDYDVSDHVSIVTFPNLNETRPRGKFTYDAVYCCNEHCCH 420
 Db 359 ISSKQIYVMMNLAERKIPETQYNTVSDHVSIVTFPNLNETRPRGKFTYDAVYCCNEHCCH 418

QY 421 RYAEIYVIVNINISCTEDYLTMRKCRMSSTTOSLAESTLQRYRSLSLXSDPSIH 480
 Db 419 RYAEIYVIVNINISCTEDYLTMRKCRMSSTTOSLVSTQVLRHRRSLXCPDNSSIR 478

QY 481 PISEPKDYLOSDGEYECIPQIFLUSGYTMIRINHSLSLSDSPPCVLPDSVYKRLP 540
 Db 479 PISEPKDYLOSDGEYECIPQIFLUSGYTMIRINHSLSLSDSPPCVLPDSVYKRLP 538

QY 541 SSVKAEITIGLTKISMEKVPENNLQOIRYGLSGKQVOKMEVYDAKSRSVLPV 600
 Db 539 SSVKAEITIGLTKISMEKVPENNLQOIRYGLSGKQVOKMEVYDAKSRSVLPV 598

QY 601 PDLCAVAVOVGRKRLDGLGYNSMSPATYVMDIKVPRGEPFMIINGDMKKKNV 660
 Db 599 PDLCAVAVOVGRKRLDGLGYNSMSPATYVMDIKVPRGEPFMIINGDMKKKNV 658

QY 661 TLLMKPLMKNDLSYQRYVINHTSCNGTWSDEYNGHTFELMTQEAHTVTVLAINSI 720
 Db 659 TLLMKPLMKNDLSYQRYVINHTSCNGTWSDEYNGHTFELMTQEAHTVTVLAINSI 718

QY 721 GASVAPNVLTFSPMKRVNIVOSLSAVPLNSCVIYMSIPSDYKLMYFIEKKNLND 780
 Db 719 GASVAPNVLTFSPMKRVNIVOSLSAVPLNSCVIYMSIPSDYKLMYFIEKKNLND 778

QY 781 GEIKMLRISSSVKKYIYHDFIPEKYOFSLYPIFMGVKPKIINSFTODDIEKHSDA 840
 Db 779 GEIKMLRISSSVKKYIYHDFIPEKYOFSLYPIFMGVKPKIINSFTODDIEKHSDA 838

QY 841 GLTVYVPIIISSSILLGLTLLSHORAKKLEWEDVPRKNCVMAOGLNFOKPEFHEFLT 900
 Db 839 GLTVYVPIIISSSILLGLTLLSHORAKKLEWEDVPRKNCVMAOGLNFOKPEFHEFLT 898

QY 901 KHTASTGCPILLEPETISDIDSVTSKKNKDMAPTYVSLSTT-DEKGSVCISDOP 958
 Db 899 KHTASTGCPILLEPETISDIDSVTSKKNKDMAPTYVSLSTT-DEKGSVCISDOP 958

QY 960 NSVNFSEAEGETEYVDESOROPFYVATLISNKSSETGEOGLNNSSTGKFCSSKNP 1018
 Db 959 NSVNFSEAEGETEYVDESOROPFYVATLISNKSSETGEOGLNNSSTGKFCSSKNP 1018

QY 1020 LKDSFNSSMELAEQAFLLSDQHPNIIISPHLTFSEGLDELLECNFPDENNDKSIY 1079
 Db 1019 LKDSFNSSMELAEQAFLLSDQHPNIIISPHLTFSEGLDELLECNFPDENNDKSIY 1077

QY 1080 LGVTSIKKRESGYLLTDKSRVSCPPAPCLETDIRVLQDSCSHFVENNINLGTSSKRTFA 1139
 Db 1078 LGVSSGKKRENDMLTDEAGVLCFPAHCLFSDIRILQESCSHVENNINLGTSG-KNFV 1136

QY 1140 SYMPOTCSTQTHKIKENKMDLTV 1165
 Db 1137 PYMPOTCSTQTHKIKENKMDLTV 1162

RESULT 2

568438
 1leptin receptor, splice form Ob-Rb - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1998 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
 C:Accession: S68438; S68441
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68438
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 664-1162 <LEP>

A:Cross-references: EMBL:049107; NID:g1195486; PIRN:AAC52421.1; PID:g1195487
 A:Experimental source: splice form Rb; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Note: only a part of the translation is shown
 A:Accession: S68441
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-796, GMCVYLEND, <LEP2>
 A:Cross-references: EMBL:049110; NID:g1195492; PIRN:AAC52424.1; PID:g1195493
 A:Experimental source: splice form Re; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Note: this sequence from splice form Re is included to produce a complete sequence
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
 C:Accession: S68441
 A:Gene: Ob-Rb
 C:Keywords: alternative splicing; appetite

Query Match 76.2%; Score 4766.5; DB 2: Length 1162;
 Best Local Similarity 75.4%; Pred. No. 9,6e-302;
 Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;

QY 1 MICOKFCVLLHMEFIYVITAFNLSTYPTPMRKLSCMPNSTYDYFLPAGLSKNTNS 60
 Db 1 MTCOKFYVLLHMEFLVITAFNLALNLAAPTSPMRKFLPCAPSTTDDSLSPAGVNNNSL 60

QY 61 NGHEFVAEPEKFNSSGTHFNLSKTTTHCCFRSDORNCISLADNIGKTFVSTVNSLVF 120
 Db 61 KGASEALVEAKFNSTGIYVELSKTIFHCFCGNGONCSALNGTNGEKTALASVVKPLVF 120

QY 121 QOIDAMNNIOCMKLGDKLFTCYVESLFKNLFRNRYNKVHLVLPVLEDSPLVPQKS 180
 Db 121 ROLGVNMDICMKMGDLTLETCHEMPLKMPFKYDSKHLHLYDLPVLDLPLPKDS 180

QY 181 FOMVHCNSVHECCCLVPPYPAKNDLTLLMCLKITSGGVIFOSPLMSVOPINMKVDPDP 240
 Db 181 FOMVHCNSVHECCCLVPPYPAKNDLTLLMCLKITSGGVIFOSPLMSVOPINMKVDPDP 240

QY 241 LGHMEITDDGNLKISWSSPPLVPPLQOVKYSNSTYIREDKIVSATSLVDSILP 300
 Db 240 LGHMEITDDGNLKISWSSPPLVPPLQOVKYLENS-TIVRAAEIVSDTSLVDSILP 298

QY 301 GSSYEVOVGRKRLDGCINSDMSTPRVFTTQDYIYFPPKILTVSGNSVSHCIYKKNKI 360
 Db 299 GSSYEVOVGRKRLDGCINSDMSTPRVFTTQDYIYFPPKILTVSGNSVSHCIYKKNKI 358

QY 361 VPSKEIYVMMNLAERKIPQSDYDVSDHVSIVTFPNLNETRPRGKFTYDAVYCCNEHCCH 420
 Db 359 ISSKQIYVMMNLAERKIPETQYNTVSDHVSIVTFPNLNETRPRGKFTYDAVYCCNEHCCH 418

Oy 421 RYAEALVIDVNIINISCEIDGVLTKMCRWSTSTQSLAEFTLQARHRSSTLYCSOIPSTH 480
 Db 419 RYAEALVIDVNIINISCEIDGVLTKMCRWSTSTQSLAEFTLQARHRSSTLYCSOIPSTH 478
 Oy 481 PISEPKDCYIAGSDGFECIEIOPFIPLISGYTMWIRINHSIGSLDSEPTCVLPDSVVKPLPP 540
 Db 479 PTSEPRKNCVLIQIRGFGFECVYQPIFFILISGYTMWIRINHSIGSLDSEPTCVLPDSVVKPLPP 538
 Oy 541 SSYKAEITINIGLKIATSWKVPPEPENNLOQIRAGLSKEVQWKAYEYDAKSKSVSLPV 600
 Db 539 SWKAEITFNTGILKATSWKVPPEPENNLOQIRAGLSKEVQWKAYEYDAKSKSVSLPV 598
 Oy 601 PDLCAVYAVOVRCKRLDGLGSLYWSMNSPATVAVMDIKVPMGPEEWRRIINGPTMKKEKAV 660
 Db 599 SDLCAYVAVOVRCKRLDGLGSLYWSMNSPATVAVMDIKVPMGPEEWRRIINGPTMKKEKAV 658
 Oy 661 TLLMKPLMKNDLSCSVQRYVYINHTSCNGTSEVDGNFKFETFLTEQAHVTVVLAINSI 720
 Db 659 TLLMKPLTKNDLSCSVQRYVYINHTSCNGTSEVDGNFKFETFLTEQAHVTVVLAINSI 718
 Oy 721 GASVANFNLTFSPPMKSVNIVOSLAPPLNNSCYIVSITLSPDYKLMATFTEKMLNED 780
 Db 719 GASLVNFNLTFSPPMKSVNIVOSLAPPLNNSCYIVSITLSPDYKLMATFTEKMLNED 778
 Oy 781 GEIKMLRISSSVKKYVYHDFIPLEKYQSLPYPIFMGVGKPKILNSFODDIEKHQSDA 840
 Db 779 DGMKMLRISSNVKKFYIHDNFIPEKYQSLPYPIFMGVGKPKILNSFODDIEKHQSDA 838
 Oy 841 GLYVIVPIIISSSILLLGLTLLISHQRMKLEWEDVNPKNKNSMAQGLNQRKPEFTEHLEI 900
 Db 839 GLYVIVPIIISCVLLGLTLLISHQRMKLEWEDVNPKNKNSMAQGLNQRKPEFTEHLEI 898
 Oy 901 KHTASTYTCGPILLPEPIIISDIYDTSMKKNDEMAPTTVSILSTT-DLEKSSVCISDOP 959
 Db 899 KHAESYIIFPPLLEPEPISEIISYDTAMKKNDEWAPAMVSLITLTPPSESSISICSDOC 958
 Oy 960 NNVNFEAEDEETVEYDEESOROPVVKATVILSNSKSPSETGEOGLINSVTCFSSKNSP 1019
 Db 959 NSNFEFGSOSTOYTCEDECORQPSVKATVILSNDKLVTTDEFOGITHSVNSCISNSHSD 1018
 Oy 1020 LKDSFSSNSWEIEAQAFFILSDQHPNITSPHLTFSEGLDELKLEGNPEENNDDKSIYV 1079
 Db 1019 LKDSFSSNSWEIEAQAFFILSDQHPNITSPHLTFSEGLDELKLEGNPEENNDDKSIYV 1077
 Oy 1080 LGVTSIRKKRSGVLLLDKSKVSCPFPAPCLFTDIRVLDDSCSHPEENNINIGTSKKTTRA 1139
 Db 1078 LGVTSIRKKRSGVLLLDKSKVSCPFPAPCLFTDIRVLDDSCSHPEENNINIGTSKKTTRA 1136
 Oy 1140 SYMPOTCSTOTHKIMENKMDLTV 1165
 Db 1137 PYMPOTCSTOTHKIMENKMDLTV 1162
 RESULT 3
 568440
 A:leptin receptor, splice form Ob-Rd - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2000
 C:Accession: S68440
 R:Lee, G.H.; Pirence, R.; Montez, J.M.; Carroll, K.M.; Davyishadeh, J.G.; Lee, J.I.; F
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437, PMID:96231997
 A:Accession: S68440
 A:Status: nucleic acid sequence not shown: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-900 <LIE>
 A:Cross-references: EMBL:U49109; NID:G1195490; PTDN:AAC52423.1; PID:G1195491
 A:Experimental source: tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68

A:Gene: Ob-Rd
C:Keywords: alternative splicing; appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TM>

Query Match	60.6%	Score 3793;	DB 2;	Length 900;
Best Local Similarity	76.8%	Pred. No. 1,46-238;		
Matches 691;	Conservative	83;	Mismatches 124;	Indels 2;
				Gaps 2;
QY 1	MICQFCVLLHMEIYVITAFNLSPYTPMPKFLSCMPNSTYDYLIPAGLSKNTS	60		
Db 1	MMQCFVYLLHMEIYVITAFNLSPYTPMPKFLSCMPNSTYDYLIPAGLSKNTS	60		
QY 61	NGHYTAVERKFNSSGTHFPMNLKTHPHCCPSSEDRNCISLCAQNI EKTFTSYNSLV	120		
Db 61	KGASAEIVAEKFNSSGTHFPMNLKTHPHCCPSSEDRNCISLCAQNI EKTFTSYNSLV	120		
QY 121	QOIDANMIOGKDKDLKFLICYESLSPKLNFRNNYVHLLLYLPEVLSDPLPQKGS	180		
Db 121	ROLGVMNIDECMAKDDLFLFICHMPLERKNPKNDSKVHLLYDLPVYIDSPLEPLKDS	180		
QY 181	FQMVHNCNSVHECCBLVPPVPTAKLNDTLMLCKLTISGVIIFQSLNLSVQPIPNVKKPP	240		
Db 181	FQTVQNCNSLHG-CGCHVPVPRAKLNLYALMLYLETISAGVSFQSLNLSQPLVYKPP	239		
QY 241	LGLEHETIDGGLKLTSMSSPLVPPPLQYQKSENSTTVIREAKIYSATSLVDSLP	300		
Db 240	LGLEHETIDGGLKLTSMSSQTPAPPLQYQKLENS-TIVREAEIYSATSLVDSLP	298		
QY 301	GSSYEVQYRGRKLDGPIMSDMSPRVYTPDQVITFPRKLTISVSNVFCITYKKNKI	360		
Db 299	GSSYEVQYRKRKLDGSGWSDMSPOVETDQVYFPPPLTISVSNVFCITYKKNKI	358		
QY 361	VPSKEIYVMNMLAEKILPOSOYDVVSDHYSKYTFEMLNETKPRGKITYAUYCNEHECH	420		
Db 359	ISSKQIVMMRNLAEKIPEIQYSIVSDRYSKYTFEMLNATKPRGKITYAUYCNEHQA	418		
QY 421	RYAEIYIDVNNINISCEFDGYLTAKTCRWSTSTIOSLAESTIQLNRIHSSLYCSDIP	480		
Db 419	RYAEIYIDVNNINISCEFDGYLTAKTCRWSTSTIOSLAESTIQLNRIHSSLYCSDIP	478		
QY 481	PISERKDCYLDGDEYECFOPRIFILSGTYMIRINHSLGSDSPPTCYLPDSYVKPLP	540		
Db 479	PISERKDCYLDGDEYECFOPRIFILSGTYMIRINHSLGSDSPPTCYLPDSYVKPLP	538		
QY 541	SSVKKEITINIGLLISMKEKPYEPENNLOFOYRGISGEQWKIYEYDAKSKSVLP	600		
Db 539	SNVKEIYVNGLLISMKEKPYEPENNLOFOYRGISGEQWKIHEVFDKSKASLSLV	598		
QY 601	PDLCAVAYOVBCRKRLDGLGYVMNPNPRTVYVMDIKYMRGRPEIIRINGDTMKENK	660		
Db 599	SDLCAYVYOVBCRKRLDGLGYVMNPNPRTVYVMDIKYMRGRPEIIRINGDTMKENK	658		
QY 661	TLLMKPLMKNDSLGSQVORYVINHHTSCNGTSEDEYGNHTKFTFLNTEQAHYTVLA	720		
Db 659	TLLMKPLMKNDSLGSQVORYVINHHTSCNGTSEDEYGNHTKFTFLNTEQAHYTVLA	718		
QY 721	GASVANENLTFEPMPSKVIYOSLSAYPLNNSCYVSNLSPDYSVKIWFETIEMKLN	780		
Db 719	GASVANENLTFEPMPSKVIYOSLSAYPLNNSCYVSNLSPDYSVKIWFETIEMKLN	778		
QY 781	GEIKMLRISSSYKAKYIHDFPIEKYQSLPPIEMEGVGRKIINSTFODIERHOSDA	840		
Db 779	DOMKMLRISSNKRYIHNDFPIEKYQSLPPIEMEGVGRKIINCTTKOALDQONDA	838		
QY 841	GLYIVIPVLISSILLGLTLISHQRMKLFMEDVDPNPKNSWAQNLNFORPETHLPI	900		
Db 839	GLYIVIPVLISSCYLLGLTLISHQRMKLFMEDVDPNPKNSWAQNLNFORPETHLPI	898		

RESULT 4
568439
leptin receptor, splice form Ob-Rc - mouse


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Db 359 ISSKQIVMMNNAEKIPEDQYIVSDRVSKVTFESNKKATRPGRKFTYDAVYCCNEACGH 418
OY 421 RYAEIVIDVINISCEITDGLYTKMTCRMSSTIOSLAESTLOLRHRSLSYCSIDPSIH 480
Db 419 RYAEIVIDVINISCEITDGLYTKMTCRMSSTIOSLAESTLOLRHRSLSYCSIDPSIH 478
OY 481 PISEPRDCYLOSDGFYECIFPFIPLSGTYMMIRINHSLSGSDSPPTCYLPDSVAPLPP 540
Db 479 PISEPRDCYLOSDGFYECIFPFIPLSGTYMMIRINHSLSGSDSPPTCYLPDSVAPLPP 538
OY 541 SSVKAEITINIGLKISWEKPVPEPENNLOFOIRYGLSGKEVOMKMEYVDAKSKSYSLPV 600
Db 539 SNVKAETITNTGLKISWEKPVPEPENNLOFOIRYGLSGKEVOMKMEYVDAKSKSYSLPV 598
OY 601 PDLCAVYAVOVRCRDLGSGYWSNMSNPATYVMDIKVPMRGPEFRIINGDTMKKEKNV 660
Db 599 SDCAVYAVOVRCRDLGSGYWSNMSNPATYVMDIKVPMRGPEFRIINGDTMKKEKNV 658
OY 661 TLLMKPLMKNDLSYVORYVINHHTSCNGTSEDVGNHRTKFTPLATEQAHTVTLAINSI 720
Db 659 TLLMKPLMKNDLSYVORYVINHHTSCNGTSEDVGNHRTKFTPLATEQAHTVTLAINSI 718
OY 721 GASVANFNLTFSMPMSKVIVOSLSAYPLNSCVIYSMTLSPDYKLMFTIEMKLNED 780
Db 719 GASVANFNLTFSMPMSKVIVOSLSAYPLNSCVIYSMTLSPDYKLMFTIEMKLNED 778
OY 781 GEIKMLRISSVKKYIYIHDFIPIEKYQFSLYPIEMEGVGPRIINSFTODDIEKHQSDA 840
Db 779 DGMKMLRIPSNVKKYIYIHDFIPIEKYQFSLYPIEMEGVGPRIINSFTODDIEKHQSDA 838
OY 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVDPNPKNCSVAOGLNFOK 891
Db 839 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVDPNPKNCSVAOGLNFOK 889

RESULT 6
S74225
leptin receptor, isoform Ob-Rf - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999
C:Accession: S74225
R:Yang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.
FEBS Lett. 392, 87-90, 1996
A:Title: A novel leptin receptor isoform in rat.
A:Reference number: S74225; MUID:96368027
A:Accession: S74225
A:Molecule type: mRNA
A:Residues: 1-895 <MAN>
A:Cross-references: EMBL:U53144; NID:q1395212; PIDN:AA803088.1; PID:q1395213
A:Experimental source: strain Sprague-Dawley; tissue type brain
C:Genetics:
A:Gene: OB-R
C:Keywords: Appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TM>

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Query Match 59.6%; Score 3729; DB 2; Length 895;
Best Local Similarity 76.5%; Pred. No. 2e-234;
Matches 682; Conservative 84; Mismatches 123; Indels 2; Gaps 2;

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```

OY 1 MTCORFVLLMEFYITAFNLSPITPMRKLSCMPNNSYDFLLPAGLSKTSNS 60
Db 1 MTCORFVLLMEFYITAFNLSPITPMRKLSCMPNNSYDFLLPAGLSKTSNS 60
OY 61 NCHYETAPEKPNSSGTHSNLSKTFHCCFSEODRNSLCDNTEGTFVSTVSIYE 120
Db 61 NCHYETAPEKPNSSGTHSNLSKTFHCCFSEODRNSLCDNTEGTFVSTVSIYE 120
OY 121 QOIDANNTQCMKLKDLKFLICYVESLFKNLERNYKYVHLLVLEDESEPLVPOKS 180
Db 121 QOIDANNTQCMKLKDLKFLICYVESLFKNLERNYKYVHLLVLEDESEPLVPOKS 180
OY 121 ROLGVMDIECMWKGDLTFLICMEBLLKNPKNYSKVALHLYDLEVIDDPLPLKDS 180
Db 121 ROLGVMDIECMWKGDLTFLICMEBLLKNPKNYSKVALHLYDLEVIDDPLPLKDS 180
OY 181 PQMVHNCNSVHCEBCLVLEVPVPAKNDLTLLMKLITSGVITPQSLMSVQPIIMVAPDP 240
Db 181 PQMVHNCNSVHCEBCLVLEVPVPAKNDLTLLMKLITSGVITPQSLMSVQPIIMVAPDP 240

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Db 181 PQMVHNCNSVHCEBCLVLEVPVPAKNDLTLLMKLITSGVITPQSLMSVQPIIMVAPDP 239
OY 241 LGHMEITDDGNLKISWSSPPLVPEPLOYOVKSESTYIRPADYIVASATSLVYSLIP 300
Db 240 LGHMEITDDGNLKISWSSPPLVPEPLOYOVKSESTYIRPADYIVASATSLVYSLIP 298
OY 301 GSSYEYOVRCRDLGPGISDMSSTPRVFTTODVYIEPPKILTSVGSNSVEHCITYKENKI 360
Db 299 GSSYEYOVRCRDLGPGISDMSSTPRVFTTODVYIEPPKILTSVGSNSVEHCITYKENKI 358
OY 361 VPSKEIVMMNNAEKIPEDQYIVSDRVSKVTFESNKKATRPGRKFTYDAVYCCNEACGH 420
Db 359 ISSKQIVMMNNAEKIPEDQYIVSDRVSKVTFESNKKATRPGRKFTYDAVYCCNEACGH 418
OY 421 RYAEIVIDVINISCEITDGLYTKMTCRMSSTIOSLAESTLOLRHRSLSYCSIDPSIH 480
Db 419 RYAEIVIDVINISCEITDGLYTKMTCRMSSTIOSLAESTLOLRHRSLSYCSIDPSIH 478
OY 481 PISEPRDCYLOSDGFYECIFPFIPLSGTYMMIRINHSLSGSDSPPTCYLPDSVAPLPP 540
Db 479 PISEPRDCYLOSDGFYECIFPFIPLSGTYMMIRINHSLSGSDSPPTCYLPDSVAPLPP 538
OY 541 SSVKAEITINIGLKISWEKPVPEPENNLOFOIRYGLSGKEVOMKMEYVDAKSKSYSLPV 600
Db 539 SNVKAETITNTGLKISWEKPVPEPENNLOFOIRYGLSGKEVOMKMEYVDAKSKSYSLPV 598
OY 601 PDLCAVYAVOVRCRDLGSGYWSNMSNPATYVMDIKVPMRGPEFRIINGDTMKKEKNV 660
Db 599 SDCAVYAVOVRCRDLGSGYWSNMSNPATYVMDIKVPMRGPEFRIINGDTMKKEKNV 658
OY 661 TLLMKPLMKNDLSYVORYVINHHTSCNGTSEDVGNHRTKFTPLATEQAHTVTLAINSI 720
Db 659 TLLMKPLMKNDLSYVORYVINHHTSCNGTSEDVGNHRTKFTPLATEQAHTVTLAINSI 718
OY 721 GASVANFNLTFSMPMSKVIVOSLSAYPLNSCVIYSMTLSPDYKLMFTIEMKLNED 780
Db 719 GASVANFNLTFSMPMSKVIVOSLSAYPLNSCVIYSMTLSPDYKLMFTIEMKLNED 778
OY 781 GEIKMLRISSVKKYIYIHDFIPIEKYQFSLYPIEMEGVGPRIINSFTODDIEKHQSDA 840
Db 779 DGMKMLRIPSNVKKYIYIHDFIPIEKYQFSLYPIEMEGVGPRIINSFTODDIEKHQSDA 838
OY 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVDPNPKNCSVAOGLNFOK 891
Db 839 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVDPNPKNCSVAOGLNFOK 889

RESULT 7
S68441
leptin receptor, splice form Ob-Re - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68441
R:Lee, G.H.; Pirocna, R.; Montez, J.M.; Carroll, K.M.; Darvishadeh, J.G.; Lee, J.I.;
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68441
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-805 <LEE>
A:Cross-references: EMBL:U49110; NID:q1195492; PIDN:AA52424.1; PID:q1195493
A:Experimental source: splice form Re; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439. PIR:
C:Genetics:
A:Gene: Ob-Re
C:Keywords: alternative splicing; appetite

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Query Match 53.4%; Score 3340; DB 2; Length 805;
Best Local Similarity 76.2%; Pred. No. 3.5e-205;

```



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Qy 999 GEEGLINSSTK-CFSSKNSP-----LKDSFNSGWELEAFAFLISDQHNIIISPHLTF 1053
Db 770 PSYVFSRSESTQPLDLSSEERPELDQVDSYDGDDELIPROPYKONSCOPE-ACPELISH 828
Qy 1054 SEGDELLEKLEGN 1066
Db 829 FERSNOV--LSGN 839

RESULT 9
A:Accession: A36337
A:Gene: g130 precursor - human
A:Species: Homo sapiens (man)
A:Date: 12-Apr-1991 #sequence.revision 12-Apr-1991 #text.change 28-Jul-2000
A:Accession: A36337
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HTB>
A:Cross-references: GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
A:Gene: GDB:11657; GP130
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
A:Superfamily: cytokine receptor homology
A:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 5.5%; Score 345.5; DB 2; Length 918;
Best Local Similarity 19.8%; Pred. No. 2.6e-14;
Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;

Qy 337 PPKILTSVGSVNSFHCIYK--ENKIYPSKEIYMMMLAEKIPSOQYDVVSDHVSQVTF 393
Db 33 PESPVOVLSHNFATVAVCVLKEKMDYFHVANVYWKTN-HFTIPEQYTIINRTASSYTF 91

Qy 394 FNLNETKRGKFTYDAVYCCNEHCHHRYAEIYDV-----NINISC-ETDGYLTK 444
Db 92 TDI-----ASLNIOQLTCNLTFTGQLEQNVYGITLISGLPEPKNLSCVING--KK 141

Qy 445 MTCRWSTIOSLAESTLOLRHRSSTICSDIPSIHPISSEPKDYLQSDGYECI--FQP 502
Db 142 MRCMDG-----RETHLETNFTLSEMAT-----HKFA---DCKAKDPTSCVVDYST 188

Qy 503 IFLISGYTMMIRINHSLSGLSDSPPTCVLPDSVVKPLPPSSVKAETIN-----IGLKTSW 558
Db 189 YFVNV-IEVWVEAEENALCKVTSDIINFDPYVKKPNPHNLS--VINSELSILKLTW 244

Qy 559 EKP-----VFENNLOQPIRIGLSGEQWKMVEYDAKSKSVSLPVDL--CAVYAAVQ 611
Db 245 TNPSTKSVYIILKYNIOYFTKAST-----WSQIPEDTASRSSTYVDLKFTEYVERI 299

Qy 612 RCKRLDGLGYSNNSNPAYTVVMDIKVPMRGPEFRIRINGDTMKKEKNVTLTKPLMKND 671
Db 300 RCMEDGKGYSNMSSEASGLTYEDR--PSKAPSFYKIDPSHTQGRVQVLMKLLPPE 358

Qy 672 SLCSVQRYVINHHRTSCNGTSEDVGNH---TKFTLMTQEAHTVTVALINSIGASVANF 727
Db 359 ANGLITIDEVY-----LTRMKSHLONTVNTKLTIVNLTRNRLATLIVRNLVGSDAAV 413

Qy 728 NLITSMPSKYNIVQSLAYPLNNSCVYVSWLSRDKMLFTIEKNLNLEDGE--TKW 785
Db 414 LTIPLCOFOATHPMDLAEP--KDMMLAVEMWTPPRESVK--KYLLEMCVLSDKACITDM 470

Qy 786 LRISSVKRYIHHFIPIEKYQSLYPIFMGVGKPKII----- 825
Db 471 QOEDGTIVRTYLRGLNLSKCYLITVTPVYADGSGPESIRAYLKQAPPSKGPYVTKV 530

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Qy 826 -----NSFTQDDIEKHSDAGLY- 843
Db 531 GKNEAVLEMDQLPYDVONGEIRNTYIFRYTILIGNETAVANNVSHTEYLSLSTSDT-LYM 589
Qy 844 -----VIVPIIISSTI-LTCTLLSHOR--MKK 869
Db 590 VRMAAYTDEGKDGKDEFTTTPKPAQGEIEAVVPCVLAFLITLLGLVPCFKNKDLTK 649

Qy 870 LEWEDVPNPKNCNWAQGLNFQKPEFTEHLFIKHTASVTCGPLLEPETISEDVDSWK 929
Db 650 HWPVNPDPSPKSHIAQWSPHNP-----RH-----NFN 677

Qy 930 NKDEMPPTVYSLSTDLKNGVSCISDQFNSVNFSEAEGETVEYDESOQRP---VKY 986
Db 678 SKDQW-----YSDGNFTDVSVAIEAND--KKPEPELKS 710

Qy 987 AFLISNSKPSFTEGROGLINSVTRKCFSSKNSPLKDSFNS 1028
Db 711 LDLEKKEKINTEGHSSGIGSS---CMSSSRPSISSDSENS 749

RESULT 10
A:Accession: A44257
A:Interleukin-6 signal transducing molecule gp130 - rat
A:Species: Rattus norvegicus (Norway rat)
A:Date: 30-Apr-1993 #sequence.revision 18-Nov-1994 #text.change 28-Jul-2000
A:Accession: A44257
A:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transduc
A:Reference number: A44257; MUID:93052397
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <MAN>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBI:P118486)
A:Superfamily: cytokine receptor homology
A:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 5.4%; Score 339.5; DB 2; Length 918;
Best Local Similarity 20.8%; Pred. No. 6.3e-14;
Matches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;

Qy 327 VETTDVLT-----XFPKILTSVGSVNSFHCIYKKEKIVPSKE--IYMMNLAE 374
Db 14 IFLITESTIGOLVPCGYTYPERPVQSGNSFTATCVLKEKLCLOYSVNATYIWKTNHV- 72

Qy 375 KIPSOQYDVSDHVSQVTFEFLNETKPRGKFTYDAVY-----CCNEHCHHRYAEIYV- 428
Db 73 AVPKQYVIVNRTASSVTF-----TDVVPQNVOLQTCNLTLSFGQLEQNVYGIT 119

Qy 429 -----DVNINISC-ETDGYLTKMTCRWSTIOSLAESTLOLRHRSSTICSDIPSIH 480
Db 120 ILSGYPPDIPNLSQIVNGG--KNMLCO-----LDPGREYLETNYLTKSEMAVE----- 167

Qy 481 PISEKDKYLOSDGYECI--FQPIFLISGYTMMIRINHSLSGLSDSPPTCVLPDSVVKPL 538
Db 168 ---KPPDCRTK-HGTSSCMGITPIYFN-IEVWVEAEENALGNVSSCPINFPDVKVPS 222

Qy 539 PPSVKAETITNI-GILKISW-----EKVPENNLOQPIRIGLSGEQWKMVEYDAK 592
Db 223 PPHNLSVYNSELSILKLANVNSGLDILRKSDIOYRTDASV-----NIQVPLEDTV 277

Qy 593 SKSVSLPVDL--CAVYAVQYCKRLDGLGYSNNSNPAYTVVMDIKVPMRGPEFRIRIN 650
Db 278 SPRTSFTVQDLKPFTEYFIRISIKENKGYMSDSEASGTYEDR--PSKAPSFYKYN 336

Qy 651 GDTMKKEKNVTLTKPLMKNDSLCSVQRY--VINHHRTSCNGTSEDVGNHKTFTLWEDQ 708
Db 337 ANHPQYRSARLIMKTLPLSEANGKITIDYEVLVTSQSKVSQSYTV--NGTELLIVNLTN 393

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QY 195 -----ECLVPPYATLNTLMLCKLITSGVIFPSPLMSVOPINNVKPPDPLGLHMETT- 248
Db 90 CYOLEKTSIKIPALSHGVEYETIINSLHDSGSTSKFTLNEONVSLI- PDTEILMLSDDF 148
QY 249 DDGNLKMSSPPLVPFPLOYOKVSENSTYIVR---EADKIVATSUL----- 294
Db 149 STSTLYLKNRNGSV-FPHRSNVIV---ELVLRKESMELKLYVHNNTLNGKOTLHMS 204
QY 295 --VDSILPGSSYEVOVR---GKRLDGPGLMSDMSPTPVFT---TQDYIYPPKILTSVG 345
Db 205 WASDMPLECALHFEVIRCYIDNLHPSGLEMSDMSPVKNISIMIPDSQKVPQDQVILVG 264
QY 346 SNVSFHCITKKNKIVKSEIYVMMNLAEKIPQSOYDV---SDHVSATVPFNLETNPR 402
Db 265 SDITFCVC-----SQEYV---LSALIGHTMCPILHLDGENVA- IKIRINISVSASS 310
QY 403 GKFTDVAVCCNEHCCHRYALVYIDVNIINISCTEDGLTKMCRMSSTIOSLA---E 459
Db 311 GT---NVFTTEDNIFGVIVRAGVIPPDPPOOLNCTEHD-LKEITCSMNPGRVATLVGPRA 366
QY 460 STLQLRHRSLSYCSDIPSIHPISEPKDCYLOSDEYECIFQPIFLSGYTMWIRINSL 519
Db 367 TSYLVESFGKYVRLKRAEAPTNES-----YQLRQMLPNOEIVNFTLANHPL 416
QY 520 GSLDSPPCVLPDSVYKLPSPSVAEETTINGLKISMEK-----VFPEEN 566
Db 417 GRSOSTILVNTTEKYR-PHTPISEFKV-DINSTAVKLSMHLPGNPAKINFLCEIKRKN 474
QY 567 NLQFQIRGLSGKEYOMMEYVDAKSKSVSLPVPDLCAVAVOYRCRLDGLGYKWSMS 626
Db 475 SVOEBRANTINGVE-----NSSYLVADKINPPTLYIFTRICS-TEFFMKWSKMS 523
QY 627 NPATVYVMDIVPMGPEFWRIINDTKKKNVTLMLPKLNKNDLSGVORYVINHTS 686
Db 524 NKKOHLTEAS-PSKGPPTWREMSD---GKNLITYMKPLPIINA---NGKILSYMS 574
QY 667 CNG-----TMSDVGNNHKTFTLMTQAHVTVLAINSGAVANFNLFSPMKRNIV 741
Db 575 CSSDETOISLEIPDPQKAEIRLDKNDYIISVAKNSVSPSKIASMETIPNDLKE 634
QY 742 QSLASVPLNNSCVIYSWILSPS---DYKLMTFIEMKN-LNEDDEIKWLRI-SSSVKY 795
Db 635 QVYGM-----GKGIILTMHYDPMTCDY-----VIMCNSSRREPLMDRKVPNSSTEV 685
QY 796 YIHDHFIPIEKYQFSLYPIFMEG-----VG-----KPKIINSTODD----- 832
Db 666 IESDEFRRGIRYRNFYLCGRNOGYQLLRSMIGYIELAPIYVNFVEDTSADSLVKE 745
QY 833 -----LEKHOSD----- 839
Db 746 DIPVELRGLFNGLYFEGKERDTSKMRVLESGRSDIKVKNITDISOKTLRIADLOCKT 805
QY 840 -----AGLYVI-----VPYIISLILGLTLISHOR-M 867
Db 806 SYHLVLRATDOGVPEKSMYVTKENSVGLIATILIPAAVAYIGVTSILCYKREKI 865
QY 868 KKLMEVDVNPKNKCSMAOGLNFQK-----PETFEHLTKHTASVTCGPLL 912
Db 866 KETFPDIPNPENC---KALOFKSVCSGSSALKTLEMPCTPNNVVEVLETRSAF--PKI 920
QY 913 LEPEFISDISDYSWKKNKDEMPYTVVSLSTDLKGSVC---ISDOFNSVNSEAAG 969
Db 921 EDETEIIS---PAERPERDSDAEPENHVV-----SYCPPIIEEIPRPADEAG 968
QY 970 T-EVYVED-ESORQPFVYKATLISNKSPEETGEQGL-----INSSVTKCSF- 1014
Db 969 TAQVYIIVQSNYOP-----QAKPEEEDNDPVGAGYKRPQMLPINSTVEDIAAE 1019
QY 1015 ---SKNSPLKFSNMSWEIEAQAFFILSDOHPNIIS 1049
Db 1020 EDDLKTAGYRBPQANVTW-----NLVSP 1042

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RESULT 13
C38252
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C:Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FUK>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63176.1; PID:g183049
A:Note: clones PHG11 and PH5
A:Accession: A38252
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FUK>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A:Note: clone PHO3
R:Ralsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0330
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <LAR>
A:Cross-references: GB:X55721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A:Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A:Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 855-863 <SET>
A:Cross-references: GB:S71484; NID:g240883; PIDN:AB200650.1; PID:g240884
A:Experimental source: granulocyte
A:Note: sequence extracted from NCBI backbone (NCBI:71484, NCBI:71485)
R:Hanlu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
A:Accession: S68332
A:Molecule type: protein
A:Residues: 234-269 <HAN>
C:Genetics:
A:Gene: GDB:CSF3R
A:Cross-references: GDB:126430; OMIM:138971
A:Map position: 1p35-1p34.3
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-863/Product: granulocyte colony-stimulating factor receptor, long form #status p
F:25-680,708-863/Product: granulocyte colony-stimulating factor receptor, short form
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TM>
F:654-863/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (asn) (covalent) #status pred

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Query Match 4.6%; Score 288.5; DB 2; Length 863;
Best local similarity 20.0%; Pred. No. 1.2e-10;
Matches 156; Conservative 125; Mismatches 280; Indels 219; Gaps 38;

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QY 341 LTVSGSNVSFHCITKRE-NKIVPSKEIYVMMNLAEKIPQSOYDVSD--HYSKVTFEFLN 397
DB 35 IYHLDPTASCTIIONGSHDPRQILMRIG-AELQPGRGQRSLSDQSEIITLPHLN 93
QY 398 ETKPRGKFTYDAVCCNEHCCHRYALVYID-----VININISCTEDGLTKMT 446

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Db 94 HQ-----AFISC-----CLMNGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSLI 141
Qy 447 CWMSTSIQSLAES-TLOLRHRSLSYCSIDIPISHPISPKCYLQSDGFYECI----- 499
Db 142 COMEGPETHLPSTSLKFSKRG-----NCQFGSDILDCVPRDGS 184
Qy 500 -----FOPIFLSGYTMWRIRHNSIGSLDSPPTCYLPDSVYKPLRP-----SSVKAET 548
Db 185 HCCIRKHLILYQNGIWOAENALGTSMPOLCLDPMOVYKLEPMLRTMDPSDEA-AP 243
Qy 549 INIGLKISWEKVPFP--ENNLOFOIRYGLSGKEVQMKYEVYDAKRSVSLPVP----- 601
Db 244 PQAGCLOLCWE-PMQPGHLINOKCELRRKPRGSEASMLVY-----PLPLEALQ 291
Qy 602 -DLCAV-----YAVORCKRLDGLGYWSMNSPAYTVMDIKVPRCP-----EFMRITN 650
Db 292 YELCGLPATAYATLOIRCIKRWPLPGHWSDMW-PS---LELTERAPTVRLDTWMR--- 343
Qy 651 GDTMKKKNVTLMKPLKNDLSGVORYVINHTS-----CNGTMSBDVGNHTKF 701
Db 344 -QROLDPRVOLFWRKPVPLEEDSGRIQGYVSWRPSGAGAILPLCNTT-----ELSC 395
Qy 702 TELMTEQAHVTYVLAINSIGASVANFNLFSPWPSKVNIVOSLSAYPLNSCVIWSILS 761
Db 396 TELHPSAEQVALVAYNSAGTSRPT-PVYFS--ESRGALTRFLHMAPRPSLWGMW--E 450
Qy 762 PSDYKLMFTIEM-----KNLNDGELKW-LRISSSYKKYIYIDHPIEKYQFSLXP 813
Db 451 PNPMPQGVIVLEWGLGPPSASNSNK---TWMEQNGRATGFLKENIRPOLYEIYTP 506
Qy 814 IFMEGVGPKRIINSFTODDIEKHQSDAGL-----YIVIVYIISSTILLGLTLLI 862
Db 507 LYQDTMGPSQAHYAYASQEMAPSHAPELHLKHIGKTAQLEWVPEPELKSPLTHYT--- 563
Qy 863 SHQRNKKLEWEDVPPPKNSMAOGLNFO-----KPEFHEHLFIR-----HTASVT 907
Db 564 -----TFW---TNAQNSFSAILNASSRGFVLHGLEPASLYHILMAASQAGATNSTV 913
Qy 908 CGPILLEPPTISEDIV-----DTSW-----KNKDEMPPTVYSLSTIDLE 949
Db 614 LTLMLTPEGSEHLITLGLFGLLLLLTCLCGTAWLCCSPNKRNPIMPSPVPPAHSSLSGW 673
Qy 938 -TIVVSL-----STYDLKGSV---CISDFNSVNSEAGTEVEYEDESQROP 982
Db 674 VPTIMEELPGPROGOMLCOTSEMSRALTPHPCVDAPFOLPGTGPTRITKLYLEDEKKP 733

RESULT 14
JX0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
C:Accession: JX0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JX0329; MUID:91079757
A:Accession: JX0329
A:Molecule type: mRNA
A:Residues: 1-783 <LARP>
A:Cross-references: GB:X55720; NID:931698; PIDN:CAA39252.1; PID:931699
C:Keywords: glycoprotein; transmembrane protein
F:1-74/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,133,389,474,579,610/Binding site: carbohydrate (asn) (covalent) #status predict

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Query Match 4.5%, Score 284, DB 2; Length 783;

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Best Local Similarity 20.3%, Pred. No. 2e-10;
Matches 153; Conservative 121; Mismatches 287; Indels 192; Gaps 35;

Qy 341 LTVSANSFHCITAKE-NKIYPSKEIYMMMLAKTIQSOQDVSD--HVSQYFFNIN 397
Db 35 IYHLDPTTASCIRKONSHLDPEOILRLG-AELOPGROORISDQESITLPHLIN 93
Qy 398 ETRPGKFTYDAVYCCNECHHRYAEIYVD-----VINISCEFDGLTKMT 446
Db 94 HQ-----AFISC-----CLMNGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSLI 141
Qy 447 CWMSTSIQSLAES-TLOLRHRSLSYCSIDIPISHPISPKCYLQSDGFYECI----- 499
Db 142 COMEGPETHLPSTSLKFSKRG-----NCQFGSDILDCVPRDGS 184
Qy 500 -----FOPIFLSGYTMWRIRHNSIGSLDSPPTCYLPDSVYKPLRP-----SSVKAET 548
Db 185 HCCIRKHLILYQNGIWOAENALGTSMPOLCLDPMOVYKLEPMLRTMDPSDEA-AP 243
Qy 549 INIGLKISWEKVPFP--ENNLOFOIRYGLSGKEVQMKYEVYDAKRSVSLPVP----- 601
Db 244 PQAGCLOLCWE-PMQPGHLINOKCELRRKPRGSEASMLVY-----PLPLEALQ 291
Qy 602 -DLCAV-----YAVORCKRLDGLGYWSMNSPAYTVMDIKVPRCP-----EFMRITN 650
Db 292 YELCGLPATAYATLOIRCIKRWPLPGHWSDMW-PS---LELTERAPTVRLDTWMR--- 343
Qy 651 GDTMKKKNVTLMKPLKNDLSGVORYVINHTS-----CNGTMSBDVGNHTKF 701
Db 344 -QROLDPRVOLFWRKPVPLEEDSGRIQGYVSWRPSGAGAILPLCNTT-----ELSC 395
Qy 702 TELMTEQAHVTYVLAINSIGASVANFNLFSPWPSKVNIVOSLSAYPLNSCVIWSILS 761
Db 396 TELHPSAEQVALVAYNSAGTSRPT-PVYFS--ESRGALTRFLHMAPRPSLWGMW--E 450
Qy 762 PSDYKLMFTIEM-----KNLNDGELKW-LRISSSYKKYIYIDHPIEKYQFSLXP 813
Db 451 PNPMPQGVIVLEWGLGPPSASNSNK---TWMEQNGRATGFLKENIRPOLYEIYTP 506
Qy 814 IFMEGVGPKRIINSFTODDIEKHQSDAGL-----YIVIVYIISSTILLGLTLLI 862
Db 507 LYQDTMGPSQAHYAYASQEMAPSHAPELHLKHIGKTAQLEWVPEPELKSPLTHYT--- 563
Qy 863 SHQRNKKLEWEDVPPPKNSMAOGLNFO-----KPEFHEHLFIR-----HTASVT 907
Db 564 -----TFW---TNAQNSFSAILNASSRGFVLHGLEPASLYHILMAASQAGATNSTV 913
Qy 908 CGPILLEPPTISEDIV-----DTSW-----KNKDEMPPTVYSLSTIDLE 949
Db 614 LTLMLTPEGSEHLITLGLFGLLLLLTCLCGTAWLCCSPNKRNPIMPSPVPPAHSSLSGW 673
Qy 950 KGSVCISDFNSVNSEAGTEVEYEDESQROP 982
Db 674 VPTIMEELPGPROGOMLCOTSEMSRALTPHPCVDAPFOLPGTGPTRITKLYLEDEKKP 706

RESULT 15
JX0312
differentiation-stimulating factor/leukemia inhibitory factor receptor 1 precursor -
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C:Accession: JX0312; J02181; S38942
R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
J. Biochem. 115, 557-562, 1994
A:Title: Three different cDNAs encoding mouse D-factor/LIF receptor.
A:Reference number: JX0312; MUID:94334302
A:Accession: JX0312
A:Molecule type: mRNA
A:Residues: 1-1092 <TOM>
A:Cross-references: DDBJ:D26177; NID:9473718; PIDN:BA05165.1; PID:dl005707; PID:9825
A:Accession: J02181
A:Molecule type: mRNA
A:Residues: 1-717, 'EA' <TOM1>

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 06:54:01 ; Search time 39.61 Seconds

(without alignments)
1138.810 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254
Sequence: 1 MICQKFCVVLHMEFIYIT.....QFCSTQTHKIMKMDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	6246	99.9	1165	LEPR_HUMAN
2	4784.5	76.5	1162	LEPR_RAT
3	4766.5	76.2	1162	LEPR_MOUSE
4	366	5.9	917	IL6B_MOUSE
5	345.5	5.5	918	IL6B_HUMAN
6	339.5	5.4	918	IL6B_RAT
7	313	5.0	837	GCGR_MOUSE
8	294.5	4.7	1097	LIFR_HUMAN
9	284	4.5	836	GCGR_HUMAN
10	281.5	4.5	1092	LIFR_MOUSE
11	220.5	3.5	862	112S_HUMAN
12	220	3.5	830	PRLR_COILI
13	220	3.5	874	112S_MOUSE
14	209.5	3.3	831	PRLR_CHICK
15	190	3.0	831	PRLR_MEICA
16	184	2.9	2481	FLNC_XENLA
17	173.5	2.8	1493	NEOL_MOUSE
18	172	2.8	2012	DSGA_HUMAN
19	170.5	2.7	1461	NEOL_HUMAN
20	169.5	2.7	1443	NEOL_CHICK
21	166.5	2.7	2029	LAR_DROME
22	165	2.6	630	PRLR_ORENT
23	162	2.6	1447	DCC_MOUSE
24	158.5	2.5	462	IL6A_RAT
25	154.5	2.5	2386	FLNC_HUMAN
26	153.5	2.5	460	IL6A_MOUSE
27	151	2.4	1377	NEOL_RAT
28	150.5	2.4	610	PRLR_RAT
29	147.5	2.4	3063	GHR_MACMU
30	146	2.3	3063	CA1C_HUMAN
31	145.5	2.3	2477	FLNC_RAT
32	144.5	2.3	1302	NRG_DROME
33	144	2.3	581	PRLR_CERBL

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	AA
1	LEPR_HUMAN	AC	STANDARD	PRT	1165 AA.
2	LEPR_HUMAN	P48357			
3	01-FEB-1996 (Rel. 33, Created)				
4	01-FEB-1996 (Rel. 33, Last sequence update)				
5	01-MAR-2002 (Rel. 41, Last annotation update)				
6	Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).				
7	LEPR OR OBR.				
8	Homo sapiens (Human).				
9	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
10	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
11	NCBI_TaxID=9606;				
12	SEQUENCE FROM N.A.				
13	TISSUE=Brain;				
14	MEDLINE=96128129; PubMed=8548812;				
15	Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,				
16	Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,				
17	Muir C., Sanker S., Morlaty A., Moore K.J., Smutko J.S.,				
18	Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;				
19	"Identification and expression cloning of a leptin receptor, OB-R.;"				
20	Cell 83:1263-1271(1995).				
21	SEQUENCE FROM N.A.				
22	Thompson D.B., Ossowski V., Sutherland J., Apel W.,				
23	Bislerfeldt J.;				
24	Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.				
25	VARIANT ARG-223.				
26	MEDLINE=96270489; PubMed=8666155;				
27	Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;				
28	"The hypothalamic leptin receptor in humans: identification of				
29	incidental sequence polymorphisms and absence of the db/db mouse and				
30	fa/fa rat mutations.;"				
31	Diabetes 45:992-994(1996).				
32	VARIANT ARG-109; ARG-204; ARG-223 AND ASN-656.				
33	MEDLINE=97289527; PubMed=9144432;				
34	Echwald S.M., Soerensen T.D., Soerensen T.I., Tybjærg-Hansen A.,				
35	Andersen T., Chung W.K., Leibel R.L., Pedersen O.;				
36	"Amino acid variants in the human leptin receptor: lack of association				
37	to juvenile onset obesity.;"				
38	Biochem. Biophys. Res. Commun. 233:248-252(1997).				
39	VARIANT ARG-109; ARG-223 AND ASN-656.				
40	MEDLINE=97431549; PubMed=9287054;				
41	Chung W.K., Power-Kebbe L., Chua M., Chu F., Aronne L., Huma Z.,				
42	Soerensen M., Udall J.N., Kahle B., Leibel R.L.;				
43	"Exonic and intronic sequence variation in the human leptin receptor				
44	gene (LEPR).;"				
45	Diabetes 46:1509-1511(1997).				
46	VARIANT ARG-109 AND ARG-223.				
47	MEDLINE=97301763; PubMed=9158141;				
48	Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;				

Structure and sequence variation at the human leptin receptor gene in lean and obese Pima Indians.
Hum. Mol. Genet. 6:675-679(1997).
[7]
VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
MEDLINE-99075638; PubMed-9860295;
Roth H., Korn T., Rosenkranz K., Hluney A., Ziegler A., Kunz J., Slegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
"Transmission disequilibrium and sequence variants at the leptin receptor gene in extremely obese German children and adolescents.";
Hum. Genet. 103:540-546(1998).
[8]
VARIANTS ARG-109; ARG-223 AND ASN-656.
MEDLINE-97318795; PubMed-9175732;
Gotooda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L., Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;
"Leptin receptor gene variation and obesity: lack of association in a white British male population";
Hum. Mol. Genet. 6:869-876(1997).
-1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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DR EMBL; U43168; AAA93015.1; .
DR EMBL; U59263; AAB09673.1; JOINED.
DR EMBL; U59248; AAB09673.1; JOINED.
DR EMBL; U59249; AAB09673.1; JOINED.
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DR EMBL; U59252; AAB09673.1; JOINED.
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DR EMBL; U59254; AAB09673.1; JOINED.
DR EMBL; U59255; AAB09673.1; JOINED.
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DR EMBL; U59259; AAB09673.1; JOINED.
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DR HSP; P40189; IBOU.
DR MIM; 601007; .
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; signal; Repeat; Polymorphism.
FT SIGNAL 1 21 LEPTIN RECEPTOR.
FT CHAIN 22 1165 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 22 841 POTENTIAL.
FT TRANSMEM 842 862 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 863 1165 FIBRONECTIN TYPE-III 1.
FT DOMAIN 1166 1230 FIBRONECTIN TYPE-III 2.
FT DOMAIN 1231 1233 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 728 728 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 109 109 /FtId-VAR_002703.
FT VARIANT 204 204 /FtId-VAR_002704.
FT VARIANT 223 223 /FtId-VAR_002705.
FT VARIANT 656 656 /FtId-VAR_002706.
FT VARIANT 675 675 S -> T.
FT SEQUENCE 1165 AA; 132449 MM; 8FF21D9AF5125808 CRC64;
Query Match 99.9%; Score 6246; DB 1; Length 1165;
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DB 1 MICOKECVLLHWEFIYITAFNLSTPTPWRFKSCMPNSTYDFLLPAGLSKNTSNS 60
OY 61 NGHETAVEPKFNSSGTHFSLKTFHCFRSEDRCSCADBIESTKTVSTNSLVF 120
DB 61 NGHETAVEPKFNSSGTHFSLKTFHCFRSEDRCSCADBIESTKTVSTNSLVF 120
OY 121 QOIDANNMIQCMKGLDLKFLCYVESLFKFLFRNRYKVHLLVYLPVLEDSPLVPQGS 180
DB 121 QOIDANNMIQCMKGLDLKFLCYVESLFKFLFRNRYKVHLLVYLPVLEDSPLVPQGS 180
OY 181 FQWVHCNCVHECCBCLVPPVPAKINDTLMLCKITSGVIFQSPVLSVQPINWKPDP 240
DB 181 FQWVHCNCVHECCBCLVPPVPAKINDTLMLCKITSGVIFQSPVLSVQPINWKPDP 240
OY 241 LGLHMETDDGKNTKISWSSPPLVPPLOQVYKYSNSTTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMETDDGKNTKISWSSPPLVPPLOQVYKYSNSTTVIREADKIVSATSLVDSILP 300
OY 301 GSSYEVOYRGKRLDGPGLMSDMSTPRVFTQDVLYFPFKILTVSGSNVSFQIKKENKI 360
DB 301 GSSYEVOYRGKRLDGPGLMSDMSTPRVFTQDVLYFPFKILTVSGSNVSFQIKKENKI 360
OY 361 VPSKEIYVMNMLAKIKPOSDVYVSDHVSQVTFENLNETKRGKFTYIDAVYCNHEHC 420
DB 361 VPSKEIYVMNMLAKIKPOSDVYVSDHVSQVTFENLNETKRGKFTYIDAVYCNHEHC 420
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DB 481 PISPKDCYLOSDFYECIFQPIFLSGTYWIMINISLSGLSDSPICVLPDSVYKPLP 540
OY 541 SSVAEITINIGLKISWEKVPENNLOQIRYGLSGKEYQWMEYVDAKSKSVSLPV 600
DB 541 SSVAEITINIGLKISWEKVPENNLOQIRYGLSGKEYQWMEYVDAKSKSVSLPV 600
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DB 601 PDLCAVAVOYRCKRLDGLGYSWMSNPATYVMDIVPMGPEFVRIINDTKKREKNV 660

QY 661 TLLMKPLKNDLSCVQRYVINHTSCNGTWSDEVGNHTKTEFLMTEGAHTVYLAINSI 720
 D6 661 TLLMKPLKNDLSCVQRYVINHTSCNGTWSDEVGNHTKTEFLMTEGAHTVYLAINSI 720
 QY 721 GAVANFNLTSWPMKSKNVIQSLASVPLNSSCVIYVSLSPDQKLMYFIEMKNLMD 780
 D6 721 GAVANFNLTSWPMKSKNVIQSLASVPLNSSCVIYVSLSPDQKLMYFIEMKNLMD 780
 QY 781 GEIMKLRISSSVKKYYIHDFPIEKYQFSLPIFMEVGKPKLIINSTODDIEKHQSDA 840
 D6 781 GEIMKLRISSSVKKYYIHDFPIEKYQFSLPIFMEVGKPKLIINSTODDIEKHQSDA 840
 QY 841 GLYIYVPIIISSTLLGLTLLISHQRMKLLWEDVDPNFKNSMAOGLNFQKPEFHEHLEFI 900
 D6 841 GLYIYVPIIISSTLLGLTLLISHQRMKLLWEDVDPNFKNSMAOGLNFQKPEFHEHLEFI 900
 QY 901 KHTSVTCGPLLPEPTISEDIVSOTSMKNDEMPPTVYSLSTDLKSGVCSIDQFN 960
 D6 901 KHTSVTCGPLLPEPTISEDIVSOTSMKNDEMPPTVYSLSTDLKSGVCSIDQFN 960
 QY 961 SVNFSSEAGTEVTEDESOROPFYKATLISNSKPSSETGEOGLINSSVTKCFSSKNSPL 1020
 D6 961 SVNFSSEAGTEVTEDESOROPFYKATLISNSKPSSETGEOGLINSSVTKCFSSKNSPL 1020
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 D6 1021 KDSFSNSSWEIEAOAFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNRKSIYLL 1080
 QY 1081 GVTSLKKRESGVLLTDKRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTAS 1140
 D6 1081 GVTSLKKRESGVLLTDKRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTAS 1140
 QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
 D6 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 2
 LEPR_RAT STANDARD; PRT: 1162 AA.
 AC 063007; 063007; P70493; P70494; P70495; Q63385; Q63386; Q54805;
 AC P67589; Q35772;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
 GN LEP-R OR OB-R OR FA.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
 RC STRAIN-ZUCKER: TISSUE-Hypothalamus;
 RX MEDLINE-96241565; Pubmed-8673096;
 RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,
 RA Hess J.F.,
 RT "Leptin receptor missense mutation in the fatty Zucker rat.";
 RT Nat. Genet. 13:18-19(1996).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
 RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE-Brain;
 RX MEDLINE-96295531; Pubmed-8702432;
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.,
 RT "Substitution at codon 269 (glutamine--> proline) of the leptin
 RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
 RT (fa/fa) rat.";
 RT Biochem. Biophys. Res. Commun. 224:597-604(1996).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANTS A; B AND E).
 RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
 RX MEDLINE-96332408; Pubmed-8769097;

RA Takaya K., Ogawa Y., Ise N., Okazaki T., Satoh N., Masuzaki H.,
 RA Mori K., Tamura N., Hosoda K., Nakao K.,
 RT "Molecular cloning of rat leptin receptor isoform complementary
 RT DNA." Identification of a missense mutation in Zucker fatty (fa/fa)
 RT rats.";
 RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (VARIANT B).
 RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
 RT "Cloning of the rat leptin receptor.";
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).
 RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
 RX MEDLINE-96212906; Pubmed-8630068;
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.,
 RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
 RT Zucker fatty (fa/fa) rat.";
 RT Biochem. Biophys. Res. Commun. 222:19-26(1996).
 RN [6]
 RP SEQUENCE OF 1-123 FROM N.A.
 RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.,
 RT "Analysis of rat leptin receptor gene.";
 RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 694-878 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Pancreas;
 RA Ma Z.,
 RT "Identification of a leptin receptor in islet.";
 RT Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 843-892 FROM N.A. (VARIANT C).
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Bell G.I., Hara M., Rouard M., Yano H., Philippe N., Polonsky K.S.,
 RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP VARIANT FA PRO-269.
 RX MEDLINE-96314329; Pubmed-8690163;
 RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
 RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
 RA Leibel R.L.,
 RT "Phenotype of fatty due to Glu269Pro mutation in the leptin receptor
 RT (lepr).";
 RT Diabetes 45:1141-1143(1996).
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
 CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN. EXCEPT FOR FORM E
 CC WHICH COULD BE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: A, B (SHOWN HERE), C, D AND E;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
 CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHIVERING
 CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
 CC TISSUE.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb-sdb.ch).
 CC
 CC EMBL: U52966; AAC52587.1;
 CC EMBL: D84550; BAA12697.1;
 CC EMBL: D84551; BAA12698.1;
 CC EMBL: D85557; BAA12830.1;

DR EMBL: D85558: BAA12831.1; -
 DR EMBL: D85559: BAA12832.1; -
 DR EMBL: D85560: BAA12833.1; -
 DR EMBL: D84125: BAA12230.1; -
 DR EMBL: D84126: BAA12231.1; -
 DR EMBL: AB01006: BAA24899.1; -
 DR EMBL: U67207: AAB0654.1; -
 DR EMBL: AF007818: AAB63201.1; -
 DR InterPro: IPR002996: CRIA.
 DR InterPro: IPR003961: FN.III.
 DR InterPro: IPR003529: Hematopo_receptor_L_F2.
 DR Pfam: PF00041: fn3.2.
 DR PROSITE: PS01353: HEMATOPO_REC_L_F2: 1.
 KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Polymorphism; Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 1162
 FT DOMAIN 22 839
 FT TRANSMEM 840 860
 FT DOMAIN 861 1162
 FT DOMAIN 236 318
 FT DOMAIN 535 621
 FT DOMAIN 736 821
 FT CARBOHYD 55 55
 FT CARBOHYD 56 56
 FT CARBOHYD 73 73
 FT CARBOHYD 98 98
 FT CARBOHYD 187 187
 FT CARBOHYD 275 275
 FT CARBOHYD 345 345
 FT CARBOHYD 356 356
 FT CARBOHYD 431 431
 FT CARBOHYD 514 514
 FT CARBOHYD 622 622
 FT CARBOHYD 657 657
 FT CARBOHYD 668 668
 FT CARBOHYD 686 686
 FT CARBOHYD 695 695
 FT CARBOHYD 698 698
 FT CARBOHYD 726 726
 FT VASPLIC 890 894
 FT VASPLIC 895 1162
 FT VASPLIC 890 892
 FT VASPLIC 893 1162
 FT VASPLIC 797 805
 FT VASPLIC 806 1162
 FT VARIANT 269 269
 FT CONFLICT 2 2
 FT CONFLICT 12 12
 FT CONFLICT 34 34
 FT CONFLICT 751 752
 FT CONFLICT 846 846
 SQ SEQUENCE 1162 AA: 130832 MW: BA7AC2A2D2B62AF CRC64:

Query Match 76.5%; Score 4784.5; DB 1; Length 1162;
 Best Local Similarity 75.6%; Pred. No. 4.6e-316;
 Matches 882; Conservative 118; Mismatches 161; Indels 5; Gaps 5;

QY 1 MICKFCVLLHMEFIYITAFNLSTPTWRFKLSCHPSTSYDYILLPLGLSKRNTS 60
 DB 1 MTCCKFYVLLHMEFLYITAFNLSTPTWRFKLSCHPSTSYDYILLPLGLSKRNTS 60
 QY 1 NGHETAVEPEFNSGTFHSLKTFHCFRSDRNCSCANINIGKTFVTVNSLYE 120
 DB 1 KGAEEALVEAFENSTGIVSELSTKTIHCCGNGGONCSALTONTCKTASLYVKKPLVE 120
 QY 121 QQIDANNIQGWLKGLKLFICYVESLFKMLFRNTKYNKHLVYLPLEVLEDSPLVPQGS 180
 DB 121 ROLGVNNDIEGMMKGLDLEFICHEMPLKKNPKFYKDSKVLHLLDREYIDDLPLPKDS 180
 QY 181 FQMHGMSVHECECLVPPVPTAKLNTLMLCKLITSGVLFQSPPLMSVQPINNVKDDPP 240

DB 181 FQYVQNCNRYE-CECHVPVRAKVNVALMLYLETSGVFSQSPMLSLQMLVYKDDPP 239
 QY 241 LGLHMETDGNLKIISWSPPLVPEPLQYQVYSENSITTVIREADKIYSATSLVDSITLP 300
 DB 240 LGLHMETDGNLKIISWSPPLVPEPLQYQVYSENSITTVIREADKIYSATSLVDSITLP 298
 QY 301 GGSYEVQYRGRRLDGPQISWSTPRVFTTODVYIFPPKILTSVGSNVSFCITKKKKKI 360
 DB 299 GGSYEVQYRGRRLDGPQISWSTPRVFTTODVYIFPPKILTSVGSNVSFCITKKKKKI 358
 QY 361 VPSKEIVMMNLAKRIPQSDVYSDHYSKYTFPNLNETKRGKFTDVAVYCCNHEHC 420
 DB 359 ISSQIYVMMNLAKRIPQSDVYSDHYSKYTFPNLNETKRGKFTDVAVYCCNHEHC 418
 QY 421 RYAEIYVDVNIINISCELDGYLTKMTCSWTSTIOSLAESTIOLRYHRSLSYCSIDPSIH 480
 DB 419 RYAEIYVDVNIINISCELDGYLTKMTCSWTSTIOSLAESTIOLRYHRSLSYCSIDPSIH 478
 QY 481 PISEPKDCYLOSDFEYECIFQIFLDSGYTMIRINHSLSLSDPICVLPDSYVKKPLPP 540
 DB 479 PISEPKDCYLOSDFEYECIFQIFLDSGYTMIRINHSLSLSDPICVLPDSYVKKPLPP 538
 QY 541 SSVKAEITINIGLKISMEKVPENNLOFQIRGLSGEYQNMAYHYDAKSKSVSLPV 600
 DB 539 SSVKAEITINIGLKISMEKVPENNLOFQIRGLSGEYQNMAYHYDAKSKSVSLPV 598
 QY 601 PDLCAVAVQYRCRRLDGLGYWMSNFPATVVMIDIKPMRGPBEMIRINDGTJMKKKKNV 660
 DB 599 PDLCAVAVQYRCRRLDGLGYWMSNFPATVVMIDIKPMRGPBEMIRINDGTJMKKKKNV 658
 QY 661 TLKMKPLMKNDLSQVQRYVINHTSCNGTWSDEVGNHTKFTPLNTVOATVYVLAINSI 720
 DB 659 TLKMKPLMKNDLSQVQRYVINHTSCNGTWSDEVGNHTKFTPLNTVOATVYVLAINSI 718
 QY 721 GASVANFLPFSMMSKYNVYIOSIAYPLNSCYIVSLSPSYDKMLYIEKKRNKND 780
 DB 719 GASVANFLPFSMMSKYNVYIOSIAYPLNSCYIVSLSPSYDKMLYIEKKRNKND 778
 QY 781 GEIKMLRISSSVKRYHYHDFPIEKOFSLYPFMEGVGPKIINSFTODDIEKHOSDA 840
 DB 779 GEIKMLRISSSVKRYHYHDFPIEKOFSLYPFMEGVGPKIINSFTODDIEKHOSDA 838
 QY 841 GLYIYVPIISSLGTLGLTLLISHQKAKLFEDEVPNPKNSAQQGLNFOKPEFHEHFT 900
 DB 839 GLYIYVPIISSLGTLGLTLLISHQKAKLFEDEVPNPKNSAQQGLNFOKPEFHEHFT 898
 QY 901 KHTASVYCGPLLEPERISSEISVDTGSKNDEMPPTVYSLST-DLEKGSYCIDQF 959
 DB 899 KHTASVYCGPLLEPERISSEISVDTGSKNDEMPPTVYSLST-DLEKGSYCIDQF 958
 QY 959 NSVNFSEAEGETVEYDESDQRPVYKATLTSNSKPSFTGEQGLINSVYKCFSSKNRP 1019
 DB 959 NSVNFSEAEGETVEYDESDQRPVYKATLTSNSKPSFTGEQGLINSVYKCFSSKNRP 1018
 QY 1020 LKDSFSSNSWEIEAQAFFISDQHPNITSPHLTFSEGLDELKLGNEPPEBNDKKSITP 1079
 DB 1019 LKDSFSSNSWEIEAQAFFISDQHPNITSPHLTFSEGLDELKLGNEPPEBNDKKSITP 1077
 QY 1080 LGVTSIKKRRESGVLLTDKSRVCPFPACLETDIRLQDSCSHVENNINIGTSSKRTFA 1139
 DB 1078 LGVTSIKKRRESGVLLTDKSRVCPFPACLETDIRLQDSCSHVENNINIGTSSKRTFA 1136
 QY 1140 SYMPOFOTCSTQTHKIMENKMCIDLTV 1165
 DB 1137 SYMPOFOTCSTQTHKIMENKMCIDLTV 1162

RESULT 3
 LEPR MOUSE STANDARD: PRT: 1162 AA.
 ID LEPR MOUSE STANDARD: PRT: 1162 AA.
 AC P48356: 035686: 061215: 064309: 054986:
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)

01:MAR-2002 (Rel. 41, last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219 receptor).
 GN LEP-R OR OB-R OR DB.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (VARIANT A).
 RC TISSUE=Choroid plexus;
 RX MEDLINE=96128129; PubMed=8548812;
 RA Tartaglia L.A., Dembski M., Meng X., Deng N., Culpepper J., Devois R., Richards G.J., Campfield L.A., Clark F.T., Deeds J., Muller C., Sanker S., Moriarty A., Moore K.J., Smutko J.S., Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;
 RT Identification and expression cloning of a leptin receptor, OB-R.;
 RL Cell 83:1263-1271(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (VARIANT B).
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=96190816; PubMed=8608603;
 RA Chen H., Charlat O., Tartaglia L.A., Wolf E.A., Meng X., Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E., Duvk G.M., Tepper R.I., Morgenstern J.P.;
 RT Evidence that the diabetes gene encodes the leptin receptor: identification of a mutation in the leptin receptor gene in db/db mice.;
 RL Cell 84:491-495(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (VARIANTS A TO E).
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=96231997; PubMed=8628397;
 RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G., Lee J.I., Friedman J.M.;
 RT Abnormal splicing of the leptin receptor in diabetic mice.;
 RL Nature 379:632-635(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (VARIANT C).
 RC STRAIN=BA1B/C; TISSUE=Liver;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Clouff J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A., Platika D., Snodgrass H.R.;
 RT Novel B219/OB receptor isoforms: possible role of leptin in hematopoiesis and reproduction.;
 RL J. Med. 2:585-589(1996).
 RN [5]
 RP SEQUENCE FROM N.A. (VARIANT B).
 RC STRAIN=NEW ZEALAND OBSE / NZO; TISSUE=Hypothalamus;
 RX MEDLINE=97462708; PubMed=9322935;
 RA Igel M., Becker W., Heberg L., Joost H.G.;
 RT Hyperleptinemia, leptin resistance, and polymorphic leptin receptor in the New Zealand obese mouse.;
 RL Endocrinology 138:4234-4239(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (VARIANTS A AND B).
 RC STRAIN=FVB/N; TISSUE=Spleen;
 RX MEDLINE=96270520; PubMed=8692797;
 RA Ghilardi N., Ziegler S., Westner A., Stoffel R., Helm M.H., Skoda R.C.;
 RT Defective STAT signaling by the leptin receptor in diabetic mice.;
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
 RN [7]
 RP SEQUENCE FROM N.A. (VARIANT E).
 RC STRAIN=129/J;
 RX MEDLINE=98008913; PubMed=9344648;
 RA Chua S.C., Koutlas I.K., Han L., Liu S.M., Kay J., Young S.J., Chung W.K., Leibel R.L.;
 RT Fine structure of the murine leptin receptor gene: splice site suppression is required to form two alternatively spliced transcripts.;
 RL Genomics 45:264-270(1997).
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT E) COULD FUNCTION AS A TRANSPORT PROTEIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E WHICH COULD BE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS, A, B (SHOWN HERE), C, D AND E; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS. (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E: EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 CC EMBL; U42467; AA93014.1; -
 CC EMBL; U46135; AAC52408.1; -
 CC EMBL; U49106; AAC52420.1; -
 CC EMBL; U49107; AAC52421.1; -
 CC EMBL; U49108; AAC52422.1; -
 CC EMBL; U49109; AAC52423.1; -
 CC EMBL; U49110; AAC52424.1; -
 CC EMBL; U52915; AAC52599.1; -
 CC EMBL; Y10298; CAA71343.1; -
 CC EMBL; U58861; AAC52705.1; -
 CC EMBL; U58862; AAC52706.1; -
 CC EMBL; U58863; AAC52707.1; -
 CC EMBL; AF039456; AAB95334.1; -
 CC EMBL; AF039443; AAB95334.1; JOINED.
 CC EMBL; AF039444; AAB95334.1; JOINED.
 CC EMBL; AF039445; AAB95334.1; JOINED.
 CC EMBL; AF039446; AAB95334.1; JOINED.
 CC EMBL; AF039447; AAB95334.1; JOINED.
 CC EMBL; AF039448; AAB95334.1; JOINED.
 CC EMBL; AF039449; AAB95334.1; JOINED.
 CC EMBL; AF039450; AAB95334.1; JOINED.
 CC EMBL; AF039451; AAB95334.1; JOINED.
 CC EMBL; AF039452; AAB95334.1; JOINED.
 CC EMBL; AF039453; AAB95334.1; JOINED.
 CC EMBL; AF039454; AAB95334.1; JOINED.
 CC EMBL; AF039455; AAB95334.1; JOINED.
 CC HSSP; P40189; IBCU.
 CC MGD; MGI:104993; Lepr.
 CC InterPro; IPR002996; CRA.
 CC InterPro; IPR003961; FN.III.
 CC InterPro; IPR003529; Hematopo_Receptor_L_F2.
 CC Pfam; PF00041; fn3; 3.
 CC SMART; SM00060; fn3; 3.
 CC PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 CC Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 CC Polymorphism; Alternative splicing.
 CC SIGNAL 1 21 POTENTIAL.
 CC CHAIN 1 21 LEPTIN RECEPTOR.
 CC DOMAIN 22 1162 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 840 839 POTENTIAL.
 CC DOMAIN 861 1162 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 236 318 FIBRONECTIN TYPE-III 1.
 CC DOMAIN 535 621 FIBRONECTIN TYPE-III 2.
 CC DOMAIN 736 821 FIBRONECTIN TYPE-III 3.
 CC CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 686 686 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 695 695 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 726 726 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VASPLIC 890 894 PETE -> RDTL (IN ISOFORM A).
FT VASPLIC 895 1162 MISSING (IN ISOFORM A).
FT VASPLIC 890 892 PET -> VTV (IN ISOFORM C).
FT VASPLIC 893 1162 MISSING (IN ISOFORM C).
FT VASPLIC 890 900 PETEHLFTKH -> DISHEFVFLTR (IN ISOFORM D).
FT VASPLIC 901 1162 MISSING (IN THE ISOFORM D).
FT VASPLIC 797 805 DNEFDTEKY -> GACTVLEMD (IN ISOFORM E).
FT VASPLIC 806 1162 MISSING (IN ISOFORM E).
FT VASPLIC 541 541 V -> I (IN STRAIN NOZ).
FT VASPLIC 651 651 V -> I (IN STRAIN NOZ).
FT VASPLIC 1044 1044 T -> I (IN STRAIN NOZ).
FT CONFLICT 140 140 F -> I (IN REF. 6).
FT CONFLICT 720 720 A -> T (IN REF. 5).
SQ SEQUENCE 1162 AA; 130788 MW; 0E1E75B076BA60A2 CRC64;

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Query Match 76.2%; Score 4766.5; DB 1; Length 1162;
 Best Local Similarity 75.4%; Pred. No. 7.7e-315;
 Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;

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QY 1 MICOQFVLLHMEFIYITAFNLSPITTPMRKLSMPNSTYDFLLPAGLSKNTSNS 60
DB 1 MHCQFVYVLLHMEFIYITAFNLSPITTPMRKLSMPNSTYDFLLPAGLSKNTSNS 60
QY 61 NCHYTAVERPNSGTHFNSLKTTHCCPSREDDRNCSLCAADIEGKTFTVNSLVE 120
DB 61 KGASAIYEAFFNSGIVPELSKTFHFCFNGEQNCSALTDMTEKTLASVYKASVF 120
QY 121 QOIDLNNMIQCLKGLDKLFCYVESLFKNLFRNRYKHLLYLPEVLEDSPLVPKOS 180
DB 121 ROLSVNMIECMKGDLLFLFCHMEPLKPNPKNDKSKVHLLYLPEVLEDSPLVPKOS 180
QY 181 FOMVHCNSVHECECLVVPVPTAKINDTLMLCLKTSGSVIFQSPLSMVOPINWKPDP 240
DB 181 FQYVQCNCSLKG-CECHVVPVPRKLNVALMLLETTSAGVSFQSPLSMVOPINWKPDP 239
QY 241 LGLHMEIDDDGKLKISMSPLVPPLOYVAKYSENSTTVREAKIYSATSLVDSILP 300
DB 240 LGLHMEVTDGKLKISMSQTMAPPLOYVAKYLENS-TIVREAEIYVATSLVDSILP 298
QY 301 GSSYEYQVRGRKLDGPGIMSDMSTPRVFTQDVIFPKRILTSVGSNSVFCIKYKKNKI 360
DB 299 GSSYEYQVRGRKLDGSGVMSDSPOVFTQDVYFPFKRILTSVGSNSVFCIKYKKNKI 358
QY 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSATVFENLFTKPRGKFTYDAYVCCNEHECH 420
DB 359 ISSKQIVMMNLAEKIPQSQYDVVSDHVSATVFENLFTKPRGKFTYDAYVCCNEHECH 418
QY 421 RYAEIYVADVNTINISCEFDGYLTKMTCSWSTSTOSLAEISLQRLRYHSSSLYCSIPSIH 480
DB 419 RYAEIYVADVNTINISCEFDGYLTKMTCSWSTSTOSLAEISLQRLRYHSSSLYCSIPSIH 478
QY 481 PISEKDCYILSDGFYECIFQPIFLLSGYTMMIRINHSLSGSDSPRTVLPDSVYKPLPP 540
DB 479 PISEKDCYILSDGFYECIFQPIFLLSGYTMMIRINHSLSGSDSPRTVLPDSVYKPLPP 538
QY 541 SSVAAEITINIGLKLISKEKFPVFNENLQFQIRGLSGKEVQMKYEVYDAKSKSVSLPV 600
DB 539 SSVAAEITINIGLKLISKEKFPVFNENLQFQIRGLSGKEVQMKYEVYDAKSKSVSLPV 598
QY 601 PDLCAVYAVQVRCKRLDGLGYWSMNSPATYVMDIKYPMKGPPEWRLINDGYMKKEKNV 660
DB 599 PDLCAVYAVQVRCKRLDGLGYWSMNSPATYVMDIKYPMKGPPEWRLINDGYMKKEKNV 658

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DB 599 SDLCAYVYVQVRCKRLDGLGYWSMNSPATYVMDIKYPMKGPPEWRLINDGYMKKEKNV 658
QY 661 TLMLKPLKNDLSGVORYVIVNHHTSCNGTWSEDEGNHKEFLNTEFOAHYTVLAISNI 720
DB 659 TLMLKPLKNDLSGVORYVIVNHHTSCNGTWSEDEGNHKEFLNTEFOAHYTVLAISNI 718
QY 721 GASVANFNLTEPMSKSNVIVOSLSAYPLNSCVIVSWLSPSDYKLYFETIEMKNLND 780
DB 719 GASVANFNLTEPMSKSNVIVOSLSAYPLNSCVIVSWLSPSDYKLYFETIEMKNLND 778
QY 781 GEIKMLRISSVYKYYIHDFPIPEKTOPSLYPIPMEGVGRKIIINSTODDIEKHQSDA 840
DB 779 DGMKVLRLPSNVKRYIHDFPIPEKTOPSLYPIPMEGVGRKIIINSTODDIEKHQSDA 838
QY 841 GLYVIVPVIYIISILLGLTILSHORMKLEMDVDPNKNCSNAGLNFQKPEFHEFLFI 900
DB 839 GLYVIVPVIYIISILLGLTILSHORMKLEMDVDPNKNCSNAGLNFQKPEFHEFLFI 898
QY 901 KHTASVTCGPLLEPETISEDISVDTSMKNDEMPTTVSLSTT-DLEKGSVCISDOF 959
DB 899 KHAESVIRGPLLEPETISEDISVDTSMKNDEMPTTVSLSTT-DLEKGSVCISDOF 958
QY 960 NSVNSSEAEGETYVYEDSSQOPFYKATILISNSKPSFTGEOGLNSVTKCFPSKRSK 1019
DB 959 NSANFSSQSQTQVTCEDCQOPSVYKATILISNKLVTETDEQGFHSVPVSCJSSNHP 1018
QY 1020 LKDSFNSMTEAQAFLPSDQHPNIIISPHLTFESGDELKLGPNPEENNDKSIY 1079
DB 1019 LKDSFNSMTEAQAFLPSDQHPNIIISPHLTFESGDELKLGPNPEENNDKSIY 1077
QY 1080 LGVTSIKKRESGVLLTDKSRVSCPPAPCLPTDILVYLDOSCHFEVENNINIGTSKRTFA 1139
DB 1078 LGVTSIKKRESGVLLTDKSRVSCPPAPCLPTDILVYLDOSCHFEVENNINIGTSKRTFA 1136
QY 1140 SYMPOFORCSTQTHKIMENKMODLTV 1165
DB 1137 SYMPOFORCSTQTHKIMENKMODLTV 1162

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RESULT 4
 IL6B_MOUSE STANDARD; PRT; 917 AA.
 AC Q00560;
 DT 01-FEB-1995 (Rel. 31, Created).
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin 6 signal transducer) (Membrane glycoprotein 130) (GP130).
 GN IL6ST.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Macrophage;
 RA MEDLINE=92291532; PubMed=1602143;
 RX Saito M., Yoshida K., Hibi M., Tega T., Kishimoto T.;
 RT "Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130, and its regulated expression in vivo.";
 RL J. Immunol. 148:4066-4071(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE CELLS.

CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
CC 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
CC DURING THE REST OF EMBRYOGENESIS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; X62646; CAA44515.1; -
DR EMBL; M83336; AAA37723.1; -
DR HSSP; P40189; IBOU
DR MGD; MGI:96560; I16st.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003962; FN.III.repeat.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 4.
DR PRINTS; PR00014; FN1YPE111.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; signal;
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 917 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 617 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 618 639 POTENTIAL.
FT DOMAIN 26 917 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 124 220 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 221 322 FIBRONECTIN TYPE-III 1.
FT DOMAIN 323 420 FIBRONECTIN TYPE-III 2.
FT DOMAIN 422 515 FIBRONECTIN TYPE-III 3.
FT DOMAIN 516 611 FIBRONECTIN TYPE-III 4.
FT DOMAIN 723 741 FIBRONECTIN TYPE-III 5.
FT DISULFID 28 54 SER-RICH.
FT DISULFID 48 103 BY SIMILARITY.
FT DISULFID 134 144 BY SIMILARITY.
FT DISULFID 172 180 BY SIMILARITY.
FT DISULFID 456 464 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 917 AA; 102452 MW; FCEPD220BC2466F4 CRC64;
Query Match 5.9%; Score 366; DB 1; Length 917;
Best Local Similarity 20.9%; Pred. No. 5.9e-17;
Matches 191; Conservative 140; Mismatches 338; Indels 244; Gaps 42;

QY 474 SDIPSIHPISPKDCYQSDGFYECI--FQPIELSGYTMIRIHSLGSLDSPPTCYLP 531
DB 166 TE-----KFPDC--QSKHGTSCMVSYPYLVN-IEVWEALNALGKSSSEINDP 214
QY 532 DSVNPLPPSSKAEIITINI-GLKISWEKVPYPPNNIOFOIRYLSG-----KRYO--- 582
DB 215 VDKVPTPTPTNIVTNSSELISITLKW-----VSSGLGLDLKSDIQYRT 261
QY 583 -----WKMEYVDAKSKVSLPVPDL--CAVAYQVRCKRLDGLGWSMNSPATAVMD 635
DB 262 KDASTWIDQPLEDTPMSPTSTFYQDLKPFTEVFRIRISIKSGKIVSDMSSEASGTYTE 321
QY 636 IKVPRGPEPMRIINGDTMKKEKNVTLLMKPLMKNDLSLSQRY--VINHTSCNGTWSE 693
DB 322 DR-PSRPSFWKTKNPSHGOEYRSVRLIMKALPLSEANGKIIDYHVLLTOSKVSQFYTV 380
QY 694 DVGNHTKFTPLMTBOAHVTVYLAISIGASVAFNFTLTSWP-MKVNIVQSLAAFLPMS 752
DB 381 --TGTELVNLTNDRYVASLARKKVGKSAAY-LTTPSPVTVAYSVVNLKAPF-KDN 435
QY 753 CVIYSMILSPSDYKIMFYELIEMKNLNEDEGEI--KWLRISSVKKYVLIHDFIPERKQFS 810
DB 436 LLWVEM--TPPKPKYSKTIEMCVLSENAFCYEDWQEDATVNRTHLGRLLSEKCYQIT 493
QY 811 IYPIFMG----- 818
DB 494 VTPVATGPGGSGESLKAYLKQAAPARGPTVTKVGNKEAVLAWDQIPVDQNGFIRNYS 553
QY 819 -----VGRKRII--NSFTQDDIEKHOSDAGLY----- 843
DB 554 ISYRTSVKEMVAVHDSTTEYTLSSSDT-LYVMAAYTDEGKOGPEFTTTPKFA 612
QY 844 -----VIYVPISSSI-LLGLTLLISHOR--MKLFMEDVNPVKNCSMAOGLNPKPBT 894
DB 613 QGEIATVAVPCLALLTLTLGLVLCFKNRDLIKHINPNVDESKSHQAQSPHTPP-- 670
QY 895 FEHLFIKHTASVTCGPLLEPETISEDIVDSVTSKMKDEMDPTVVSLLSTTDLEK---- 950
DB 671 -RHNFNSKQDMSDGNF-----TVSVVEIEANNNKPCDD--LKSVDLKKKEV 717
QY 951 -----GVCISIDQFNSVNFSEAGTEVYDEDSGR--PVKATATLSNKRPSPT 998
DB 718 STEGSHSGIGSGSSCMSSSRPSSISNE-----ENESQSTASVTEYSTVHSSYRIQOV 769
QY 999 GHEOGLINSSVVK-FFSSKNP-----LKDSFNSSSWEIQAQAFILSDQPNITSPHLTF 1053
DB 770 PSVOVFSKSESTQPLLDSEFPEDQLVDSDVSGDEILRPQYFKONCSQPE-ACPEISH 828
QY 1054 SEGDELKLTLEGN 1066
DB 829 FERSNOV--LSCN 839
RESULT 5
ID IL6B_HUMAN STANDARD; PRT; 918 AA.
AC P40189; O9U041;
DT 01-FEB-1995 (Rel. 31, last sequence update)
DT 01-FEB-1995 (Rel. 31, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (CD130) (Oncofstatin M
DE receptor) (CDw130) (CD130 antigen).
GN I16ST
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Myeloma, and Placenta;
RX MEDLINE=91084844; PubMed=2261637;

RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 RL gp130.";
 RN Cell 63:1149-1157(1990).
 RP [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE-Synovium;
 RX MEDLINE-20341529; PubMed-10880057;
 RA Tanaka M., Kishimura M., Ozaki S., Osaka F., Hashimoto H., Okubo M.,
 RA Murakami M., Nakao K.;
 RT "Cloning of novel soluble gp130 and detection of its neutralizing
 RT autoantibodies in rheumatoid arthritis.";
 RL J. Clin. Invest. 106:137-144(2000).
 RN [3]
 RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE-21269388; PubMed-11098061;
 RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
 RT "determination of the disulfide structure and N-glycosylation sites of
 RT the extracellular domain of the human signal transducer gp130.";
 RL J. Biol. Chem. 276:8244-8253(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE-98169383; PubMed-9501088;
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674(1998).
 CC -1- FUNCTION: Signal-transducing molecule. The receptor systems for
 CC IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for
 CC initiating signal transduction. Binds to IL-6/IL-6-R (alpha chain)
 CC complex, resulting in the formation of high-affinity IL-6 binding
 CC sites, and transduces the signal. Does not bind IL-6. May have a
 CC role in embryonic development (By similarity).
 CC -1- SUBUNIT: Heterodimer of type I and a beta chain.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and
 CC secreted (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2/gp130-
 CC RAS; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Found in all the tissues and cell lines
 CC examined. Expression not restricted to IL-6 responsive cells.
 CC -1- DISEASE: gp130-RAPS is an autoantigen found in rheumatoid
 CC arthritis (RA) but it is not specific to patients with RA.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
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 CC -----
 DR EMBL: M57230; AA559155.1; -
 DR EMBL: AB015706; BAA78112.1; -
 DR PIR: A36337; A36337.
 DR PDB: 1BOU; 26-AUG-98.
 DR MIM: 600694; -
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003861; FN_III.
 DR InterPro: IPR003962; FN_III_repeat.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam: PF00041; fn3; 3.
 DR PRINTS: PR00014; FNTYPEIII.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 KW Repeat; 30-structure; Alternative splicing.
 FT SIGNAL 1 22
 FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).
 FT

FT TRANSMEM 620 641 POTENTIAL.
 FT DOMAIN 642 918 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 124 222 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 223 324 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 325 423 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 424 517 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 518 613 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 725 755 SER-RICH.
 FT DISULFID 28 54
 FT DISULFID 48 103
 FT DISULFID 134 144
 FT DISULFID 172 182
 FT DISULFID 458 466
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .).
 FT VARSPLIC 325 329 RPSA -> N1ASE (IN GP130-RAPS).
 FT VARSPLIC 330 918 MISSING (IN GP130-RAPS).
 SQ SEQUENCE 918 AA: 103522 MW: 86135672DD10D53 CRC64;
 Query Match 5.5%; Score 345.5; DB 1: Length 918;
 Best local similarity 19.8%; Pred. No. 1,4e-15;
 Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;
 QY 337 PKILITSGVSNVSPHCIIYKK---ENKIYPSKEIWMMLAEKIPQSYDVSADHSKYTF 393
 DB 33 PESPVYQJHSNPTAVCAVLKEKCMDFHVNANYIKTN-HFTIPKEQYTIINRTASVTF 91
 QY 394 FPLNETKPKGKTYTAVYCNHNECHHRYAEIYDV-----NINSC-ETGCIYLT 444
 DB 92 TDI-----ASLMDIOLCNLTFTGQLEQNYGITIISGLPERPKNLCIVNGG--RK 141
 QY 445 MCRWSTYIQSLASTLQLRHRSLSVCSQIPSHIPSEPKDCLQSDGFYECI--FOP 502
 DB 142 MCEMDGCG-----RETHLENTTLKSEVAT-----HKRA--DCIAKBDTPSCVNDST 188
 QY 503 IELLSGYTMIRINHSLSIDSPPTCVLPDSYKPLPSSVKAETITN---IGLLKISW 558
 DB 189 VYFVN-IEVWVAEENALGKVTSDHINFDVYKKNPNHNL--VINSEELSLIKLTW 244
 QY 559 EKP-----VFPENNIQFOIRYGLSGREVQMKRYEYDAKSKVSJLPVPL--CAYVAVQ 611
 DB 245 TNPISIKSVITILKYNIOYRKDKAST-----WSQIPBEDASTRSSITVODLKPFTEVFRI 299
 QY 612 RCKRLDGLGYSMNMPAYTVVMDIKVPMRGPEFRITNGDMKKEKNTLLMKPLMKND 671
 DB 300 RCKMKEDGKGYSDWSEBSGITYEDR-PSKAPSPFKKIDPSITQGYRYVQLWKLPPPE 358
 QY 672 SLCSVQRYVINHTSCNGTSESDVGNH---TKFTFLMTEQAHVTVVLAINSIGASVANF 727
 DB 359 ANGKILDEYEV-----LTRMKSHLQNYVNAKTLVNLINDRYLATLVRLNLYGKSDAAV 413
 QY 728 NLTFSPKSKVNIQVSLNAYPLNNSCVYSLTSDKRMKFIIEKMNLMDEG--IKW 785
 DB 414 LTIAPCDQFQNHPPVNDLAKFP-KDMMMLVWEVTPRESVK--KYILEWCVLDKAPCTIDW 470
 QY 786 LRISSVKKRYVHDFIFLEKYQSLYPIFMGVGKPKII----- 825
 DB 471 QOEDSTVHRTILRGNLASKCLITVTVPYADGPGSPESIAIYALKQAPPSKGPYRTKKV 530
 QY 826 -----NSFTQDDIERHOSDAGLY- 843
 DB 531 GKNEAVLEMDQLPVDVQNGFIRNTYIFRTIIGNETAVNVDSHREYLSLSLTSOT-LYM 589
 QY 844 -----VIYPIVITSSSI-LLLGTLLISHOR--MKK 869

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Db 550 VMAAYTBGCGDGEPTFTTPKFAQGEIEAIVPVCIAFLTTLGLVCFCKNRDLKK 649
Qy 870 LFMEDVPMKNCMAQNGINFORFETFEHLFIKHTASVTCGPIILPELTISEDIVDTSMK 929
Db 650 HIMPVPPDSKSHIKQNSPHPP-----RH-----NFN 677
Qy 930 NKDEMPTTVSLSTDLKSGVCSIDQFNSVNSEAEGETYEDESQROPF---VKY 986
Db 678 SKDQM-----YSDGNETDVSAVEIAND---KKPFEDDLKS 710
Qy 987 ATLINSKPSPEGEGLINSVTKCFSSKNSPLKDFSNSS 1028
Db 711 LDLFKREKINTEGHSSGIGGSS---CMSSSRPSISSSENES 749

RESULT 6
IL6B_RAT STANDARD: PRT: 918 AA.
AC P40190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (GPI30).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130."
RL Genomics 14:666-672(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CMF, AND IL-11 CAN UTILIZE GPI30 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, M92340; -, NOT_ANNOTATED_CDS.
CC PIR, A44257; A44257.
CC HSSP, P40189; 1BQU.
CC InterPro: IPR002966; CRIA.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR003529; Hematopo_receptor_L_F2.
CC Pfam, PF00041; fn3; 3.
CC SMART, SM00060; FN3; 3.
CC PROSITE, PS01353; HEMATOPO_REC_L_F2; 1.
CC Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
CC Repeat.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.

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FT DOMAIN 23 618 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 619 640 POTENTIAL.
FT DOMAIN 641 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 124 221 FIBRONECTIN TYPE-III 1.
FT DOMAIN 222 323 FIBRONECTIN TYPE-III 2.
FT DOMAIN 324 422 FIBRONECTIN TYPE-III 3.
FT DOMAIN 423 516 FIBRONECTIN TYPE-III 4.
FT DOMAIN 517 612 FIBRONECTIN TYPE-III 5.
FT DOMAIN 724 754 SER-RICH.
FT DISULFD 28 54 BY SIMILARITY.
FT DISULFD 48 103 BY SIMILARITY.
FT DISULFD 134 144 BY SIMILARITY.
FT DISULFD 172 181 BY SIMILARITY.
FT DISULFD 457 465 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAc. . .) (POTENTIAL).
SQ SEQUENCE 918 AA; 102450 MW; 9E1B86FCF087E7 CRC64;

Query Match 5.4%; Score 339.5; DB 1; Length 918;
Best Local Similarity 20.8%; Pred. No. 3.7e-15;
Matches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;

Qy 327 VPTTQDVI-----FPPKILTSVGSNSFHCYKKNKIVNSKE---IVMMNLAE 374
Db 14 ILLTIESIQALVEPCGYIYFPPVQVQSGNSFTATCYLKEKCIQVSVANTYIVKMTNW 72
Qy 375 KIPQSOYDVNSDVSKVYFFNINETKPRCKFTYDAVY-----CCNEHECHRYAEIYV 428
Db 73 AVPKEDQVYVINTASVVF-----TDVVFQVQVLTCTNLSFGQIEQVNYGIT 119
Qy 429 -----DVNINISC-ETDGYITKTKCRWSTIOSIASTIQLKIHRSLSYCSIDPSIH 480
Db 120 ILSGYPPDIPMLSCIVNGG--KNMICQ-----LDPRGTYLETNYTLKSEWATE---- 167
Qy 481 PISEPKDVLQSDGFEYECI--FQPIFLSGYTMIRINSLGSLSPPCVLPDSVVKPL 538
Db 168 ---KEPDCNTR-HGTSICMAGTPIYFVN-IEVWEAEALGNVSSCPINFPVDKVKFS 222
Qy 539 PSSVKAETITINI-GLKLSW-----EKVPEPNMLQFQIRYGLSGKEVQWRYEYDAK 592
Db 223 PPHNLSTNSEELSLIKLAWNSGLDSLRLKSDIQYTKDAST-----WIOVPLEDTV 277
Qy 593 SKSVSLPVVDL--CAVYAVQVCKRLDGLGYMSNNSPYYTVMMIKVMPKRPERRIIN 650
Db 278 SPRTSTPYDQLPFEYVYRIRSIKENGKGYWSDSEASGTYTDDR--PSKAPSEFYKVN 336
Qy 651 GPTMKKEKVVTLMLPKMNDLSQVQRY--VINHTSCNGTMSDDYCHGTFEFLMTQ 708
Db 337 AHPPOEYRSARLIKMTLPISSEANGKILDEYVLQSKYSQYTYT---NGTEIVTLTNK 393
Qy 709 AHTVYVLAINSIGASVANENLTFSWPMKRV-NIVQSLAVPLNSGCVIYSWILSPDYKL 767
Db 394 RYVASLAAARNVVGKSPATV-LTIPGSHFASHPVVDLKAFP-KDNLIAWEM--TPSPKRV 449
Qy 768 MYFIEMKLNDELGEI--KWLRISSSVKRYIHDHPIPIEXQFSLYPIFMGVGKPF--- 822
Db 450 NKYILIEWCVLSNSPCIPDWOQEDGTVNRTHLRSGLSKCYLITVTVVPGPGPSPESM 509
Qy 823 -----KI 824
Db 510 KAYLQAAAPSKGPYATKRVGKNEAVLEMDHLPVYQNGFINNYSTYSTVGKEMVAVV 569

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QY 825 INFTODDIEKHOSDAGLY-----VIVPVIIS 852
 DB 570 DSHTEYTLSSLDL-LLYVHMAAYTEEGKDGPEFTTTLKFAOGLIAYVPCIAL 628
 QY 853 SI-LLGLTLLISHOR--MKLEWEDYVNPKNCSMAOGLNQRKETEHLF-----IKHTA 904
 DB 629 LHTLLGLAVLEFCFKRDLIKHIMPVDPKSHIAQMSPTTP--RHNFNSKQDMISDA 685
 QY 905 SYTCGPLELLETISDYSVTSMKNKDEMPPTVSLSTVLEK-----950
 DB 686 NPT-----DVSVLEIANNNKRCPPDLSL--DLFKKIKISTEGHSSGIG 728
 QY 951 GSVICIDQFNSVNFSEAEGETVEYDESOQR--PFVKYATLLISNKRSPETGEGLINNS 1008
 DB 729 GSSCGMSSSRPSSISSE-----ENESASQSTASTVQYSTVHSGYRHOVPSVQVPSRSE 780
 QY 1009 VTK-CFSSKNSP---LKDFSSNSWEIEAOAFILSDQHPNIIISPHLT 1052
 DB 781 STQPLDSERPEDLDLVDSVSGDELPRQYFKQSCSOPG-ASPDVS 828

RESULT 7
 GCSR.MOUSE STANDARD: PRT: 837 AA.
 AC P40223;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R).
 GN CSF3R OR CSFGR
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90235283; PubMed=2158661;
 RA Fukunaga R., Ishizaka-Ikeda E., Seto Y., Nagata S.;
 RT Expression cloning of a receptor for murine granulocyte colony-
 stimulating factor.";
 RL Cell 61:341-350(1990).
 RN [2]
 RP STRUCTURE BY NMR OF 225-333;
 RX MEDLINE=9731327; PubMed=9187659;
 RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
 RT Solution structure of an extracellular domain containing the MSXMS
 motif of the granulocyte colony-stimulating factor receptor and its
 interaction with ligand.";
 RL Nat. Struct. Biol. 4:498-504(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
 CC ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
 CC THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M58288; AAA37673.1;
 DR PIR: A34898; A34898.
 DR PDB: 1GCF; 22-OCT-97.
 DR PDB: 1CTO; 22-OCT-97.
 DR MGD: MGI:1339755; C6131.
 DR InterPro: IPR002996; CRIA.

DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam: PFO0041; fn3; 3.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 KW Repeat; 3d-structure.
 FT SIGNAL 1 25
 FT CHAIN 26 837
 FT
 FT DOMAIN 26 626
 FT TRANSMEM 627 650
 FT DOMAIN 651 837
 FT DOMAIN 26 118
 FT DOMAIN 122 228
 FT DOMAIN 229 333
 FT DOMAIN 334 431
 FT DOMAIN 432 528
 FT DOMAIN 529 624
 FT DISULFID 132 143
 FT DISULFID 249 296
 FT DISULFID 267 310
 FT CARBOHYD 51 51
 FT CARBOHYD 94 94
 FT CARBOHYD 129 129
 FT CARBOHYD 166 186
 FT CARBOHYD 279 279
 FT CARBOHYD 392 392
 FT CARBOHYD 408 408
 FT CARBOHYD 474 474
 FT CARBOHYD 487 487
 FT CARBOHYD 582 582
 FT CARBOHYD 613 613
 SO SEQUENCE 837 AA; 93406 MW; 42295989E2C8531 CRC64;

Query Match 5.0%; Score 313; DB 1; Length 837;
 Best Local Similarity 20.0%; Pred. No. 2e-13;
 Matches 183; Conservative 125; Mismatches 311; Indels 298; Gaps 40;

QY 337 PKILTVGSNNVSPHC-IYKKNKIYPSKEIYMMNMLAEKIQSOQDVVSD--HNSKVF 393
 DB 33 PP--VRLDDPYLVASCTISPNCSKIDQAKILRLQDEPTQGDQNHLLPDTQSLTL 90
 QY 394 FILNETKPRGKFTY-----DAVCCNEHECHRYAEVLIVDININISCTDGYLTMTK 447
 DB 91 PLHNTQ---ALFCVLVPEDESVQLDAQELHAGRPRA-----SPNLSGLMLHTNLSVC 143
 QY 448 RNSTSTIOSLAESTQLRYHSSLYCSDIPIPISEPKCYLQSDGFEYCIPO- 502
 DB 144 QWEPGETHLPTSF-I-LKSFRR-----ADCOYQGDIPDCVAKRRONNC 187
 QY 503 -----IFLSGYTWIRIRNHSLSGLSDSPPTCVLDPSVYKPLPSSVYAEIINTI----- 551
 DB 188 STPRNNLLIYOYMAIWOVENMLGSESPKICLDLPDQVVKLEPMLQALDIPDVVSHOP 247
 QY 552 GLIKTISMEKPPVPPENNL--QFOIRYGLSGEYQMKYEVYDAKSVSLPVDLCA----- 605
 DB 248 GCLMLSM-KPMKPSRYMECEELKRPQOLKGNMVL--VFHLPSKDOF--ELGGLHQA 301
 QY 606 -YVAVQVQCKRLDGLGYSNWSNPATVYVMDIKVPMRGPEFMRITNGTKKK- 658
 DB 302 PYVTIOMRCIRSSLPQFNSPMS-PG---LQLRPTMKAP---TIRLDTWCKQLDPGT 352
 QY 659 -NYTLIMKPLMNDLSICSVQRYVINHHNS-----CNGTWSDDVGNHRTFTLMTDQ 708
 DB 353 VSVOLFMRKFTPLQEDSGOIGYLLSMNSPDHOGODIHLNLT-----QLSCIFLPS 405
 QY 709 AHTVTVLAINSIGASVANPNLFESWPMKVNIVOSLSAYPLNNSCVIYSM--ILSPSDY 765
 DB 406 AONTLVAVANKAGTSSPT---TVFLENBGRVYTGILHMAQDLNITWDMKPSLLPOCY 462
 QY 766 KLMYFLIEMK---NLNDEGEIKMLRISSSVKYYIHDHFIPIEKYQPSLYPIFMEGVGK 821

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Db 463 -----LIEEMSSPSYNNSSYKMWLEPNCNTGILKLNINFPOLRYTVAELYGIQIP 517
OY 822 PKINSFT----- 829
Db 518 PNVVTFPAGERAPPAALHLKVGSTMAOLEWVPEARLGMPLTHYTFIWDAGDHSF 577
OY 830 -----ODDIEKHQSDAGLY-----VIVPV 848
Db 578 SVTLNISLHDFVLKLEPASYLHYIYLMATSRAGSTNGTLRTLPDSDNLIFGLICLV 637
OY 849 IISSTILLGTLILSHQMKLFMEDVPRPKMSNAQGINPKPFFELFKHIAASYVC 908
Db 638 LLSTTCVV--TWLCKCKRKRTSFMDSVDPDPAHSSLSWL----- 674
OY 909 GLLLEPETISDIDSVNKMKNDEMPYVLSLSTPDEKGSVCIS--DQNSVNES-- 965
Db 675 -PTIMEET-----FOLPSW-----DSSVPSIRKITELEDKPKTHWDSSESGNSGLP 722
OY 966 -----EAGETEVYEDESQOROPVYKAYALLINSKPSGTGEE-----Q 1002
Db 723 ALVQAVVLQGDREIS--NOSOP-----PSRTGDQVLYGVLESPTSQVW 766
OY 1003 GLINSVTKCFSSKNSPLKDSFNSWEIEAQAFLISQHN-----IISPHLFS-- 1054
Db 767 QYIRSDSTOPLIGPFPSPKSTENIMFHSRQETIV--POPNOEDDCVGFPPDFLEFO 824
OY 1055 -----EGDELKLEGNF 1067
Db 825 GLVHGVGE-----QCGF 837

RESULT 8
LIFR_HUMAN STANDARD; PRT: 1097 AA.
AC P42702;
ID LIFR_HUMAN
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukemia inhibitory factor receptor precursor (LIF-R).
GN LIFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA MEDLINE=92007727; PubMed=1915266;
RA Geating D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.B.,
RA King J., Price V., Cosman D., Beckmann M.P.;
RA "Leukemia inhibitory factor receptor is structurally related to the
RA IL-6 signal transducer, gp130."
RA EMBO J. 10:2839-2848(1991).
RT LIFR.
RL EMBL J. 10:2839-2848(1991).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
CC MEMBRANE-BOUND AND A SECRETED FORM.
CC -1- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
CC MAY ARISE BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL: X61615; CAA43805.1;
DR MIM: 151443;
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
DR Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KV Alternative splicing: Repeat.
FT SIGNAL 1 44
FT CHAIN 45 1097
FT DOMAIN 45 833
FT TRANSMEM 834 858
FT DOMAIN 859 1097
FT DISULFID 55 65
FT CARBOHYD 64 64
FT CARBOHYD 85 85
FT CARBOHYD 131 131
FT CARBOHYD 143 143
FT CARBOHYD 191 191
FT CARBOHYD 243 243
FT CARBOHYD 303 303
FT CARBOHYD 390 390
FT CARBOHYD 407 407
FT CARBOHYD 426 426
FT CARBOHYD 445 445
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FT CARBOHYD 572 572
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FT CARBOHYD 729 729
FT CARBOHYD 787 787
SQ SEQUENCE 1097 AA; 123742 MW; C8602897E359FCE5 CRC64;

Query Match 4.7%; Score 294.5; DB 1; Length 1097;
Best Local Similarity 19.2%; Pred. No. 5.3e-12;
Matches 215; Conservative 179; Mismatches 385; Indels 339; Gaps 52;

OY 161 LLYVLEPELSDPLVPQKSGFQVHC-----NCS-----VHECC----- 194
Db 35 LLYIMQVNSQ-----KKGAPHLKCVTNLQVNMQSWKAPSGISRGTDYEVCIENRSRS 89
OY 195 -----ECVYVPRPAKNTDILMLCKITSGVIFQSLMVSQPLNHVKKRPPLGIMHEIR 248
Db 90 CYOLEKTSIKIRPALSHGDEYITINSLHDFGSSSTKFTLNEQVSLI--PDTPETILNSADF 148
OY 249 DDGNLKISWSPPLVFPFLQYOVKYSSENSTYAIR-----EADKIVSAVSLI----- 294
Db 149 SSTSLYLAKNNDGSAV--FPIRNSVW----EIKYLKRSMLVLYVTHNTLNKDTLHMS 204
OY 295 --VDSLPGSSSEYQVVR-----GKRLDGPQISWDSSTPRVFT--TQDYVIFPKKILTSVG 345
Db 205 WASMDPLECAIHFEVETRCIDMLHFSGLEMSWSPVKNISWIPQSVYVFPQDKYILWG 264
OY 346 SWSFPCIKKKNKIKVPSKEIYMMMLAKIPQSOVDV--SDIVSKYTFPFLNLTNR 402
Db 265 SDITFCV-----SQEKV-----LSALIGHTNCPPLHLDGEVNA--IKRINISVAS 310
OY 403 GFETDAVVCNHEHCNHRAYELVYDVININSCETDGLTKMTCWSTSTQSLA---E 459
Db 311 GF---NVVFTEDNIFGYIYFAGYPPDPQOLNCEHD--LKEILCSNNGRTALVGPRA 366
OY 460 STQLQRYHRSLSYCDSPISHPIDSEPKDQYLOSDFGYECIFOPITLISGYTMIRINSL 519
Db 367 TSYTLVESPSGKYVRUKRAEAPTNES-----YQLFQMDPQDIEYNTLVNAHNL 416
OY 520 GUSDPTVPLVDSVYKPLPPSSVKAELTINIGLKISERK-----VFPPN 566

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Db 417 GRSQSTILVNITEKY-PHTPTISFKVK-DINSTAVKLMSHLPEGNKINFLCEIEIKKS 474
Qy 567 MLOFOIYRGISGEVQMKWEYVDASKSVSLPVDLCAYAVQVCRKRLDGLGYSNMS 626
Db 475 SVGEQKNVITIKGE-----NSSYLALDKLNPLYLTYFRICS-TEFFMKSKMS 523
Qy 627 NPATYVMDIKVMPGPEPMRIINGDTMKKEKNVTLKPLMKNDLSGVQRYVINHHHS 686
Db 524 NKKQHLITTEAS-PSKGPDMREMSD-----GKNLIYMPDLPINEA-----NGKILSYNVS 574
Qy 687 CNG-----TWSEDSVGHNTKFTPLWTEQAHVTVYLAINSIGASVANLTFSPMSVNVY 741
Db 575 CSSEDETQSISEIPDQHKATRLDNDYIISVAAVNSVSSPEPSIASMEIPNDLKTIE 634
Qy 742 QSLSAVPLNSSCYIVSMILSPS---DYKLMEFLIEKN-LNEDGRIKWLRI-SSSVKRY 795
Db 635 QVVGW-----GKILLTMVHDPNNTCDY-----YIKMCSRSRSPCLMDRKVPSNTEIV 685
Qy 796 YIHDHPIPLEKIOFSLYPIFMES-----VG-----KKRIINSFTQDD----- 832
Db 686 IESDEFRPGIRYNFELYCGRNQGYQLRSMIGYIELLADIVAPNPTVEDSADSLVKWE 745
Qy 833 -----IEKHSD----- 839
Db 746 DIPVEELRGLRGYLFYFGKGERDTSKMYLSEGRSDIKVKNITDISQKTLRIADLGKT 805
Qy 840 -----AGLYVI-----VPYIISSSILLTLLISHR-M 867
Db 806 SYHLVRAVATDGVGPEKMYVTVTKENSVGLIAILIPAAVAVIGVAVSILCYRRREMI 865
Qy 868 KILFEDVNPKNKCSWAQGLNFOK-----PEPFEHLFIKHTASVTCGPIL 912
Db 866 KEFFYEDINPENC---KALQFKSVCEGSSALKTELEMPCTPNNEVELETSASF--PKI 920
Qy 913 LEPETSEDSIVDTSMKNDEMPTVYSLSTDLKESVC---ISDQFNVSNESEAG 969
Db 921 EDIEIIS---PAEREDSDAPEENHVV-----SYCPPIIEEIPNPADEAG 968
Qy 970 T-EVYTED-ESORQPEVKYATILSNKPSBETGEQGL-----INSSVTKCFE- 1014
Db 969 TAQVITIVQSMOP-----QAKPEDEQNDPVGAGYKRPQMHPLINSTVEDIAE 1019
Qy 1015 -----SKNSPLKDSFSSNMELEAOFILSDQHNITSP 1049
Db 1020 EDLDKTAGYRPOANVTW-----NLVSP 1042

```

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RC TISSUE-Placenta;
RA MEDLINE-91062348; PubMed-1701053;
RX Fukushima R., Seto Y., Mizushima S., Nagata S.;
RT "Three different mRNAs encoding human granulocyte colony-stimulating
factor receptor";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-92091782; PubMed-1530796;
RA Seto Y., Fukushima R., Nagata S.;
RT "Chromosomal gene organization of the human granulocyte colony-
stimulating factor receptor";
RL J. Immunol. 148:259-266(1992).
RN [4]
RP DOMAINS STRUCTURE.
RX MEDLINE-92007729; PubMed-1717255;
RA Fukushima R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;
RT "Functional domains of the granulocyte colony-stimulating factor
receptor";
RL EMBO J. 10:2855-2865(1991).
RN [5]
RP STRUCTURE BY NMR OF 227-334.
RX MEDLINE-97331327; PubMed-9187659;
RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
RT "Solution structure of an extracellular domain containing the WSXWS
motif of the granulocyte colony-stimulating factor receptor and its
interaction with ligand";
RL Nat. Struct. Biol. 4:498-503(1997).
RN [6]
RP 3D-STRUCTURE MODELING OF 125-331.
RX MEDLINE-98037802; PubMed-9368043;
RA Layton J.E., Iaria J., Smith D.K., Treutlein H.R.;
RT "Identification of a ligand-binding site on the granulocyte colony-
stimulating factor receptor by molecular modeling and mutagenesis";
RL J. Biol. Chem. 272:29735-29741(1997).
CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
EVENTS AT THE CELL SURFACE.
CC -1- SUBUNIT: DIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,
WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
OF THE RECEPTOR.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; GCSFR-1 (SHOWN HERE),
GCSFR-2, GCSFR-3 AND GCSFR-4/D7; SEEM TO BE PRODUCED BY
ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
CC THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
CC -1- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME;
ALSO KNOWN AS SEVERE CONGENITAL NEUTROPHILIA (SCN).
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD114 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".
CC
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CC
DR EMBL, X55721; CA39253.1; -
DR EMBL, X55720; CA39252.1; -
DR EMBL, S71484; AA20660.1; -
DR EMBL, M59818; AA63176.1; -
DR EMBL, M59819; AA63177.1; -
DR EMBL, M59820; AA63178.1; -
DR PIR, JH0329; JH0329.

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RT "Three different cDNAs encoding mouse D-factor/LIF receptor".
 RL J. Blochem. 115:557-562(1994).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
 CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
 CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
 CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
 CC MEMBRANE-BOUND AND A SECRETED FORM.
 CC -1- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
 CC MAY ARISE BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN,
 CC AND EMBRIS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF
 CC THE SECRETED FORM.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@sdb.ch).
 CC -----
 CC EMBL: S73496; AAC60698.1; -
 CC DR EMBL: S73495; AAC60697.1; -
 CC DR EMBL: D26177; BAA05165.1; -
 CC DR EMBL: D17444; BAA04258.1; -
 CC MGD: MGI:96788; 11ft.
 CC InterPro: IPR002996; CRIA.
 CC InterPro: IPR003961; FN_III.
 CC DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 CC Pfam: PF00041; fn3; 4.
 CC DR SMART: SM00060; FN3; 3.
 CC DR PROSITE: PS01553; HEMATOPO_REC_L_F2; 1.
 CC KM Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 CC Alternative splicing; Repeat.
 CC KW SIGNAL. 1 43
 CC FT CHAIN 44 1092 LEUKEMIA INHIBITORY FACTOR RECEPTOR.
 CC FT DOMAIN 44 828 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 829 853 POTENTIAL.
 CC FT DOMAIN 854 1092 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 53 63 BY SIMILARITY.
 CC FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 567 567 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 647 647 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 658 658 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 724 724 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 782 782 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARPSPIC 718 719 AP -> EA (IN SECRETED ISOFORM).
 CC FT VARPSPIC 720 1092 MISSING (IN SECRETED ISOFORM).
 CC SEQUENCE 1092 AA; 122573 MW; 6F02B8C8E154DE70 CRC64;

Query Match 4.5%; Score 281.5; DB 1; Length 1092;
 Best Local Similarity 18.8%; Pred. NO. 4e-11;
 Matches 217; Conservative 177; Mismatches 392; Indels 371; Gaps 57;

Qy 178 KGSFQVHCNCVHECCCELVFVPP-----TAK---LNDTLLMC--LKITSQGVTFOSP- 225
 Db 45 KRGVDDLCCTNNMRYMCTWPAFLGVSBGYKDKICIDRFHSCAPLETINVKIPALSPG 104

Qy 226 -----LMSVDPINNVKPPPLGLHMETDD--(N)KISWSS-PLVPF 265
 Db 105 DHEVITINLVNGFSQKFTLNKENVSLPEPEL---LDLSADFTSLILKMDRBSALPH 161
 Qy 266 P--LQYQVKSNSYTVREADKIVSATSLL-----VSIJLPGSSVEYQVNGK 311
 Db 162 PNAATWEIKVLONPRT---EPVALVLTMLTSLGKDTVOHMWNTSPLPLOCATHSVIRW- 217
 Qy 312 RLDGGI-----WMSWSPRYVT---TQDVIFPPKILTSVSN/SPICIKKKEKIVY 363
 Db 218 HDSPHFSQYKMSDMSPLKINISWIRNTEVNFPODKVYLAOSNHTTCC-----MSFT 270
 Qy 364 KEIVWMM-NIAEKIQSOQYDVSDHVSQVTFEPLNETKPRGK---TVDAVYCCNEHC 418
 Db 271 KVLSQLIGNTLAPLHLVGGQYVAIH-----LNVFSENSGNITETDDV----- 317
 Qy 419 HIRYAEI---YVIDVINISCTEDGYLTKMCRNSTISQSL---AESL----- 462
 Db 318 ---YGTVFAGYPPDPVKLSCTETHD-LKEIICSNPGRITGLVGRKTEYLFPSISGK 373
 Qy 463 QLRHYR-----SLKCSDPISHPISSEPCDYLOSGDFECIFQPLFLLSGYTMIRIH 517
 Db 374 SAVFHRIGELTYETRLGV-QMHPQGEIHN-----TLLTG-----RN 409
 Qy 518 SLGSLDSEPTCYLPDSYVKKPLPPSSVKAETITIGLKI SWKP-VPPENMLQFOIRYGL 576
 Db 410 PLGQASAVAVINWTERVA-PHDPTSLKVK-DINSYVFESWYLPNFIRKINLLQIEICK 467
 Qy 577 SGKEVQMKMYEYDAKSKSVSLPYVDL--CANYANOVCKRLDGJAGYSNMSNRPATYVM 634
 Db 468 ANSKKEVRNATIRGAEDSYHAADVKLNPYATYTRVRCSS-KTFWKMSRWSDERHLLTT 526
 Qy 635 DIKVMRGPPEFRIINGCTMKKEKNVTLMKNDKISQVQVIVIHHTSCNGTMSGD 694
 Db 527 E-ATSKGPDTRKREMSD---GRNLIYWKRLPINEA---NGKILSYNCS----- 571
 Qy 695 VGNHTKFFFLMTQAH-----TVYVLAINSQASVANFHTSPWPKYNIQVS 743
 Db 572 LNEETQSVLEFPDQHRAEIQLSKNDYIISVARSAGSSPSKIASMEIPDDITVEQA 631
 Qy 744 LSAYFLNSSCVIVSWILSPS---DYKLMVFTEEMKN--LNEDEGLKVLRI-SSSKYKYYI 797
 Db 632 VGL---GNRIFLTWRHDPNMTCDY---YKMCNSSRSECLMDWKKVPBSNSTEYIE 682
 Qy 798 HDHFTPIRKYQSLPIPMEG-----VG-----KPKILNSFTQDD----- 832
 Db 683 SDQFQPGVRYNLYLGCINGQLLRSLIIGYEELAPVAPNFTVEQTSADSIYKMDI 742
 Qy 833 -----TEKHQSDAGL----- 842
 Db 743 PVEELRGFLRGYLFQKGERDTPKTRSLRPHHSIDIKLNITDISQKLRADLOGKTSY 802
 Qy 843 -----YVIVPVYISSIILLGTLISHQK--KK 869
 Db 803 HLIVRAYHGLGPEKSMFVYTKENSGLLITLIPVAVAVYGVVISILCYRRKREWKE 862
 Qy 870 LFMEDVPKPKNSAAGLNQKPETFEHLFIKHTASVYCGPLLEPETISEDIVDSWK 929
 Db 863 TFFPIRPNENC---KALQFOKSVCEGSNALKTELMNCTP-----NNVEYLESRS 910
 Qy 930 NKDEMPPTVVSLLSTDLEKGSV-----CISQFQSVNFSEMEG--TEVYIE 975
 Db 911 IVPKIEDETEIISVAPERGERSEVDPENHVAVSYCPRIIEEITNPADADEGASQVYVI 970
 Qy 976 D-ESQROPFVRYATLISKRSPEGEQGLINSSVTKCFSSKNSPLKQSFSSSWELDAQ 1034
 Db 971 DVQSKTYQOAK-----AEEEDV-----DPV----- 991
 Qy 1035 AFFIISDQHPNI---ISPHLTFSEGLDELRLKLEGNPEENDKKSIIYLVGYTSIKKRESG 1091
 Db 992 ---VAGYKKPQMRPLPISRAVEDTAADEDEGKTAGYRQGANNTYNNL-----VSPSPRS- 1042
 Qy 1092 VLLTDKSRVSCPPFAPC 1108

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DR Proactin receptor precursor (PRL-R).
 GN PRLR.
 OS Columba livia (Domestic pigeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Columbiformes; Columidae;
 OX NCBI_TaxID=8932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Crossed;
 RX MEDLINE=94283267; PubMed=7516866;
 RA Chen X., Horseman N.D.;
 RT "Cloning, expression, and mutational analysis of the pigeon prolactin
 receptor".
 RL Endocrinology 135:269-276(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 or send an email to license@sdb.ch).
 CC -----
 DR EMBL: U07684; AAA20646.1; -.
 DR HSP: P16471; I893.
 DR InterPro: IPR002996; CRA1.
 DR InterPro: IPR003561; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 4.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 KW SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT TRANSMEM 440 460
 FT DOMAIN 461 830
 FT DOMAIN 25 122
 FT DOMAIN 123 226
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316
 FT CARBOHYD 336 336
 SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69EFP CAC64;
 Query Match 3.5%; Score 220; DB 1; Length 830;
 Best Local Similarity 20.8%; Pred. No. 3.9e-07;
 Matches 165; Conservative 126; Mismatches 308; Indels 194; Gaps 37;
 QY 476 IPSHIPSEPKCYLQSGFYECIFQPIPLLSG-----YTMIRINSL 519
 DB 56 LPTNTLYLRSKD---SEETIEEC---PDYMGSGPSCYFDKHTNTPMTTYNTYVAMNEI 109
 QY 320 GSLDSPCYLPDSVVKLPFP--SSVKAETINIGLLKISWEKVPFPE-----NNLQROI 572
 DB 110 GSNSSDPQIVDTSTVQDPAPVNLSETKTSASTYLLAKMSPPPLADVTSNSHYREL 169

QY 573 RYGLSGKEYOMKMYEYDASKSVSLPVPDLCAV-----YAVQRCRKLGLGYMSN 624
 DB 170 RLKPEKE-EM-----ETVSQVQTOYKKVRLRAGAVVYQVCHV-LD-IGEMSE 216
 QY 625 WSNPAYTYVMIDIKVPMRGDEFRRIINGDTMKKEKNVTLMPKMNDSLCVSQRYVINHH 684
 DB 217 WSSERHIIHPNESP---PEKPTIIRKCSPEKE-TFTCMWKP----- 254
 QY 685 TSCNCTWSESDVGNHNTKFTFLMTEQA-----HT-----YTV 714
 DB 255 -----GSDGHPYVNTYLLSKBEEERYECPOYKTLGPNSCYDKKHTSFWTYITV 307
 QY 715 IAINSIGASVAN---FNLFSPWMS-KVNIYOSLAPLNSSCVIVSWLSP-SDYKIMY 769
 DB 308 KATNEIGSNVSDPLVDVTVYQVDPVNVTELLKTYNRKRYLVLTWSPPLADVRSGM 367
 QY 770 FTIEBK-NINDEGELIKWLRISSVAKKYYIHDFTIEKYOFSLYIEHGCKPKIINSF 828
 DB 368 LTLDELRLKPEAEEMETIFEGQOTHYKMSFLNPKRYVOIH-----CKPDHGSW 420
 QY 829 TODDIEKHQ-----SDAGLYIVPVYIISSTILLG-TLISHQHKKLFMEDVPMPK 879
 DB 421 SEMSLEKTLQIPTDRIDKQMVMTIVGVLSLCLVMSWTMYLKGTYKMAFLPPVPGPK 480
 QY 880 NCSMAQGNFQKPEFFE-----HLFIKHTASVTCGPLLDPETI--SEDISVDT 927
 DB 481 ---IKGIDTHLEETLKGSEBELLALGCHGF--PTSDCELLIYLVEDSEDOQLMPS 533
 QY 928 WKNKDEMPPTVYVSLSTLTDLEKSGVCISDQFNSVNEFEATEVTYDESGRQFVYKA 987
 DB 534 HDNGHPSKNNAKVIKAKETSDSGRS-CDSPSLSKRESRALISTLTQDIR----- 585
 QY 988 TLISNKSKEGEEGGLINSVTKCFSSKNSPLKDFSNSSWEIACQAFILSDQHPMI 1047
 DB 586 -----DVQENNGRHHWE-TQCIASEQKTL--LFNNESKSPIWPAQLPDQPMF 633
 QY 1048 SPHLTFSSGLDELKLEGNFPE--ENNDRKSIYLVGTST-----KKRESGVLL--TDK 1097
 DB 634 AYHSTVDVHKITLCTIDVNIAPVLVENEHQPOYPIRETVADNMEKREVENLTSKTDQ 693
 QY 1098 SRV-----SCPEFAPCLETDI---RYLQDS-CSHFVENNINLGTSSKTFPSYMPQ 1144
 DB 694 TTVQVQKNRPNDKSPFSKPLMDYVEHKVRODEVAVALLKHKEHSGKIEKTYPGTSKE 753
 DB 754 YTKVSTVVDHNL 766
 RESULT 13
 ID 112S.MOUSE STANDARD; PRT: 874 AA.
 AC P97378;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-
 2) (IL-12R-beta2).
 GN IL12RB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97098510; PubMed=8943050;
 RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
 RA Gately M.K., Gubler U.;
 RT "A functional interleukin 12 receptor complex is composed of two
 beta-type cytokine receptor subunits".
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A

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CC LOW AFFINITY.
CC -1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U64199; AAB36676.1;
DR HSSP: P40189; 1B0U.
DR MGD: MGI:1270861; 1112rb2.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 4.
DR PRINTS: PR00014; RNTYPEIII.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS001353; HEMATOPO_REC_L_F2; 1.
DR Receptor: Transmembrane; Glycoprotein; Signal; Repeat.
DR SIGNAL: 1 20 INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.
FT CHAIN 21 874 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 21 639 POTENTIAL.
FT DOMAIN 640 636 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 657 874 FIBRONECTIN TYPE-III 1.
FT DOMAIN 137 230 FIBRONECTIN TYPE-III 2.
FT DOMAIN 240 322 FIBRONECTIN TYPE-III 3.
FT DOMAIN 436 523 FIBRONECTIN TYPE-III 4.
FT DOMAIN 534 622 FIBRONECTIN TYPE-III 4.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 874 AA; 98196 MW; 582EAD21BF1BD67 CRC64;
Query Match 3.58; Score 220; DB 1; Length 874;
Best Local Similarity 20.38; Pred. No. 4.2e-07;
Matches 166; Conservative 95; Mismatches 286; Indels 270; Gaps 42;

```

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OY 650 NGDTKKKKNVTLTKPLMKNDLSGVORYINHTSCNGTWSEVGNHKTFTLMTF-- 707
D 347 KODIDYDROQIISLFWKSNINSEARGKILHYQVTLQEVTKTKTIACTHTHTS---WTRVI 402
OY 708 ---QAHVTYLAISIGSVANFNLTFSMPMSKVIV-----QSLAVPLINSSCV 754
D 403 PRFGMTASVSANSGASAP-----THNIVDLCTGLLAHQVSKSENMDNI 452
OY 755 IVSWTILSP---SDYKLMFIEMKLNEDGET---KMLR-----ISSYKRYI 797
D 453 LVTW---QPPKADSNVREIYEMRL-QPGSTTKPPHMLRPPDNNSALLISENKPIC 509
OY 798 HD-----HEPII-----ERYQ----- 808
D 510 YEIRVHALSESQGCSSIRGDSKHKAPVSPHITAITEKERELFSTHTHPPEQRCIL 569
OY 809 -FSLYPIRMEVGKRII-----NSFTQDDIEKH----- 836
D 570 HYRIYKRESDTAQPELCEIQRSONSHPISSLOPRVYVLMKTVAVTAGESPOGNERE 629
OY 837 ---QSDAGLYVIVPIYISSILLGLTLLISHQRMK-----KLEW---EDVPNKNCSW 883
D 630 FCPQKAMMKAFVISSICIAITVGTSTIRYRQAKFTLLSLKIQVYSRTIPDPANSTW 689
OY 884 AGLNFKQPEFTEHLLFKHTASVTCGPLLEPETISEDIVDTSKKNKDEMMPTTVSIL 943
D 690 VK-----KY-----PILEKIQLPDQ-NLIMAMPPEEPPLIIEVL 726
OY 944 -----STPDEKGVCSISQPFNSVNSEGEVTEYEDDSQOP 982
D 727 YHMPVVRQPYFRKRGQFGYSTKQDAMYIANQATQTITAEIRQLVNIYKVLSESDP 786
OY 983 FVKYATLIS-----NSKPESETGEGLINSYVKCFSSKNSPKUSFSNSMEIEAQ- 1034
D 787 DSKLANLSPLTIVTVNVLPS---HEGVLPSNIDLSPEHEDP-----IDSPFLQHQ 836
OY 1035 ---AFFILSDQHPNII-SPHLTFSE---GLDELLKLE 1064
D 837 ISLSIFASSSLRPLIFGGERLTLRLKMGYSLMSNE 873

```

RESULT 14

PRLR_CHICK STANDARD; PRT: 831 AA.

AC 004594;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Prolactin receptor precursor (PRL-R) (cPRLP).

GN PRLR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OK NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WHITE LEGHORN; TISSUE=Kidney;

RC MEDLINE=93075121; PubMed=1445292;

RA Tanaka M., Maeda K., Okubo T., Nakashima K.;

RT "Double antenna structure of chicken prolactin receptor deduced from

RT the cDNA sequence."

RL Biochem. Biophys. Res. Commun. 188:490-496(1992).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

CC PROLACTIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -----

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CC or send an email to license@sib-sib.ch).

CC EMBL: D13154; BAA02439.1; -
DR PIR: J01655; J01655.
DR HSRP: P14787; IAN3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR SMART: SM00041; tn3; 4.
DR Prosite: PS01352; Hematopo_REC_L_F1; 1.
DR Receptor: Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 438 PROLACTIN RECEPTOR.
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 439 459 POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94102 MW; 104E75791DCADBE9 CRC64;

Query Match 3.3%; Score 209.5; DB 1; Length 831;
Best Local Similarity 20.4%; Pred. No. 2e-06;
Matches 174; Conservative 127; Mismatches 291; Indels 263; Gaps 46;

OY 476 IPSHIPSEPKDCYLOSDFECIFOPIFLLSG-----YIMWIRINSL 519
DB 56 IPTNTLFYSKD---SESEIYEC---PDRTSGPNSCYFNKNHTSPMTFNITVATNEI 109
OY 520 GSLDPPPCVLPDSYVKKPLPSSVKAET--TINIGLKISMKKPYRPE---NNL-QFOIR 573
DB 110 GSNSSDPQVVDVTSIVQPSFVNLLETRKRSANIMYLAKWSPPLADASSNHLHYELR 169
OY 574 YGLSGEYQWKKMEYVYDAKSKSVSLPVDLCAV-----YAVQVRCKRLDGLGYWSNM 625
DB 170 IKPEKE-EM-----ETISYGVOTQCKINLNLMGMRVYVQRC-TLDP-GENSEM 216
OY 636 SNPATVVMADIKVPMRGEFWRITNGDTMKKEKNVTLMLKPLKNDLSLCSQVRYVINHT 685
DB 217 SSERHILIPSGSP---PEKPTIICRSPEKE-TFTCWMKPKLDG-----GAPT 261
OY 666 SCNGWSD-----VGNHT-----KFTFLWTEQAHITYVALNISTGASVAN- 726
DB 262 NTLTLLSYEGEBOYECPDYRTAGPNSCYFPKKTHTSEWT--IYNTVATNEMGSSNSDP 319
OY 727 --FNLTF--SWPMKVINIQTSLAYPLN--SSCVIYSMILSP--SDYLMWFIEM--KNLNE 779
DB 320 HYVDVTIYQDPFVNVNLELKK-PINKKPYLVLTWSPPLADVNSGULTLEYELRLKPE 378
OY 780 DGEIMLRISSSVKKYVYIHDHPIREKYOFSLYIFMEGVGPKLIINSFTODIEKH--- 836
DB 379 EGE-EMETIFEGQOTQYKMFSLNPKKTYIQH-----CKPDHGSMSSESSNYIOI 430
OY 837 -----QSAGLYVIVPYLISSILILG--TLISHORAKKLWEDVPRNKNCSMAOGLNFQ 890
DB 431 PNDPRVKMDIWMIVGLVGLISLCLIMSWTNVLKGYRMITFMLPVPGRK-----IKGIDTH 486

OY 891 KPEI-----FEHLFIKH-----TASYT- 907
DB 487 LLETFKSEELSLALCCHGLPRTSDCEBLLIYELVEDESEDOQLMPSHONGHRSNAKTR 546
OY 908 -----C-GPLL-----EPETISEDIVTSKKNKDEMPPT 938
DB 547 KETDSDSGRSCDSPSLLSSEKRETCALPVLQTOEVDVDEKKAARSMET--QYVASE 604
OY 939 VYSLSTDDLEKGSYCIDQF--NS-----VNFSEAGTEYTYDESOR 980
DB 605 KRALLSNSESAAKSTWPAVQCPNSQPPMPAVHSYDAKHTLTNTNVVAALVDEDEH 664
OY 981 QPFVYATLISNKSSETEGEQGL-----INSYTKCFSSKNSPLKDSFSSNSWEIRAQ 1034
DB 665 QSOCLTFETIPEMKQ--GEMENLHKSKEQTQAQVKQRSNRLPFLAALMDYEVHK- 722
OY 1035 AFFILSDHPNITISHLTPSEGDELKLEGNPEENNDSKY-----YLCVTSIK 1086
DB 723 --VIRQDEPVALKH-----KENSGLIEKYITSGASKETRYKSTVM 762
OY 1087 KRESGVLLTDRSVSCPEPA---PCLFTDIRYLODSCSHFVENNTN-----LG 1131
DB 763 DHNITVLMPD-SRVP-HTPASQEPAKETSQSIQOQO---VEKNASYCLTAPDCKRETG 816
OY 1132 TSSKRTFASYPQFO 1146
DB 817 GSEYMDPSSPMPSFK 831

RESULT 15
PRLR_MELGA STANDARD: PRT: 831 AA.
ID PRLR_MELGA 091094: 091092:
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (PRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney.
RX MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo.";
RL Biol. Reprod. 55:1081-1090(1996).
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE-Ovary;
RA Plets-Ovary;
RL Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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DR EMBL: L76587; AAB01544.1; -
DR EMBL: U22947; AAA75038.1; -

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 06:52:56 ; Search time 96.26 Seconds
(without alignments)
2093.695 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254
Sequence: 1 MTCQKFCVLLHWEFIYIT.....QTCSTQTHKIMNKMDLTV 1165

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6254	100.0	1165	4	Q92921
2	5967	95.4	1163	6	Q9MYL2
3	5941.5	95.0	1194	6	Q9MYL0
4	5269	84.3	1165	6	Q02671
5	4831.5	77.3	958	4	Q92920
6	4826	77.2	896	4	Q92919
7	4819.5	77.1	958	4	Q13592
8	4816	77.0	906	4	Q13593
9	4814	77.0	896	4	Q13594
10	4761.5	76.1	1162	11	Q9QW63
11	4591	73.4	925	6	Q9MYK9
12	4590	73.4	894	6	Q9MYL1
13	3970.5	63.5	848	6	Q9MZS2
14	3729	59.6	895	11	Q62960
15	2790.5	44.6	1147	13	Q9DDK1
16	2775	44.4	1148	13	Q9IBAT

17	2693	43.1	1146	13	Q9IBV6	Q9IBV6 gallus gall
18	1074	17.2	246	11	Q35773	Q35773 rattus norv
19	981.5	15.7	273	11	Q9QWV5	Q9QWV5 mus musculus
20	801	12.8	203	6	Q28604	Q28604 ovis aries
21	683	10.9	161	6	Q28606	Q28606 ovis aries
22	660.5	10.6	173	6	Q9XSN9	Q9XSN9 sus scrofa
23	616	9.8	147	6	Q9S257	Q9S257 sus scrofa
24	588	9.4	152	6	P79115	P79115 bos taurus
25	497	7.9	123	6	Q9N1P9	Q9N1P9 sus scrofa
26	477	7.6	121	6	Q18980	Q18980 bos taurus
27	456	7.3	145	13	Q9IAJ2	Q9IAJ2 gallus gall
28	444	7.1	881	13	Q57519	Q57519 xenopus lae
29	409.5	6.5	918	13	Q9W609	Q9W609 gallus gall
30	366	5.9	102	6	Q9XSH3	Q9XSH3 equus caball
31	354	5.7	710	13	Q57520	Q57520 xenopus lae
32	325	5.2	74	11	Q9ER14	Q9ER14 rattus norv
33	312.5	5.0	1093	11	Q70535	Q70535 rattus norv
34	299	4.8	57	6	Q97778	Q97778 elephas max
35	267	4.3	979	4	Q99650	Q99650 homo sapien
36	251.5	4.0	2302	11	Q88488	Q88488 rattus norv
37	232.5	3.7	970	11	Q88821	Q88821 mus musculus
38	228	3.6	971	11	Q70458	Q70458 mus musculus
39	213	3.4	57	13	Q9QWY8	Q9QWY8 gallus gall
40	213	3.4	861	6	Q9BE62	Q9BE62 bos taurus
41	197	3.1	1598	4	Q9P214	Q9P214 homo sapien
42	195	3.1	6875	6	Q28733	Q28733 oryctolagus
43	191.5	3.0	1114	5	Q9VSG6	Q9VSG6 drosophila
44	189.5	3.0	26926	4	Q10466	Q10466 homo sapien
45	188	3.0	26926	4	Q10466	Q10466 homo sapien

ALIGNMENTS

RESULT 1
ID Q92921 PRELIMINARY; PRT; 1165 AA.
AC Q92921;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96398968; PubMed=8805376;
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RT "A role for leptin and its cognate receptor in hematopoiesis";
RT Curr. Biol. 6:1170-1180(1996).
DR EMBL: U66497; AAB07497.1; -;
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; fn3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602DDA CRC64;

Query Match 100.0%; Score 6254; DB 4; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTCQKFCVLLHWEFIYITARNLSPTIPWPKFSQMPNNTYDFLLPAGLSKTSNS 60
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Db 1 MICQKFCVLLHMEFIYITAFNLSPITPMRFKLSGMPNSTYDFLLPAGLSKNTS 60
QY 61 NGHYETAVPEKFNSSGTHFSNLSKTTFFHCCFRSEODRNCSLADNIEGTFVSTNSLVF 120
Db 61 NGHYETAVPEKFNSSGTHFSNLSKTTFFHCCFRSEODRNCSLADNIEGTFVSTNSLVF 120
QY 121 QOIDANMNIOCMKGLDKLFICYVESLFRNLPFRNYKYVHLVLEPELDESPVPOKS 180
Db 121 QOIDANMNIOCMKGLDKLFICYVESLFRNLPFRNYKYVHLVLEPELDESPVPOKS 180
QY 181 FQMVHNCNSVHRCCECLVVPYPAKINDTLMLCKLITSGGVITQSPPLMSVQPIINMKPDDP 240
Db 181 FQMVHNCNSVHRCCECLVVPYPAKINDTLMLCKLITSGGVITQSPPLMSVQPIINMKPDDP 240
QY 241 LGLHMEITDDGMLKISWSSPPLVPPLOYQVYKSENSSTVIREADKIYATSLVDSTLP 300
Db 241 LGLHMEITDDGMLKISWSSPPLVPPLOYQVYKSENSSTVIREADKIYATSLVDSTLP 300
QY 301 GSSYEYQVGRKRLDGPGLWSMDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEYQVGRKRLDGPGLWSMDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VASKEIYVMMNLAERKIPQSOQDVVSDHVSQVTFENLNKPKGKTFYDAVCCNEHECHH 420
Db 361 VASKEIYVMMNLAERKIPQSOQDVVSDHVSQVTFENLNKPKGKTFYDAVCCNEHECHH 420
QY 421 RYAEIYVIDVINISCEETDGYLTKMCRWSTSTIOSLASTPQLRYHRSLSYCSIDIPSIH 480
Db 421 RYAEIYVIDVINISCEETDGYLTKMCRWSTSTIOSLASTPQLRYHRSLSYCSIDIPSIH 480
QY 481 PISEPDCYLOSDGFECEJFOPIFLLSGTYMIRINHSLGSLDSPPTCYLPDSVYKPLRP 540
Db 481 PISEPDCYLOSDGFECEJFOPIFLLSGTYMIRINHSLGSLDSPPTCYLPDSVYKPLRP 540
QY 541 SSVKAEITINIGLTKISMEKVPFPENNLOFOIRYGLSGKEVOMKMEYDADAKSKSLVP 600
Db 541 SSVKAEITINIGLTKISMEKVPFPENNLOFOIRYGLSGKEVOMKMEYDADAKSKSLVP 600
QY 601 PDLCAVYAVQVBRKRLDGLGYWSNNSNPAYTVMDIKVMRGPPEFRIIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVBRKRLDGLGYWSNNSNPAYTVMDIKVMRGPPEFRIIINGDTMKKEKNV 660
QY 661 TLLMPLKMNDSLCVQRYVINHHTSCNGTSEDVGNHTKFFLWTEQAHYTVLAINSI 720
Db 661 TLLMPLKMNDSLCVQRYVINHHTSCNGTSEDVGNHTKFFLWTEQAHYTVLAINSI 720
QY 721 GASVANFNLTFSMPKSVIYOSLSAYPLNSSCVIYSLTSPSDYKLYMFIEMKLNLD 780
Db 721 GASVANFNLTFSMPKSVIYOSLSAYPLNSSCVIYSLTSPSDYKLYMFIEMKLNLD 780
QY 781 GEIKMLRISSVKKYIYHDFPIEKYQPSLYPIEMEGVGPRIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSVKKYIYHDFPIEKYQPSLYPIEMEGVGPRIINSFTODDIEKHQSDA 840
QY 841 GLYIYVPIYISSILLGLTSLSHQAMKLEWDVNPKNCSMAOGLNFQKPEPTEHLEFI 900
Db 841 GLYIYVPIYISSILLGLTSLSHQAMKLEWDVNPKNCSMAOGLNFQKPEPTEHLEFI 900
QY 901 KHTASVTCPLLEPETISEDIVSTPMKNDKEMPTVAVSLSTDLKGGVCSIDQDN 960
Db 901 KHTASVTCPLLEPETISEDIVSTPMKNDKEMPTVAVSLSTDLKGGVCSIDQDN 960
QY 961 SVNFSAEGETEYTEDESORQPFVYKATLISNSKPSETEEOGLINSVTKCFSSKNSPL 1020
Db 961 SVNFSAEGETEYTEDESORQPFVYKATLISNSKPSETEEOGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEAQAFFILISDQHPNIIISPHLTFSEGLDELKLEGNFPENNDKSIIYL 1080
Db 1021 KDSFNSNSWEIEAQAFFILISDQHPNIIISPHLTFSEGLDELKLEGNFPENNDKSIIYL 1080
QY 1081 GYTSIKKKRSGVLLTDKSKVSCFPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GYTSIKKKRSGVLLTDKSKVSCFPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFFAS 1140

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QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 2
Q9MYL2 PRELIMINARY; PRT: 1163 AA.
AC Q9MYL2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR LONG FORM.
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys."
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF222960; AAF34683.1;
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ
SEQUENCE 1163 AA; 132295 MW; 6B7B89108F51895 CRC64;

Query Match 95.4%; Score 5967; DB 6; Length 1163;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 114; Conservative 18; Mismatches 31; Indels 2; Gaps 1;
QY 1 MICQKFCVLLHMEFIYITAFNLSPITPMRFKLSGMPNSTYDFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHMEFIYITAFNLSPITPMRFKLSGMPNSTYDFLLPAGLSKNTS 60
QY 61 NGHYETAVPEKFNSSGTHFSNLSKTTFFHCCFRSEODRNCSLADNIEGTFVSTNSLVF 120
Db 61 NGHYETAVPEKFNSSGTHFSNLSKTTFFHCCFRSEODRNCSLADNIEGTFVSTNSLVF 120
QY 121 QOIDANMNIOCMKGLDKLFICYVESLFRNLPFRNYKYVHLVLEPELDESPVPOKS 180
Db 121 QOIDANMNIOCMKGLDKLFICYVESLFRNLPFRNYKYVHLVLEPELDESPVPOKS 180
QY 181 FQMVHNCNSVHRCCECLVVPYPAKINDTLMLCKLITSGGVITQSPPLMSVQPIINMKPDDP 240
Db 181 FQMVHNCNSVHRCCECLVVPYPAKINDTLMLCKLITSGGVITQSPPLMSVQPIINMKPDDP 240
QY 241 LGLHMEITDDGMLKISWSSPPLVPPLOYQVYKSENSSTVIREADKIYATSLVDSTLP 300
Db 241 LGLHMEITDDGMLKISWSSPPLVPPLOYQVYKSENSSTVIREADKIYATSLVDSTLP 300
QY 301 GSSYEYQVGRKRLDGPGLWSMDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEYQVGRKRLDGPGLWSMDSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VASKEIYVMMNLAERKIPQSOQDVVSDHVSQVTFENLNKPKGKTFYDAVCCNEHECHH 420
Db 361 VASKEIYVMMNLAERKIPQSOQDVVSDHVSQVTFENLNKPKGKTFYDAVCCNEHECHH 420
QY 421 RYAEIYVIDVINISCEETDGYLTKMCRWSTSTIOSLASTPQLRYHRSLSYCSIDIPSIH 480
Db 421 RYAEIYVIDVINISCEETDGYLTKMCRWSTSTIOSLASTPQLRYHRSLSYCSIDIPSIH 480
QY 481 PISEPDCYLOSDGFECEJFOPIFLLSGTYMIRINHSLGSLDSPPTCYLPDSVYKPLRP 540
Db 481 PISEPDCYLOSDGFECEJFOPIFLLSGTYMIRINHSLGSLDSPPTCYLPDSVYKPLRP 540
QY 541 SSVKAEITINIGLTKISMEKVPFPENNLOFOIRYGLSGKEVOMKMEYDADAKSKSLVP 600
Db 541 SSVKAEITINIGLTKISMEKVPFPENNLOFOIRYGLSGKEVOMKMEYDADAKSKSLVP 600
QY 601 PDLCAVYAVQVBRKRLDGLGYWSNNSNPAYTVMDIKVMRGPPEFRIIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVBRKRLDGLGYWSNNSNPAYTVMDIKVMRGPPEFRIIINGDTMKKEKNV 660
QY 661 TLLMPLKMNDSLCVQRYVINHHTSCNGTSEDVGNHTKFFLWTEQAHYTVLAINSI 720
Db 661 TLLMPLKMNDSLCVQRYVINHHTSCNGTSEDVGNHTKFFLWTEQAHYTVLAINSI 720
QY 721 GASVANFNLTFSMPKSVIYOSLSAYPLNSSCVIYSLTSPSDYKLYMFIEMKLNLD 780
Db 721 GASVANFNLTFSMPKSVIYOSLSAYPLNSSCVIYSLTSPSDYKLYMFIEMKLNLD 780
QY 781 GEIKMLRISSVKKYIYHDFPIEKYQPSLYPIEMEGVGPRIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSVKKYIYHDFPIEKYQPSLYPIEMEGVGPRIINSFTODDIEKHQSDA 840
QY 841 GLYIYVPIYISSILLGLTSLSHQAMKLEWDVNPKNCSMAOGLNFQKPEPTEHLEFI 900
Db 841 GLYIYVPIYISSILLGLTSLSHQAMKLEWDVNPKNCSMAOGLNFQKPEPTEHLEFI 900
QY 901 KHTASVTCPLLEPETISEDIVSTPMKNDKEMPTVAVSLSTDLKGGVCSIDQDN 960
Db 901 KHTASVTCPLLEPETISEDIVSTPMKNDKEMPTVAVSLSTDLKGGVCSIDQDN 960
QY 961 SVNFSAEGETEYTEDESORQPFVYKATLISNSKPSETEEOGLINSVTKCFSSKNSPL 1020
Db 961 SVNFSAEGETEYTEDESORQPFVYKATLISNSKPSETEEOGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEAQAFFILISDQHPNIIISPHLTFSEGLDELKLEGNFPENNDKSIIYL 1080
Db 1021 KDSFNSNSWEIEAQAFFILISDQHPNIIISPHLTFSEGLDELKLEGNFPENNDKSIIYL 1080
QY 1081 GYTSIKKKRSGVLLTDKSKVSCFPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GYTSIKKKRSGVLLTDKSKVSCFPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFFAS 1140

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QY 361 VPSKETVMMNLAETKIPQSDYDVSDHVSQVTFPNINETKPRGKFTYDAVYCCNEHECH 420
 DB 359 VSSKKIVMMNLAETKIPQSDYDVSDHVSQVTFPNINETKPRGKFTYDAVYCCNEHECH 418
 QY 421 RYAEIVIDVNIINISCEITDGLTKMTCRSTSTIOSLAESTIOLRHRSLCSDPSIH 480
 DB 419 RYAEIVIDVNIINISCEITDGLTKMTCRSTSTIOSLAESTIOLRHRSLCSDPSIH 478
 QY 481 PISEPKDYLQSDGFYECEIFQPIFLLSGYTMIRINHSIGSLDSDPPCYLPDSVVKPLDP 540
 DB 479 PISKPRDYLQSDGFYECEIFQPIFLLSGYTMIRINHSIGSLDSDPPCYLPDSVVKPLDP 538
 QY 541 SSVKAEITINIGLTKISWEKPVPEPENNLOFQIRYGLSGKEIOCMKIDYDAKSKSVSLPV 600
 DB 539 SSVKAEITINIGLTKISWEKPVPEPENNLOFQIRYGLSGKEIOCMKIDYDAKSKSVSLPV 598
 QY 601 POLCAVYAVOVCKRDLGIGYWSMNSNPAYVYMDIKVPMRGPEFRIINIGDTMKKEKNV 660
 DB 599 POLCAVYAVOVCKRDLGIGYWSMNSNPAYVYMDIKVPMRGPEFRIINIGDTMKKEKNV 658
 QY 661 TLLMPLMKNDLSQVQRYVINHHSTSCNGTWSGVDGNNHTKFTFLMTEQAHYTVLAINSI 720
 DB 659 TLLMPLMKNDLSQVQRYVINHHSTSCNGTWSGVDGNNHTKFTFLMTEQAHYTVLAINSI 718
 QY 721 GASVANFNITFSMPKSVIVOSLSAYPLNNSCVYLSLSPDKLMTFLIEMKMLNED 780
 DB 719 GASVANFNITFSMPKSVIVOSLSAYPLNNSCVYLSLSPDKLMTFLIEMKMLNED 778
 QY 781 GEIKMLRISSVKKYIYHHTPIEKOFSIPIEMEGGPKIINSFODDTEKHOSDA 840
 DB 779 GEIKMLRISSVKKYIYHHTPIEKOFSIPIEMEGGPKIINSFODDTEKHOSDA 838
 QY 841 GLVIVPVISSISILLGLTLLISHQMKLFEVDYVNPKNCSWAQGLNFOKPEFHELF 900
 DB 839 GLVIVPVISSISILLGLTLLISHQMKLFEVDYVNPKNCSWAQGLNFOKPEFHELF 898
 QY 901 KHTASTGCPPLLEPTIEDISVDTSMKNKDBMPTVYVSLSTLTDLEKGSYCIDQEN 960
 DB 899 KHTASTGCPPLLEPTIEDISVDTSMKNKDBMPTVYVSLSTLTDLEKGSYCIDQEN 958
 QY 961 SSVFSAEGETEYTESOROPFVKATLINSKPSGTEGEOGLINSVTKCCKSSNPL 1020
 DB 959 SSVFSAEGETEYTESOROPFVKATLINSKPSGTEGEOGLINSVTKCCKSSNPL 1018
 QY 1021 KDSFNSSWEIEAQAFILSDQHPNIIISPHLTFSEGLIDELKLEGNPRENNKKSIIYL 1080
 DB 1019 KDSFNSSWEIEAQAFILSDQHPNIIISPHLTFSEGLIDELKLEGNPRENNKKSIIYL 1078
 QY 1081 GYTSIKRSGSVLLTDKRSVCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSŠKKTFS 1140
 DB 1079 GYTSIKRSGSVLLTDKRSVCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSŠKKTFS 1138
 QY 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165
 DB 1139 YMPQFOTCSTQTHKIMENKMDLTIV 1163
 RESULT 3
 Q9MYL0 PRELIMINARY: PRT: 1194 AA.
 AC Q9MYL0: 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update).
 DR LEPTIN RECEPTOR LONG INSERT ISOFORM.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ADIPOSE TISSUE.

RX MEDLINE-98408931; PubMed-9738551;
 RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bockin N.L., Hansen B.C.,
 RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
 expression in the adipose tissue of normal, hyperinsulinemic, and type
 II 2 diabetic rhesus monkeys."
 RN Obes. Res. 6:353-360(1998).
 RP SEQUENCE FROM N.A.
 RC TISSUE=ADIPOSE TISSUE;
 RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bockin N.L., Hansen B.C.,
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF225874; AAF35388.1;
 DR HSSP: P16471; 1B93.
 DR InterPro: IPR002996; CRAA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3_1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 1194 AA; 135824 MW; 76D023E659911AA9 CRC64;

Query Match 95.0%; Score 5941.5; DB 6; Length 1194;
 Best Local Similarity 93.1%; Pred. No. 0;
 Matches 114; Conservative 18; Mismatches 31; Indels 33; Gaps 2;

QY 1 MTCQKCVVLLHMEFTYVITAFNLSPITPWRKLSGMPNNTYDFFLPAGLSKTSNS 60
 DB 1 MTCQKCVVLLHMEFTYVITAFNLSPITPWRKLSGMPNNTYDFFLPAGLSKTSNM 60
 QY 61 NGHYETAPEPKFNSGTHSNLSKTFHCCFSEDRNCSLCAENIEGKTFVSTNSLVE 120
 DB 61 NGHYETAPE--FNSSDTHSNLSKTFHCCFSEDRNCSLCAENIEGKTFVSTNSVVF 118
 QY 121 QOIDANNIQCWLKGLDKLFCVSESLFNKLFENYKYVHLVYLPEVLEDSPLVPOKGS 180
 DB 119 QOQGANNNIQCWLKGLDKLFCVSESLFNKLFENYKYVHLVYLPEVLEDSPLVPOKGS 178
 QY 181 FQVWHNCNSVHECCDELVPVPTAKNDTLLMCKITISGCVTEOSPMSVQPTMMVPRDP 240
 DB 179 FQVWHNCNSVHECCDELVPVPTAKNDTLLMCKITISGCVTEOSPMSVQPTMMVPRDP 238
 QY 241 LGLHMETDGNLKNISMSPPPLVPFLOYOVKXSENSTYVREPAUKIVSATSLVDSIIP 300
 DB 239 LGLHMETDGNLKNISMSPPPLVPFLOYOVKXSENSTYVREPAUKIVSATSLVDSIIP 298
 QY 301 GSSYEVOVRCKRLDGPGLWSDMSTPRVFTTQDYVIEPPKILTSVGSNVSFHCITYKKENKI 360
 DB 299 GSSYEVOVRCKRLDGPGLWSDMSTPRVFTTQDYVIEPPKILTSVGSNVSFHCITYKKENKI 358
 QY 361 VPSKETVMMNLAETKIPQSDYDVSDHVSQVTFPNINETKPRKFTYDAVYCCNEHECH 420
 DB 359 VSSKKIVMMNLAETKIPQSDYDVSDHVSQVTFPNINETKPRKFTYDAVYCCNEHECH 418
 QY 421 RYAEIVIDVNIINISCEITDGLTKMTCRSTSTIOSLAESTIOLRHRSLCSDPSIH 480
 DB 419 RYAEIVIDVNIINISCEITDGLTKMTCRSTSTIOSLAESTIOLRHRSLCSDPSIH 478
 QY 481 PISEPKDYLQSDGFYECEIFQPIFLLSGYTMIRINHSIGSLDSDPPCYLPDSVVKPLDP 540
 DB 479 PISKPRDYLQSDGFYECEIFQPIFLLSGYTMIRINHSIGSLDSDPPCYLPDSVVKPLDP 538
 QY 541 SSVKAEITINIGLTKISWEKPVPEPENNLOFQIRYGLSGKEIOCMKIDYDAKSKSVSLPV 600
 DB 539 SSVKAEITINIGLTKISWEKPVPEPENNLOFQIRYGLSGKEIOCMKIDYDAKSKSVSLPV 598
 QY 601 POLCAVYAVOVCKRDLGIGYWSMNSNPAYVYMDIKVPMRGPEFRIINIGDTMKKEKNV 660
 DB 599 POLCAVYAVOVCKRDLGIGYWSMNSNPAYVYMDIKVPMRGPEFRIINIGDTMKKEKNV 658

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QY 661 TLLMKPLMKNDLSQVORYYINHTSCNGTWSVDGNHTKFTFLMTQAHVTVLAINST 720
DB 659 TLLMKPLMKNDLSQVORYYINHTSCNGTWSVDGNHTKFTFLMTQAHVTVLAINST 718
QY 721 GAVANFNILFSPMKSKVNIYVSLSAVPLNSSCVIYVSLSPDYKLMFTIEMKMLND 780
DB 719 GAVANFNILFSPMKSKVNIYVSLSAVPLNSSCVIYVSLSPDYKLMFTIEMKMLND 778
QY 781 GELMKLRISSSVKKYYIHDFPIEKYOFSLYPIFMEGVGKPKIINSFTQODIERKHQSDA 840
DB 779 GELMKLRISSSVKKYYIHDFPIEKYOFSLYPIFMEGVGKPKIINSFTQODIERKHQSDA 838
QY 841 GLYVIVPVIISSSILLGLTLLISHORMKKLFMEDVDPNPKNSWAGLNFOK----- 891
DB 839 GLYVIVPVIISSSILLGLTLLISHORMKKLFMEDVDPNPKNSWAGLNFOKINGVYMLPR 898
QY 892 -----PEFHEHFIKHTASVTGCPILLPEPTISSEDSIVTSYTSK 929
DB 899 LVUNSOAVIHPRPKVELQETFEHLFIKHTASVTGCPILLPEPTISSEDSIVTSYTSK 958
QY 930 NKDEMPITVVSLLSTTDELEKGSVCISDOFNSVNSEAEGETEYVDESOQROPFVYATL 989
DB 959 NKDEMPITVVSLLSTTDELEKGSVCISDOFNSVNSEAEGETEYVDESOQROPFVYATL 1018
QY 990 ISMSKSEFGEEOGLINSYTKCFSSKNSPLKDSFNSNSWELEAOAFILSDOHPNIIISB 1049
DB 1019 ISMSKSEFGEEOGLINSYTKCFSSKNSPLKDSFNSNSWELEAOAFILSDOHPNIIISB 1078
QY 1050 HLFESGDELKLEGNFPENNNDKSIYLLGTSIKKRESGVLLDKSRVSCPPFAPOC 1109
DB 1079 HLFESGDELKLEGNFPENNNDKSIYLLGTSIKKRESGVLLDKSRVSCPPFAPOC 1138
QY 1110 FDIIRVLQDSCHFEVENNINLGTSKRTFASVYMPQFOTCSTQTHKIMKMDLTIV 1165
DB 1139 FDIIRVLQDSCHFEVENNINLGTSKRTFASVYMPQFOTCSTQTHKIMKMDLTIV 1194

RESULT 4
ID 002671 PRELIMINARY; PRT: 1165 AA.
AC 002671;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR.
GN LEPR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_taxid=9823;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Men T.Y., Lacroix D.A., Ruiz-Cortes Z.T., Song J.H., Palin M.-F.,
RT Murphy B.D.;
RT "Porcine Leptin (Ob) receptor complete coding sequence."
RL Submitted (Sep-1998) to the EMBL/Genbank/DBJ databases.
RN 12
RP SEQUENCE OF 408-470 FROM N.A.
RX MEDLINE=9722487; PubMed=9069130;
RA Ernst C.W., Kapke P.A., Verle M., Rothschild M.F.;
RL Mamm. genome 8:226-226(1997).
DR EMBL; AF092422; AAC61766.1;
DR HSSP; U72070; AAC48707.1;
DR HSSP; P16471; IBB3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

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DR PROSITE; PS01353; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 1165 AA; 132548 MW; 1BB562FEA282F12 CRC64;

Query Match      84.3%; Score 5269; DB 6; Length 1165;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 980; Conservative 73; Mismatches 110; Indels 4; Gaps 4;

QY 1 MIOKRCVLLHHEFTYTAFTNLSPITPMWPKISCMPSNTYVYFLLPAGISKNTSNS 60
DB 1 MTCPEFVALHWEFTYTAFTDLATPTPMKFKISCMPPNTYD-FLLPAGISKNTSL 59
QY 61 NGHYETAVEPKENSSGTHSNL-SKTFHCCFSEEDRNCISLADNIEKTFVSTVNSLV 119
DB 60 NGHDEAVETELINISCTYLSNLSSKTFHCCFSEEDRNCISVHADNIAKAFVSAVNSLV 119
QY 120 FOQIDANNIQCWLKGDLLFCIVYSELKNTLFRRNRYVHLLYLPEVLEDSPLVPQNG 179
DB 120 FOQTGANNNIQCWMKEDLLFCYMESELFKNPFKNIDLVHLLYLLEVLDESPPLVPQNG 179
QY 180 SFQVAVNCNSVHECCCELYPVPTAKLNDTLMLCKITSGVIFQSPFAMSVOPINMYKPP 239
DB 180 SFQSVQNCNSARECCCHVPVSAKNTYLLMLKLTSGGAVFHPFLMSVOPINMYKPP 239
QY 240 PLGLHMETDGGNLKISWSSPPLVPPLOQYVYKSENSTTVIREADKIVSATSLVDSIL 299
DB 240 PLGLHMETDGTNLKISWSSPPLVPPLOQYVYKSENSTTNMREADEIVSDTSLVDSVL 299
QY 300 PSSSYVQVQGRKRLDGPGLISDMSTPFTQDVYIFPKILITSGVNSNPFICYKKNK 359
DB 300 PSSSYVQVQGRKRLDGPGLISDMSTPFTQDVYIFPKILITSGVNSNPFICYKKNK 359
QY 360 IYPSKEIYVMNMLAEKIPQSOYDVVSDHYSKYTFNLNETKRGKFTYDAVYCCNEHECH 419
DB 360 IYSSKTIYVMNMLAEKIPQSOYDVVSDHYSKYTFPMNMTFKRGKFTYDAVYCCNEHECH 419
QY 420 HRYAELIYIDVININISCEFDGYLTAKMTGWSSTSTOSLAESTLQLRHYHSSLYCSDIS 479
DB 420 HRYAELIYIDVININISCEFDGYLTAKMTGWSSTSTOSLAESTLQLRHYHSSLYCSDIS 479
QY 480 HPISPEKDCYLOSDGFYECIFQPIFLSGYTMIRINHSGLSDSPPCVLDSSVKKPLP 539
DB 480 HPISPEKDCYLOSDGFYECIFQPIFLSGYTMIRINHSGLSDSPPCVLDSSVKKPLP 539
QY 540 PSSVKAETITINIGLTKISWEKVPFENNLOFQIRYGLSGKEYQVMKYEYVDAKSKSVSLP 599
DB 540 PSSVKAETITAKIGLTKISWEKVPFENNLOFQIRYGLSGKEYQVMKYEYVDAKSKSVSLP 599
QY 600 VPDLCAYVAVOYRCRLDGLGYWSMNSPAYTVVMDIKVPMRGPIEFWRIINDYMKKEKN 659
DB 600 VPDLCAYVAVOYRCRLDGLGYWSMNSPAYTVVMDIKVPMRGPIEFWRIINDYMKKEKN 659
QY 660 VTLMLKPLMKNDLSQVORYYINHTSCNGTWSVDGNHTKFTFLMTQAHVTVLAINST 719
DB 660 VTLMLKPLMKNDLSQVORYYINHTSCNGTWSVDGNHTKFTFLMTQAHVTVLAINST 719
QY 720 IGASVANFNILFSPMKSKVNIYVSLSAVPLNSSCVIYVSLSPDYKLMFTIEMKMLNE 779
DB 720 IGASVANFNILFSPMKSKVNIYVSLSAVPLNSSCVIYVSLSPDYKLMFTIEMKMLNE 779
QY 780 DGEIKWLRISSVKKYYIHDFPIEKYOFSLYPIFMEGVGKPKIINSFTQODIERKHQSD 839
DB 780 DGEIKWLRISSVKKYYIHDFPIEKYOFSLYPIFMEGVGKPKIINSFTQODIERKHQSD 839
QY 840 AGLYIVPVIISSSILLGLTLLISHORMKKLFMEDVDPNPKNSWAGLNFOKPEFHEH 899
DB 839 AGLYIVPVIISSSILLGLTLLISHORMKKLFMEDVDPNPKNSWAGLNFOKPEFHEH 898
QY 900 IKHTASVTCGPIILPEPTISEDSIVTSWKNKDEMPITVVSLLSTT-DLEKGSVCISDO 958
DB 899 IKHTASVTCGPIILPEPTISEDSIVTSWKNKDEMPITVVSLLSTT-DLEKGSVCISDO 958

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QY 959 FNSVNFSAETEVYEDESOROPVYKATILISNKSBSFTEEOGLINSVTKCPSSKNS 1018
Db 959 RSSAFSEAESEMETTRDENRORSIPYATLLSSPKSGEETEOEOLVSLSRCSFSSNS 1018
QY 1019 PLKSFSSNSWEIAQAFILISDHPNIIISPLTFSEGLDELTLKEGFPENNDRKITY 1078
Db 1019 LPKSFSSNSWEIETQAFILISDHPNITSPLHSFSEGLDELTLKEGFPENNDRKITY 1078
QY 1079 YLGVTYSIKKRESGVLLTDKSHVSCFPAPCLFTDTRVLQDSCSHFVENNINLGTSSKRTF 1138
Db 1079 YLGVTYSIKKRESGVLLTDKSHVSCFPAPCLFTDTRVLQDSCSHFVENNINLGTSSKRTF 1138
QY 1139 ASYMPOTOTCTOTCHKIMENKMDLTV 1165
Db 1139 VSYMPOTOTCTOTCHKIMENKMDLTV 1165

RESULT 5
QY 092920 PRELIMINARY; PRT; 958 AA.
AC 092920;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RF SEQUENCE FROM N.A.
RX MEDLINE=9638968; PubMed=8805376;
RA Bennett B.D., Solar G.P., Yuan J.O., Mathias J., Thomas G.R.,
RA Matthews W.;
RT "A. role for leptin and its cognate receptor in hematopoiesis."
RL EMBL: U66496; AAB07496.1; -.
DR HSBP; P16471; IIP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KM Receptor.
SQ SEQUENCE 958 AA; 109392 MW; 3F5B5C5A187E803A CRC64;

Query Match 77.3%; Score 4831.5; DB 4; Length 958;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 904; Conservative 5; Mismatches 24; Indels 25; Gaps 3;

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QY 301 GSSEYVQYRGRLDQPGIWSDMSTPRVFTTQDVITYEPKRIITSVASNVSEHCITYKENKI 360
Db 301 GSSEYVQYRGRLDQPGIWSDMSTPRVFTTQDVITYEPKRIITSVASNVSEHCITYKENKI 360
QY 361 VPSKEIYVMMMLAEKIPQSOYDVVDVSDHYSKYTFEFLNTEIKRGKTYTAAVYCCNHECHH 420
Db 361 VPSKEIYVMMMLAEKIPQSOYDVVDVSDHYSKYTFEFLNTEIKRGKTYTAAVYCCNHECHH 420
QY 421 RYAEIYVDVNVINISCFEDGYLTWKTCRMSTIOSLAEESTJOLRHHSSLYCSDIPSIH 480
Db 421 RYAEIYVDVNVINISCFEDGYLTWKTCRMSTIOSLAEESTJOLRHHSSLYCSDIPSIH 480
QY 481 PISEKDCYLOSDGFECIFQPIFLSGYTMIRINHSIGLSDSPPTCYLPDPSVYKPLPP 540
Db 481 PISEKDCYLOSDGFECIFQPIFLSGYTMIRINHSIGLSDSPPTCYLPDPSVYKPLPP 540
QY 541 SSVKAEITINIGLTKISNEKVPFPENNLOFOIRGLSGREYQWKAEYVYDAKSASVSLPV 600
Db 541 SSVKAEITINIGLTKISNEKVPFPENNLOFOIRGLSGREYQWKAEYVYDAKSASVSLPV 600
QY 601 PDLCAVYAVOYRCKRLDGLGYWSMNSNPATYVMDIKYPMRGPEWRIINGDTMKERKNV 660
Db 601 PDLCAVYAVOYRCKRLDGLGYWSMNSNPATYVMDIKYPMRGPEWRIINGDTMKERKNV 660
QY 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTSESDVGNHTKFFELTLDQAHVTYLAINSI 720
Db 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTSESDVGNHTKFFELTLDQAHVTYLAINSI 720
QY 721 GASVANFNLTSWPMKSNVYOSLSAYPLNSSCVVSNLSFSDYKLMFTIEMKNLMD 780
Db 721 GASVANFNLTSWPMKSNVYOSLSAYPLNSSCVVSNLSFSDYKLMFTIEMKNLMD 780
QY 781 GEIKMLRISSSVKRYIINDHPIPIEKYQFSLYPIPMEGVGKRIINSTODDIEKHQSDA 840
Db 781 GEIKMLRISSSVKRYIINDHPIPIEKYQFSLYPIPMEGVGKRIINSTODDIEKHQSDA 840
QY 841 GLYIVPVISSISILLGTLTLLSHQRMKLEWEDVPNPKNSMAOGLNFKR-----PE 893
Db 841 GLYIVPVISSISILLGTLTLLSHQRMKLEWEDVPNPKNSMAOGLNFKOKEGSMFKV 900
QY 894 TPEHFLIKHT-ASYVCGP-----LLEPEIISDIDISVDTSMKKKDE 933
Db 901 SHHSHLISSTQGHKCHGRQGPLHAKRTDLCGLVYLTLPLLSYDPAKSPSVRNTQE 958

RESULT 6
QY 092919 PRELIMINARY; PRT; 896 AA.
AC 092919;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RF SEQUENCE FROM N.A.
RX MEDLINE=97215244; PubMed=9061609;
RA Lucin S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
RA Bennett B.D., Solar G.P., Yuan J.O., Mathias J., Thomas G.R.,
RA Matthews W.;
RT "Cloning and characterization of a human leptin receptor using a
RT biologically active leptin immunoadhesin."
RL J. Mol. Endocrinol. 18:77-85(1997).
RM EMBL: U66495; AAB07495.1; -.

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DR EMBL: U50748; AAC23650.1; -
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 DR SEQUENCE 896 AA; 102489 MW; D371C7A1186DEB3 CRC64;

Query Match 77.2%; Score 4826; DB 4; Length 896;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTCQKFCVLLHMERIVYITAFNLSTPTPMRFKLSGMPNSTYDYFLIPAGLSKNTS 60
 DB 1 MTCQKFCVLLHMERIVYITAFNLSTPTPMRFKLSGMPNSTYDYFLIPAGLSKNTS 60
 QY 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
 DB 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
 QY 121 QOIDANMNIQCLWKGLDLKFLICYVESLFKNLFERNYKVVHLLYVLEVEDSPLYPQGS 180
 DB 121 QOIDANMNIQCLWKGLDLKFLICYVESLFKNLFERNYKVVHLLYVLEVEDSPLYPQGS 180
 QY 161 FQMVHNCNSVHECCGCLVVPYPAKNDLMLCKLTSGGVIFQSPLMVQPIPMVKPPPP 240
 DB 161 FQMVHNCNSVHECCGCLVVPYPAKNDLMLCKLTSGGVIFQSPLMVQPIPMVKPPPP 240
 QY 241 LGLHMEITDDGDLKLSMSGSPPLVPPLOYQVYKSENSSTTVIREADKIYSATSLVDSILP 300
 DB 241 LGLHMEITDDGDLKLSMSGSPPLVPPLOYQVYKSENSSTTVIREADKIYSATSLVDSILP 300
 QY 301 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
 DB 301 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
 QY 361 VPSKRIYVMNMNLAERIKIPSOYDVVSDHVSKYTFEFLNLETKRGKRTTYAAYCCNHECHH 420
 DB 361 VPSKRIYVMNMNLAERIKIPSOYDVVSDHVSKYTFEFLNLETKRGKRTTYAAYCCNHECHH 420
 QY 421 RYAEIYVIDVNIINISCEDGYLTKMKCRKSTSTIOSLAESTIQLRYHSSLSYCSIDIPSIH 480
 DB 421 RYAEIYVIDVNIINISCEDGYLTKMKCRKSTSTIOSLAESTIQLRYHSSLSYCSIDIPSIH 480
 QY 481 PISEPKDCYLSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
 DB 481 PISEPKDCYLSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
 QY 541 SSVKAEITINIGLKLISMEKPVFPENNLOFOIRGLSGKEVQWKYEVYDAKSASVSLPV 600
 DB 541 SSVKAEITINIGLKLISMEKPVFPENNLOFOIRGLSGKEVQWKYEVYDAKSASVSLPV 600
 QY 601 PDLCAVYAVQVGRKRLDGLGYSNMSNPATYVMDIKVPMRGPBEMRIIINGDTMKKEKNV 660
 DB 601 PDLCAVYAVQVGRKRLDGLGYSNMSNPATYVMDIKVPMRGPBEMRIIINGDTMKKEKNV 660
 QY 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTWSGSEVDGNHTKFTFLTEQAHVTYVAINSI 720
 DB 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTWSGSEVDGNHTKFTFLTEQAHVTYVAINSI 720
 QY 721 GASVANENLUTSWPMKSNIVOSLAPPLNSSCVIVSWILSPSDYKLMFYIIEKNLMD 780
 DB 721 GASVANENLUTSWPMKSNIVOSLAPPLNSSCVIVSWILSPSDYKLMFYIIEKNLMD 780
 QY 781 GEIKMLRISSSVKKYIYIDHFIPIEKYQPSLYPIFMGVGKPKIINSTODDIEKHQSDA 840
 DB 781 GEIKMLRISSSVKKYIYIDHFIPIEKYQPSLYPIFMGVGKPKIINSTODDIEKHQSDA 840

QY 841 GLYIVPVISSILLGLTLLISHQRMKLEWEDVPNPKNSWAGLNFQK 891
 DB 841 GLYIVPVISSILLGLTLLISHQRMKLEWEDVPNPKNSWAGLNFQK 891

RESULT 7

ID Q13592 PRELIMINARY; PRT; 958 AA.
 AC Q13592;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
 RA Platiha D., Snodgrass H.R.;
 RT "Novel B219/OB receptor isoforms: possible role of leptin in
 hematopoiesis and reproduction.";
 RL Nat. Med. 2:585-589(1996).
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Signal; Receptor.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 958 B219/OB RECEPTOR ISOFORM HUB219.1.
 SQ SEQUENCE 958 AA; 109419 MW; C7E0E8D18428677B CRC64;

Query Match 77.1%; Score 4819.5; DB 4; Length 958;
 Best Local Similarity 94.1%; Pred. No. 0;
 Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MTCQKFCVLLHMERIVYITAFNLSTPTPMRFKLSGMPNSTYDYFLIPAGLSKNTS 60
 DB 1 MTCQKFCVLLHMERIVYITAFNLSTPTPMRFKLSGMPNSTYDYFLIPAGLSKNTS 60
 QY 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
 DB 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
 QY 121 QOIDANMNIQCLWKGLDLKFLICYVESLFKNLFERNYKVVHLLYVLEVEDSPLYPQGS 180
 DB 121 QOIDANMNIQCLWKGLDLKFLICYVESLFKNLFERNYKVVHLLYVLEVEDSPLYPQGS 180
 QY 161 FQMVHNCNSVHECCGCLVVPYPAKNDLMLCKLTSGGVIFQSPLMVQPIPMVKPPPP 240
 DB 161 FQMVHNCNSVHECCGCLVVPYPAKNDLMLCKLTSGGVIFQSPLMVQPIPMVKPPPP 240
 QY 241 LGLHMEITDDGDLKLSMSGSPPLVPPLOYQVYKSENSSTTVIREADKIYSATSLVDSILP 300
 DB 241 LGLHMEITDDGDLKLSMSGSPPLVPPLOYQVYKSENSSTTVIREADKIYSATSLVDSILP 300
 QY 301 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
 DB 301 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
 QY 361 VPSKRIYVMNMNLAERIKIPSOYDVVSDHVSKYTFEFLNLETKRGKRTTYAAYCCNHECHH 420
 DB 361 VPSKRIYVMNMNLAERIKIPSOYDVVSDHVSKYTFEFLNLETKRGKRTTYAAYCCNHECHH 420

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QY 421 RYAEIYIDVNIINISCEFDGYLTMTCKMSTSTIOSLAESTLOLRHYHRSLSYCDIPSIH 480
DB 421 RYAEIYIDVNIINISCEFDGYLTMTCKMSTSTIOSLAESTLOLRHYHRSLSYCDIPSIH 480
QY 481 PISEPKDCYLOSDFEYECFOPIFLLSGYTMIRINHSIGSDSPPTCYLPDSVVKPLPP 540
DB 481 PISEPKDCYLOSDFEYECFOPIFLLSGYTMIRINHSIGSDSPPTCYLPDSVVKPLPP 540
QY 541 SVKAEITINIGLKTISMKRPVPEPENNLOFQIRYGLSGEYQMKMEYVDASKSVSLPV 600
DB 541 SVKAEITINIGLKTISMKRPVPEPENNLOFQIRYGLSGEYQMKMEYVDASKSVSLPV 600
QY 601 PDLCAVYAVOVKCRKLDGLGYWSNMSNPAYTYVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
DB 601 PDLCAVYAVOVKCRKLDGLGYWSNMSNPAYTYVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
QY 661 TLLMKPLKNDLSQVORYVINHHTSCNGTWSGVEDVGNHTKFTFLMTBOAHYTVLAINSI 720
DB 661 TLLMKPLKNDLSQVORYVINHHTSCNGTWSGVEDVGNHTKFTFLMTBOAHYTVLAINSI 720
QY 721 GASVANFNLTFSMPKSKVNIYOSLSAYPLNSSCVIYTWILSPDYKLAWEIIEKMLNED 780
DB 721 GASVANFNLTFSMPKSKVNIYOSLSAYPLNSSCVIYTWILSPDYKLAWEIIEKMLNED 780
QY 781 GEIKMLRISSSVKYYIHDFPIEKOYSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKMLRISSSVKYYIHDFPIEKOYSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYIVPVYIISILLGLTLLSHQMKKLFMEDVNPKNCSNAQGLNOK -----PE 893
DB 841 GLYIVPVYIISILLGLTLLSHQMKKLFMEDVNPKNCSNAQGLNOK -----PE 893
QY 894 TFEHLFIKHT-ASYTCGP-----LLEPETISEDYDTSMKNDE 933
DB 901 SHHHLISSTQGHKHCGRPGPRLHRTKTRDLCGLVYLLTIPRLLSYDPAKSPVSRNQE 958

RESULT 8
Q13593 PRELIMINARY: PRT: 906 AA.
AC 013593:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.2 PRCURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shaffer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platica D., Snodgrass B.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hemopoiesis and reproduction."
RL Nat. Med. 2:585-589(1996).
DR EMBL: U52913; AAC50510.1; -
DR HSSP: P16471; 1B93.
DR InterPro: IPR002896; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3_2.
DR SMART: SM00060; FN3_1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 906 B219/OB RECEPTOR ISOFORM HUB219.2.
SQ SEQUENCE 906 AA: 103487 MW: 6051126F3076626 CRC64;
```

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Query Match 77.0%; Score 4816; DB 4; length 906;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 MICORFCVLLHMEFYITAFNLSPYTPMRFKLSGCMPSNTYQYFLPAGLSKNTNS 60
DB 1 MICORFCVLLHMEFYITAFNLSPYTPMRFKLSGCMPSNTYQYFLPAGLSKNTNS 60
QY 61 NGHYETAVPKPNSGTHNSLNKSTTHGCCFRSEODRNCSLADNIEGTFYSTVNSLVF 120
DB 61 NGHYETAVPKPNSGTHNSLNKSTTHGCCFRSEODRNCSLADNIEGTFYSTVNSLVF 120
QY 121 QOIDANMNQCKLKGDKLFICYVESLFENLPRNRYKHLVYVPEVLEDSPLVPQKS 180
DB 121 QOIDANMNQCKLKGDKLFICYVESLFENLPRNRYKHLVYVPEVLEDSPLVPQKS 180
QY 181 FQMVHNCNVHECCBCEGLVVPFAKINDTLMLCKITSGGVIFQSPILMSVOPINMYKPDPP 240
DB 181 FQMVHNCNVHECCBCEGLVVPFAKINDTLMLCKITSGGVIFQSPILMSVOPINMYKPDPP 240
QY 241 LGLHMETDQNLKTSWSSPPLVPPLOVQYSENSTVIREADKIVATSILDVSTLP 300
DB 241 LGLHMETDQNLKTSWSSPPLVPPLOVQYSENSTVIREADKIVATSILDVSTLP 300
QY 301 GSSYEYQVGRKLDGPGISDMSTPRVFTTODVYTPPKILTSVGSNVSFHCYKKEKNI 360
DB 301 GSSYEYQVGRKLDGPGISDMSTPRVFTTODVYTPPKILTSVGSNVSFHCYKKEKNI 360
QY 361 VPSKETVMMNTAEKIPQSQYDVSDVSKVTFENLNETKPRGKTYDAVYCCNEHECHH 420
DB 361 VPSKETVMMNTAEKIPQSQYDVSDVSKVTFENLNETKPRGKTYDAVYCCNEHECHH 420
QY 421 RYAEIYIDVNIINISCEFDGYLTMTCKMSTSTIOSLAESTLOLRHYHRSLSYCDIPSIH 480
DB 421 RYAEIYIDVNIINISCEFDGYLTMTCKMSTSTIOSLAESTLOLRHYHRSLSYCDIPSIH 480
QY 481 PISEPKDCYLOSDFEYECFOPIFLLSGYTMIRINHSIGSDSPPTCYLPDSVVKPLPP 540
DB 481 PISEPKDCYLOSDFEYECFOPIFLLSGYTMIRINHSIGSDSPPTCYLPDSVVKPLPP 540
QY 541 SSYKAEITINIGLKTISMKRPVPEPENNLOFQIRYGLSGEYQMKMEYVDASKSVSLPV 600
DB 541 SSYKAEITINIGLKTISMKRPVPEPENNLOFQIRYGLSGEYQMKMEYVDASKSVSLPV 600
QY 601 PDLCAVYAVOVKCRKLDGLGYWSNMSNPAYTYVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
DB 601 PDLCAVYAVOVKCRKLDGLGYWSNMSNPAYTYVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
QY 661 TLLMKPLKNDLSQVORYVINHHTSCNGTWSGVEDVGNHTKFTFLMTBOAHYTVLAINSI 720
DB 661 TLLMKPLKNDLSQVORYVINHHTSCNGTWSGVEDVGNHTKFTFLMTBOAHYTVLAINSI 720
QY 721 GASVANFNLTFSMPKSKVNIYOSLSAYPLNSSCVIYTWILSPDYKLAWEIIEKMLNED 780
DB 721 GASVANFNLTFSMPKSKVNIYOSLSAYPLNSSCVIYTWILSPDYKLAWEIIEKMLNED 780
QY 781 GEIKMLRISSSVKYYIHDFPIEKOYSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKMLRISSSVKYYIHDFPIEKOYSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYIVPVYIISILLGLTLLSHQMKKLFMEDVNPKNCSNAQGLNOK -----PETFEHL 898
DB 841 GLYIVPVYIISILLGLTLLSHQMKKLFMEDVNPKNCSNAQGLNOK -----PETFEHL 898

RESULT 9
Q13594 PRELIMINARY: PRT: 896 AA.
AC 013594:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
```

DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
 RA Platika D., Snodgrass H.R., Zupancic T.J., Smith-Gbur J., Mikhail A.,
 RT "Novel B219/OB receptor isoforms: possible role of leptin in
 RT hematopoiesis and reproduction."
 RL Nat. Med. 2:585-589(1996).
 DR EMBL: U52914; AAC50511.1; .
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002986; CRIA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01353; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Signal, Receptor.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 896 B219/OB RECEPTOR ISOFORM HUB219.3.
 SQ SEQUENCE 896 AA; 102516 MW; 73C431F8C578CD07 CRC64;

Query Match 77.0%; Score 4814; DB 4; Length 896;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 MICQFCVYLLHMEFIYITAFNLSTPTPRFKISCPNPSTYVFLPAGLSKNTS 60
 DB 1 MICQFCVYLLHMEFIYITAFNLSTPTPRFKISCPNPSTYVFLPAGLSKNTS 60
 OY 61 NGHYETAEPKFNSSGTFHNSLTKTFHCCFSEODRNCSCADNIEGTFYVNSLVF 120
 DB 61 NGHYETAEPKFNSSGTFHNSLTKTFHCCFSEODRNCSCADNIEGTFYVNSLVF 120
 OY 121 QOIDANNNIQCWLKGLDLKFLICYVESLEKKNLEFRNINRYKVVHLLYLPVLEDSPLVPQGS 180
 DB 121 QOIDANNNIQCWLKGLDLKFLICYVESLEKKNLEFRNINRYKVVHLLYLPVLEDSPLVPQGS 180
 OY 121 QOIDANNNIQCWLKGLDLKFLICYVESLEKKNLEFRNINRYKVVHLLYLPVLEDSPLVPQGS 180
 DB 121 QOIDANNNIQCWLKGLDLKFLICYVESLEKKNLEFRNINRYKVVHLLYLPVLEDSPLVPQGS 180
 OY 181 FQWVHCNCSVHECCCECLVPPPAKLNIDTLMLCKLITSGVIFRSPPLMSVOPINMYKPPDP 240
 DB 181 FQWVHCNCSVHECCCECLVPPPAKLNIDTLMLCKLITSGVIFRSPPLMSVOPINMYKPPDP 240
 OY 241 LGLHMEITDDGNLKIWSMSPPLVPPLOQVYKSENSSTVIREADKIYASATSLVDSILP 300
 DB 241 LGLHMEITDDGNLKIWSMSPPLVPPLOQVYKSENSSTVIREADKIYASATSLVDSILP 300
 OY 301 GSSYEVQVGRKLDGPGIWSMSTPRVFTTODVYIFPKILTSVGSNVSFHCITYKKNKI 360
 DB 301 GSSYEVQVGRKLDGPGIWSMSTPRVFTTODVYIFPKILTSVGSNVSFHCITYKKNKI 360
 OY 301 GSSYEVQVGRKLDGPGIWSMSTPRVFTTODVYIFPKILTSVGSNVSFHCITYKKNKI 360
 DB 301 GSSYEVQVGRKLDGPGIWSMSTPRVFTTODVYIFPKILTSVGSNVSFHCITYKKNKI 360
 OY 361 VPSKEITVMNMNAEKIPOSQDVVSDHVSQVTFEFLNETKPRGRTYAVVCCNHECHH 420
 DB 361 VPSKEITVMNMNAEKIPOSQDVVSDHVSQVTFEFLNETKPRGRTYAVVCCNHECHH 420
 OY 421 RYAEELYVDVNNINISCEIDGYLTAKTKRMSTSTQSLAESTQLRYHSSSLYCSIPSLH 480
 DB 421 RYAEELYVDVNNINISCEIDGYLTAKTKRMSTSTQSLAESTQLRYHSSSLYCSIPSLH 480
 OY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGTYMIRINHSGLSDSPCYGLPDSVVKPLPP 540
 DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGTYMIRINHSGLSDSPCYGLPDSVVKPLPP 540
 OY 541 SSVKAEITINIGLTKISNEKPFVPENNIQQFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600
 DB 541 SSVKAEITINIGLTKISNEKPFVPENNIQQFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600

DB 541 SSVKAEITINIGLTKISNEKPFVPENNIQQFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600
 OY 601 PDLCAVAVQVCKRLDGLGYSMNSNPAYTYVMDIKYMRGPEHRIINGDTMKKKNV 660
 DB 601 PDLCAVAVQVCKRLDGLGYSMNSNPAYTYVMDIKYMRGPEHRIINGDTMKKKNV 660
 OY 661 TLMLKPLKNDLSLCSVQRYVINHNTSCNGTSEDVGNHTKFFELTQEAHTVYLAINSI 720
 DB 661 TLMLKPLKNDLSLCSVQRYVINHNTSCNGTSEDVGNHTKFFELTQEAHTVYLAINSI 720
 OY 721 GASVANFNLTSPWMSKYNIVOSTASAYPLNSCVVSNLSSDDYKLMFIEEMKLNED 780
 DB 721 GASVANFNLTSPWMSKYNIVOSTASAYPLNSCVVSNLSSDDYKLMFIEEMKLNED 780
 OY 781 GEIKMLRISSSVKKYIHDHFIPIKQFSLPIPIMEGVGKRIINJFTQDDIEKHQSDA 840
 DB 781 GEIKMLRISSSVKKYIHDHFIPIKQFSLPIPIMEGVGKRIINJFTQDDIEKHQSDA 840
 OY 841 GLYIVIPVITSSILLGTLTISHORMKKLEWEDVNPKNCSMAOGLNFQK 891
 DB 841 GLYIVIPVITSSILLGTLTISHORMKKLEWEDVNPKNCSMAOGLNFQK 891

RESULT 10
 ID 090WG3 PRELIMINARY; PRT: 1162 AA.
 AC 090WG3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE LEPTIN RECEPTOR B.
 GN LEPR OR LEPRB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=K OBESE; TISSUE=BRAIN, HYPOTHALAMUS;
 RA Joest H.G., Taylor B.A., Phillips S.J., Becker W., Horberg L.,
 RA Joest H.G.;
 RT "Hypertension and leptin receptor variant Asp600Asn in the obese,
 RT hyperinsulinemic KK mouse strain."
 RL J. Endocrinol. 21:337-345(1998).
 DR EMBL: Y10296; CAAT7142.1; .
 DR HSSP: P16471; 1BP3.
 DR MGI: 104993; Lepr.
 DR InterPro: IPR002986; CRIA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 3.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01353; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 FT VARIANT 600 600 N -> D.
 FT SEQUENCE 1162 AA; 130787 MW; 541E77CBA46EC00D CRC64;

Query Match 76.1%; Score 4761.5; DB 11; Length 1162;
 Best Local Similarity 75.3%; Pred. No. 0;
 Matches 878; Conservative 116; Mismatches 167; Indels 5; Gaps 5;

OY 1 MICQFCVYLLHMEFIYITAFNLSTPTPRFKISCPNPSTYVFLPAGLSKNTS 60
 DB 1 MICQFCVYLLHMEFIYITAFNLSTPTPRFKISCPNPSTYVFLPAGLSKNTS 60
 OY 61 NGHYETAEPKFNSSGTFHNSLTKTFHCCFSEODRNCSCADNIEGTFYVNSLVF 120
 DB 61 NGHYETAEPKFNSSGTFHNSLTKTFHCCFSEODRNCSCADNIEGTFYVNSLVF 120
 OY 121 QOIDANNNIQCWLKGLDLKFLICYVESLEKKNLEFRNINRYKVVHLLYLPVLEDSPLVPQGS 180
 DB 121 QOIDANNNIQCWLKGLDLKFLICYVESLEKKNLEFRNINRYKVVHLLYLPVLEDSPLVPQGS 180


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Db 121 ROLGVNWDIECMKGDLLFTICMHEPLPKNPFKNYSKVHLLLYDPEVYIDDSPLPLKDS 180
Qy 181 FOMVHCNCSVHECECLVPEVPAKINDTLMLCKLTSGVGIPOSPILMSQPIPNMKPPDP 240
Db 181 FOMVHCNCSVHECECLVPEVPAKINDTLMLCKLTSGVGIPOSPILMSQPIPNMKPPDP 239
Qy 241 LGLHMETIDGDLKISWSSPPLVPPLOQYQVKSNSPTTVVREADKIVSATSILVDSILP 300
Db 240 LGLHMETIDGDLKISWSSPPLVPPLOQYQVKSNSPTTVVREADKIVSATSILVDSILP 298
Qy 301 GSSYEVOVGRKRDGPGIWSMSTPRVFTTODVYIFPPKILTVSGSNSVFCIYKKENKI 360
Db 299 GSSYEVOVGRKRDGPGIWSMSTPRVFTTODVYIFPPKILTVSGSNSVFCIYKKENKI 358
Qy 361 VPSKEIYVMMNLAEKIPQSDYDVSDHVSQVFFNLNETKPRGKFTYADVCCNEHECHH 420
Db 359 ISSKOIYVMMNLAEKIPQSDYDVSDHVSQVFFNLNETKPRGKFTYADVCCNEHECHH 418
Qy 421 RYAEIYVIVNINISCEFDGYLTMTCKMSTSTIOSLAESTLQLRVHRSILYCSIDPSIH 480
Db 419 RYAEIYVIVNINISCEFDGYLTMTCKMSTSTIOSLAESTLQLRVHRSILYCSIDPSIH 478
Qy 481 PISEPKDCYLOSDGEFECIFOPIFELLSGYTWMIRINHSIGSDSPPTCYLPDSVYKPLPP 540
Db 479 PISEPKDCYLOSDGEFECIFOPIFELLSGYTWMIRINHSIGSDSPPTCYLPDSVYKPLPP 538
Qy 541 SSKVAEITINIGLITKISMEKPVFPENNILOFOIRYGLSGKEVQOMKAYEVDAKSASVSLPV 600
Db 539 SSKVAEITINIGLITKISMEKPVFPENNILOFOIRYGLSGKEVQOMKAYEVDAKSASVSLPV 598
Qy 601 PDLCAVYAVOVRCKRLDGLGIVSNMSPAYVYMDIKYPMRGPERFWRILNGDTMKKEKV 660
Db 599 SMLCAYVAVOVRCKRLDGLGIVSNMSPAYVYMDIKYPMRGPERFWRILNGDTMKKEKV 658
Qy 661 TLMKPLKKNNSIGVORVYINHNHSCNGTWSGSEDYGNHKKFPLTEQOAHYTVLAINSI 720
Db 659 TLMKPLKKNNSIGVORVYINHNHSCNGTWSGSEDYGNHKKFPLTEQOAHYTVLAINSI 718
Qy 721 GASVANFNLTFESPMKSVKIYVOSLSAYPLNSCVIYWSLTFSPDYKLMFIEEMKNLND 780
Db 719 GASVANFNLTFESPMKSVKIYVOSLSAYPLNSCVIYWSLTFSPDYKLMFIEEMKNLND 778
Qy 781 GEIKMLRISSSVKKYIYHDFIPIEKYQSLYPIMEGVGKRIINSFTODDIKHOQSDA 840
Db 779 DCMKMLRIPSNVKKYIYHDFIPIEKYQSLYPIMEGVGKRIINSFTODDIKHOQSDA 838
Qy 841 GLYIVPVISSILLGLTLLSHORMKLEFWDVNPNCNSMAOGLNOKRETPHLP 900
Db 839 GLYIVPVISSILLGLTLLSHORMKLEFWDVNPNCNSMAOGLNOKRETPHLP 898
Qy 901 KHTASVTCGPLLLEPETISEDIVSDTSMKNKDEMMPTVYSLSTT-DIEKGSVCISDOF 959
Db 899 KHTASVTCGPLLLEPETISEDIVSDTSMKNKDEMMPTVYSLSTT-DIEKGSVCISDOF 958
Qy 960 NSVNFSEABGEFVYEDESQORPEVKYATLINSKPSKETGEOGLINSVYKCFSSKNSP 1019
Db 959 NSVNFSEABGEFVYEDESQORPEVKYATLINSKPSKETGEOGLINSVYKCFSSKNSP 1018
Qy 1020 LKDSNSNSMETEQAFLTISOHNITISPHLTFSEGDDELKLTBENFDEENDKSITY 1079
Db 1019 LKDSNSNSMETEQAFLTISOHNITISPHLTFSEGDDELKLTBENFDEENDKSITY 1077
Qy 1080 LGVYIKKRESGVLTLDKSRVSCPAPCLFDIRIVLQDSCHFVENNINLTSSKKTPA 1139
Db 1078 LGVYIKKRESGVLTLDKSRVSCPAPCLFDIRIVLQDSCHFVENNINLTSSKKTPA 1136
Qy 1140 SYMPOFOCSTQTHKIMENKMDLTV 1165
Db 1137 SYMPOFOCSTQTHKIMENKMDLTV 1162

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Q9MY9
ID Q9MY9 PRELIMINARY: PRT: 925 AA.
AC Q9MY9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LEPTIN RECEPTOR SHORT INSERT ISOFORM.
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RC MEDLINE=9840831; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bocklin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys."
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bocklin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF225875; AAF35389.1;
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ
SEQUENCE 925 AA; 105721 MW; EC09C27EC29C5F3A CRC64;

Query Match 73.4%; Score 4591; DB 6; Length 925;
Best Local Similarity 95.0%; Pred No. 0;
Matches 850; Conservative 15; Mismatches 28; Indels 2; Gaps 1;
Qy 1 MICQKRCVALLHMEFYVTAENLSYPIPWREKLSQMPNSYDYFLPAGLSKNTS 60
Db 1 MICQKRCVALLHMEFYVTAENLSYPIPWREKLSQMPNSYDYFLPAGLSKNTS 60
Qy 61 NGHYETAVERKNSGTHRSNLSKTFHCCFNSQEDORNSCLADNIEGKTFVSTVNSYF 120
Db 61 NGHYETAVERKNSGTHRSNLSKTFHCCFNSQEDORNSCLADNIEGKTFVSTVNSYF 118
Qy 121 OQIDAWNIQCMKGDGLKFLICVESLFFNLNPNRYKXHLVLEPEVLEDSPLVPOKS 180
Db 119 OQIDAWNIQCMKGDGLKFLICVESLFFNLNPNRYKXHLVLEPEVLEDSPLVPOKS 178
Qy 179 FOMVHCNCSVHECECLVPEVPAKINDTLMLCKLTSGVGIPOSPILMSQPIPNMKPPDP 238
Db 179 FOMVHCNCSVHECECLVPEVPAKINDTLMLCKLTSGVGIPOSPILMSQPIPNMKPPDP 238
Qy 241 LGLHMETIDGDLKISWSSPPLVPPLOQYQVKSNSPTTVVREADKIVSATSILVDSILP 300
Db 239 LGLHMETIDGDLKISWSSPPLVPPLOQYQVKSNSPTTVVREADKIVSATSILVDSILP 298
Qy 301 GSSYEVOVGRKRDGPGIWSMSTPRVFTTODVYIFPPKILTVSGSNSVFCIYKKENKI 360
Db 299 GSSYEVOVGRKRDGPGIWSMSTPRVFTTODVYIFPPKILTVSGSNSVFCIYKKENKI 358
Qy 361 VPSKEIYVMMNLAEKIPQSDYDVSDHVSQVFFNLNETKPRGKFTYADVCCNEHECHH 420
Db 359 VPSKEIYVMMNLAEKIPQSDYDVSDHVSQVFFNLNETKPRGKFTYADVCCNEHECHH 418
Qy 421 RYAEIYVIVNINISCEFDGYLTMTCKMSTSTIOSLAESTLQLRVHRSILYCSIDPSIH 480

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Db 419 RYAEIYVIDVNIINISCEITDGHILTKMTCRWSNTIQLAGSTIQLRARRSLCYFDPSIH 478
OY 481 PISEPKDCYLOSDFYECIFOPIFILSGYTMWIRINHSLGSDSPCTCLPDSVYKPLPP 540
Db 479 PISKPRDCYLOSDFYECIFOPIFILSGYTMWIRINHSLGSDSPCTCLPDSVYKPLPP 538
OY 541 SSVKAEITINILGLKISMEKPVFPENNLOFOIRYGLSGEKYOMKMYEVDAKSKSVSLPV 600
Db 539 SSVKAEITINILGLKISMEKPVFPENNLOFOIRYGLSGEKYOMKMYEVDAKSKSVSLPV 598
OY 601 PDLCAVYAVOVRCKRLDGLGYMSNNSPAYTYVMDIKYPMRGPETWRIINGDTMKKEKNV 660
Db 599 PDLCAVYAVOVRCKRLDGLGYMSNNSPAYTYVMDIKYPMRGPETWRIINGDTMKKEKNV 658
OY 661 TLLMPLKMNDSICSVORVYINHTSCNGTWSDEDVGNHRTKFTFLWTEQAHVTVLAINSI 720
Db 659 TLLMPLKMNDSICSVORVYINHTSCNGTWSDEDVGNHRTKFTFLWTEQAHVTVLAINSI 718
OY 721 GASVANFNLTFSPMSKNIYOSLSAYPLNSSCVIYVMSILSPSDYKLMYFIEMKNLND 780
Db 719 GASVANFNLTFSPMSKNIYOSLSAYPLNSSCVIYVMSILSPSDYKLMYFIEMKNLND 778
OY 781 GEIKMLRISSSKYKYIHDHFPIEKYOFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
Db 779 GEIKMLRISSSKYKYIHDHFPIEKYOFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 838
OY 841 GLYIVPVIYISSIILLGLTLLISHORMKKLFMEDVNPKNCSMAOGLNFOKRETF 895
Db 839 GLYIVPVIYISSIILLGLTLLISHORMKKLFMEDVNPKNCSMAOGLNFOKIRGF 893

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RESULT 12

O9MYL1 PRELIMINARY: PRT: 894 AA.

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ID AC O9MYL1
OY 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE LEPTIN RECEPTOR SHORT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OY NCBI_TaxID=9544;
RN [1]
RP TISSUE=ADIPOSE TISSUE;
RC MEDLINE=98408931; PubMed=9738551;
RX Hotia K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys";
RL Obes. Res. 6:353-360(1998).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=ADIPOSE TISSUE;
RC Hotia K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF225873; AAF35387.1;
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3_2.
DR SMART: SM00060; FN3_1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 894 AA: 102191 MW: 83CAF032238BAP9 CRC64;

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Query Match 73.4%; Score 4590; DB 6; Length 894;
Best Local Similarity 95.3%; Pred. No: 0;
Matches 849; Conservative 15; Mismatches 25; Indels 2; Gaps 1;

OY 1 MICOFCVYLLHWEFTIYTAFNLSYPTTPWRFKLSCHPNSITYYELLPAKLSNTSLS 60
Db 1 MICOFCVYLLHWEFTIYTAFNLSYPTTPWRFKLSCHPNSITYYELLPAKLSNTSLS 60
OY 61 NGHYEFAVEPKNSSGTFFSNLSKTFPHCCFRSEEDRNCSLADNIEGTFSTNSLYF 120
Db 61 NGHYEFAVE--FNSSDTFRSNLSKTFPHCCFRSEEDRNCSLACADNIEGTFSTNSLYF 118
OY 121 QOIDANMNIOCLKADLKLICYVESLFKNLEFNRYNYKVVHLLYLVPELEDSPLVPKGS 180
Db 119 QOMGANMNIOCLKADLKLICYVESLFKNPEKNKHKVHLLYLVPELEDSPLVPKGS 178
OY 181 FOMVHCNCSYHECCCLVVPYPAKINDTLMLCKITSSGYTFOSPLNSVOPINMKPPPP 240
Db 179 FOMVHCNCSYHECCCLVVPYPAKINDTLMLCKITSSGVVIFOSPLNSVOPINMKPPPP 238
OY 241 LGLHMEITDDGNLKITSMSPPLVPPLOVOYKSENSTVIREADKIVSATSLVYDSLIP 300
Db 239 LGLHMEITDDGNLKITSMSPPLVPPLOVEYKSENSTVIREADKIVSATSLVYDSLIP 298
OY 301 GSSYEVQVRGKRLDGPGLMSDMSPTPRVFTQDVLYFPPEKILTSVGSNVSFHCYKKNKI 360
Db 299 GSSYEVQVRGKRLDGPGLMSDMSPTPRVFTQDVLYFPPEKILTSVGSNVSFHCYKKNKI 358
OY 361 VPSKEITVMNMNIAEKIPQSOYDVSDHYSKYTFENLNEPKPKFTYAAVCCNHECHH 420
Db 359 VPSKEITVMNMNIAEKIPQSOYDVSDHYSKYTFENLNEPKPKFTYAAVCCNHECHH 418
OY 421 RYAEIYVIDVNIINISCEITDGHILTKMTCRWSNTIQLAGSTIQLRARRSLCYFDPSIH 480
Db 419 RYAEIYVIDVNIINISCEITDGHILTKMTCRWSNTIQLAGSTIQLRARRSLCYFDPSIH 478
OY 481 PISEPKDCYLOSDFYECIFOPIFILSGYTMWIRINHSLGSDSPCTCLPDSVYKPLPP 540
Db 479 PISKPRDCYLOSDFYECIFOPIFILSGYTMWIRINHSLGSDSPCTCLPDSVYKPLPP 538
OY 541 SSVKAEITINILGLKISMEKPVFPENNLOFOIRYGLSGEKYOMKMYEVDAKSKSVSLPV 600
Db 539 SSVKAEITINILGLKISMEKPVFPENNLOFOIRYGLSGEKYOMKMYEVDAKSKSVSLPV 598
OY 601 PDLCAVYAVOVRCKRLDGLGYMSNNSPAYTYVMDIKYPMRGPETWRIINGDTMKKEKNV 660
Db 599 PDLCAVYAVOVRCKRLDGLGYMSNNSPAYTYVMDIKYPMRGPETWRIINGDTMKKEKNV 658
OY 661 TLLMPLKMNDSICSVORVYINHTSCNGTWSDEDVGNHRTKFTFLWTEQAHVTVLAINSI 720
Db 659 TLLMPLKMNDSICSVORVYINHTSCNGTWSDEDVGNHRTKFTFLWTEQAHVTVLAINSI 718
OY 721 GASVANFNLTFSPMSKNIYOSLSAYPLNSSCVIYVMSILSPSDYKLMYFIEMKNLND 780
Db 719 GASVANFNLTFSPMSKNIYOSLSAYPLNSSCVIYVMSILSPSDYKLMYFIEMKNLND 778
OY 781 GEIKMLRISSSKYKYIHDHFPIEKYOFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
Db 779 GEIKMLRISSSKYKYIHDHFPIEKYOFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 838
OY 841 GLYIVPVIYISSIILLGLTLLISHORMKKLFMEDVNPKNCSMAOGLNFOK 891
Db 839 GLYIVPVIYISSIILLGLTLLISHORMKKLFMEDVNPKNCSMAOGLNFOK 889

RESULT 13
O9MZS2 PRELIMINARY: PRT: 848 AA.
ID AC O9MZS2
OY 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE LEPTIN RECEPTOR (FRAGMENT).

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QY 241 LGLHMETDGNLTKISMSPLVPPLOYOVKXSENSTVIREADKIVATSATSLVDSTLP 300
 240 LGLHMETDGNLTKISMSDQTKAPFLQOVKLENS-TIVRAAEIVSTSLVDSTLP 298
 QY 301 GSSYEVOVGRKRLDGGIWSMDSTPRVFTTQDVIYFPFKLTVSGSVNHFCTYKKNENK 360
 299 GSSYEVOVGRKRLDGGIWSMDSTPRVFTTQDVIYFPFKLTVSGSVNHFCTYKKNENK 358
 QY 361 VPKETIYMMNLAEKIPQSDYVDVSHSVKFEFNLETRPRGKFTYDAVCCNEHC 420
 359 ISSKQIYMMNLAEKIPQSDYVDVSHSVKFEFNLETRPRGKFTYDAVCCNEHC 418
 QY 421 RVALYIVDYNINISCEPDGYLTKMTCRMSTSTIOSLAESTIOLRYHRSLSYCDIPSIH 480
 419 RYADLYIVDYNINISCEPDGYLTKMTCRMSTSTIOSLAESTIOLRYHRSLSYCDIPSIH 478
 QY 481 PISEPDCYQSDGFECIFOPFIPLSGTYTMRIRHNSLGSLSDPYCVLPDSVYKPLP 540
 479 PISELKNVYQSDGFECIFOPFIPLSGTYTMRIRHNSLGSLSDPYCVLPDSVYKPLP 538
 QY 541 SSYKAEITINIGLKISMEKVPENNLQFQIRYGLSGKEVOMKMYEYDAKSVSLP 600
 539 SNAKAEITINIGLKISMEKVPENNLQFQIRYGLSGKEVOMKMYEYDAKSVSLP 598
 QY 601 PDICAVYAVOVGRKRLDGLGYSNMSNPAYTVVMDIKVPMRGEFWRINIGDTMKKEKNV 660
 599 SDICAVYAVOVGRKRLDGLGYSNMSNPAYTVVMDIKVPMRGEFWRINIGDTMKKEKNV 658
 QY 661 TLIMKRLMKNDSLCSVORYVINHTSCNGTWSGDNHNTKFFLMTQEAHTVVLAINSI 720
 659 TLIMKRLMKNDSLCSVORYVINHTSCNGTWSGDNHNTKFFLMTQEAHTVVLAINSI 718
 QY 721 GASVANFNLTFSWPMKSVNIYOSLSAYPLNSCVIYSWILSPSYKLMYFIEMKNLND 780
 719 GASVANFNLTFSWPMKSVNIYOSLSAYPLNSCVIYSWILSPSYKLMYFIEMKNLND 778
 QY 781 GELKMLRISSVKKYIYHDFIETIKYOSLPYFMEGCKPKIINSFTODIEKQSDA 840
 779 DGKMLRISSVKKYIYHDFIETIKYOSLPYFMEGCKPKIINSFTODIEKQSDA 838
 QY 841 GLYVIVPIIISCVLLGLTLLISHORMKKLFMEDVPRPKNSMAOGLNOK 891
 839 GLYVIVPIIISCVLLGLTLLISHORMKKLFMEDVPRPKNSMAOGLNOK 889
 RESULT 15
 Q9DDK1 PRELIMINARY; PRT: 1147 AA.
 AC Q9DDK1: 01-MAR-2001 (TREMBLREL. 16, Created)
 DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE LEPTIN RECEPTOR.
 GN OB-R..
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Richards M.P., Poch S.M., Ashwell C.M.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF321982; AAG40323.1;
 DR HSSP: P40189; 1B0U.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_LIT.
 DR Pfam: PF000041; fn3; 2.
 DR SMART: SMO0060; FN3; 4.
 KW Receptor.
 FT VARIANT 1133 1133 O -> R.
 SEQUENCE 1147 AA; 129131 MW; 3419787908F734F4 CRC64;

Query Match 44.6%; Score 2790.5; DB 13; Length 1147;
 Best Local Similarity 48.6%; Pred. No.1.9e-197;
 Matches 566; Conservative 190; Mismatches 364; Indels 45; Gaps 20;
 QY 9 VLLHMEFIVITAFNLSTYITPWRKFLSCMPNSTYDYFLP--AGLSKNTSNGHET 66
 11 VLL--DEFLVHAQAQCVHEIHPRSFLLPCLLNET--SLSPSAGVQSWSGMREYCT 65
 QY 67 AVEPRKNSGTHPSNLKTFHCRCRSDRNCSLCADDIEKTPV-STVNSLVYQOIDA 125
 66 A--ETNPS----LMDDESPLOCCLMSDNNASCSTLRGMQARMLIPSDISASBERDS 118
 QY 126 NNINOCMLKGDILFYCYEESLFKNLFRRVNYKVVHLLVYLPV-LEDSPLVPQKSGFQY 184
 119 NNINIECVWEGKLDLVCSIQ--FPKFMHLDKRVHLLVAVSEVSIJEDTSSLSLALAA 176
 QY 185 HCNCSVHECCELVPVPTAKNDTLMCLKITSGGVIFOSPLASVOPIMKVPDPPLGLH 244
 177 QCNSEYSEKCEHVSP--RLNHHTYIMLKVVYGVTPPLMSVYKPIDIVRDPDLNVH 234
 QY 245 METDGNLTKISMSPLVPPLOYOVKXSENSTVIREADKIVATSATSLVDSTLP 304
 235 LEMTERGOYKICMSEVPVPPRIEVLNIGNPGONGWOVOYALNTSLDVSMILDS 294
 QY 305 EVOVGRKRLDGGIWSMDSTPRVFTTQDVIYFPFKLTVSGSVNHFCTYKKNKIVPS 363
 295 PAOVGRKRLDGGIWSMDSTPRVFTTQDVIYFPFKLTVSGSVNHFCTYKKNKIVPS 354
 QY 364 KELYMMNLAEKIPQSDYVDVSHSVKFEFNLETRPRGKFTYDAVCCNEHC-ECHNY 422
 355 KRIYMMNLAESPEQSYLVTDVRSKYTLFNLKTRPGSEFNALVCOHNRCHNY 414
 QY 423 AELYIVDYNINISCEPDGYLTKMTCRMSTSTIOSLAESTIOLRYHRSLSYCDIPSIH 482
 415 AELYIVDYNINISCEPDGYLTKMTCRMSTSTIOSLAESTIOLRYHRSLSYCDIPSIH 474
 QY 483 SEPKDQYQSDGFECIFOPFIPLSGTYTMRIRHNSLGSLSDPYCVLPDSVYKPLPSS 542
 475 SEVKECHFOGRNHSYECTFPVFLSGYTMWIEFKSLGTLLESSPICVYADVADYKPLPSS 534
 QY 543 VRAEITINIGLKISMEKVPENNLQFQIRYGLSGKEVOMKMYEYDAKSVSLPVPD 602
 535 IKAETIRNDGLNVSANVAFANDDLKQIRYAVNKEELTWELVLSVSTRSAVIEV-Q 593
 QY 603 LCAVYAVOVGRKRLDGLGYSNMSNPAYTVVMDIKVPMRGEFWRINIGDTMKKEKNYL 662
 594 LCEVYIVQIRCALDGLGYSNMSNATVADYDAPLHGPEFKRTIYEDPATGQKNYL 653
 QY 663 LMKPLMKNDSLCSVORYVINHTSCNGTWSGDNHNTKFFLMTQEAHTVVLAINSIGA 722
 654 LMQPLMKNHSLSVGRYVYKHQSTSEVSEYVDGKTCSFMTHTHTITLAVANSIGA 713
 QY 723 SVANFNLTFSWPMKSVNIYOSLSAYPLNSCVIYSWILSPSYKLMYFIEMKNLND 782
 714 SSVANFNLTFSWPMKSVNIYOSLSAYPLNSCVIYSWILSPSYKLMYFIEMKNLND 773
 QY 783 IKMLRISSVKKYIYHDFIETIKYOSLPYFMEGCKPKIINSFTODIEKQSDA 842
 774 MKWVPRPNISKYYIYHDFIETIKYOSLPYFMEGCKPKIINSFTODIEKQSDA 832
 QY 843 YVIVPIIISCVLLGLTLLISHORMKKLFMEDVPRPKNSMAOGLNOKPETEHLFTKH 902
 833 YVIVPIIISCVLLGLTLLISHORMKKLFMEDVPRPKNSMAOGLNOKPETEHLFTKH 892
 QY 903 TASVTCGPLEPFTISEDISVTSWKNKDEMPITTVSL--TTDLKGSVCISDQNS 961
 893 PEAMSEFPLEPFTISEDISVTSWKNKDEMPITTVSL--TTDLKGSVCISDQNS 952
 QY 962 VNSSEADGEVYIEDESQROPVVKYATLINSKPSSEGEOSLINSVTKCFSSKNSPLK 1021
 953 RSFSECSAPPIPAETSON--VKATVINSGSGGLYEOKKNPRSGFDRCHLAEDPLAA 1010

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 05:18:00 ; Search time 122.79 Seconds
(without alignments)
1053.840 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254
Sequence: 1 MTCQFCVYLHMEFTYIT.....QTCSTQTHKMKMCDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6254	100.0	1165	18	AAW24051 Human MSX receptor
2	6254	100.0	1165	22	AAE12609 Human Ob receptor
3	6254	100.0	1220	18	AAW34500 Obesity receptor D
4	6250	99.9	1165	22	AAE12551 Human Ob receptor
5	6246	99.9	1165	20	AAI13474 Peptide Seq ID No:
6	6240	99.8	1165	18	AAW19116 Human Ob receptor
7	5809	92.9	1221	19	AAW62544 Human ob-receptor
8	4831.5	77.3	970	18	AAW34499 Obesity receptor C
9	4826	77.2	896	18	AAW24052 Human MSX receptor
10	4826	77.2	923	18	AAW24053 Human MSX receptor
11	4826	77.2	972	18	AAW34497 Obesity receptor A

12	4826	77.2	999	18	AAW34498 Obesity receptor B
13	4819.5	77.1	958	18	AAW38214 Human OB-R variant
14	4819.5	77.1	958	18	AAW31911 Human OB-R lepin
15	4819.5	77.1	958	18	AAW19535 Human OB-R lepin
16	4819.5	77.1	958	18	AAW22773 Human haematopoiet
17	4816.5	77.0	960	17	AAW88910 Haematopoietin rec
18	4814	77.0	896	18	AAW50003 Human OB-R variant
19	4814	77.0	904	18	AAW50002 Human OB-R variant
20	4813	77.0	908	17	AAW88911 Haematopoietin rec
21	4811	76.9	898	17	AAW88912 Variant form of hu
22	4799	76.7	908	18	AAW19536 Human haematopoiet
23	4785	76.5	908	18	AAW14841 Human haematopoiet
24	4784.5	76.5	1162	18	AAW34257 Rat wild-type ob r
25	4784.5	76.5	1162	18	AAW23398 Rat ob receptor (w
26	4778.5	76.4	1162	18	AAW23399 Rat ob receptor (f
27	4770.5	76.3	1162	18	AAW19115 Murine long form O
28	4770.5	76.3	1162	22	AAE12615 Murine long form O
29	4766.5	76.2	1162	20	AAV13473 peptide Seq ID No:
30	4574	73.1	883	19	AAW62543 Human ob-receptor
31	4554	72.8	839	18	AAW34502 Obesity receptor P
32	4421	70.7	815	20	AAV05701 Human OB receptor
33	4337	69.3	804	18	AAW34501 Obesity receptor P
34	4214.5	67.4	1015	18	AAW34259 Rat ob receptor is
35	3793	60.6	900	18	AAW22105 Murine leptin rece
36	3787	60.6	892	18	AAW34260 Rat ob receptor is
37	3787	60.6	894	18	AAW37337 OB protein recepto
38	3787	60.6	895	18	AAW34258 Rat ob receptor is
39	3785	60.5	894	18	AAW24064 Murine MSX recepto
40	3785	60.5	894	18	AAW19114 Murine short form
41	3785	60.5	894	22	AAE12608 Murine short form
42	3781	60.5	894	18	AAW37338 OB protein recepto
43	3479	55.6	842	18	AAW22102 Murine leptin rece
44	3340	53.4	805	18	AAW22106 Murine leptin rece
45	3143	50.3	783	18	AAW24054 Murine MSX recepto

ALIGNMENTS

AAW24051	RESULT 1
AAW24051	standard; Protein: 1165 AA.
AC	AAW24051;
XX	
XX	
DE	17-MAR-1998 (first entry)
DT	
XX	
XX	Human MSX receptor variant 13.2.
XX	
KW	Human; MSX receptor; variant 13.2; identification; purification;
KW	ligand; activator; antibody; agonist; proliferation; obesity;
KW	differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW	Type II diabetes; polycystic ovarian disease;
KW	cardiovascular disease; osteoarthritis; dermatological disorder;
KW	hypertension; insulin resistance; hypercholesterolaemia;
KW	hypertriglyceridaemia; cancer; cholelithiasis.
XX	
OS	Homo sapiens.
XX	
PN	W09725425-A1.
PD	17-JUL-1997.
XX	
XX	
PF	07-JAN-1997; 97WO-US00325.
XX	
PR	20-JUN-1996; 96US-0667197.
XX	
PR	08-JAN-1996; 96US-0585005.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
XX	Rodrigues ML;

DR WPI: 1997-372864/34.
DR N-PSDB: AAT85575.

PT MSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours

PS Claim 2, Pages 81-85; 219pp; English.

CC The present sequence is the human MSX receptor variant 13.2,
CC which can be used to identify and purify ligands and activators.
CC An anti-MSX receptor antibody can be used as an agonist to activate
CC the MSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the MSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. MSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.

CC Sequence 1165 AA;

Query Match 100.0%; Score 6254; DB 18; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICRCFVVLMEPIFYTAFTAFNLSYPTPPRFKLSCMPNSTYDFLLPAGISKNTNS 60
DB 1 mlcgcfcvlllweifyltafnlsyptlprwfklscompnstydfllpagskntns 60
QY 61 NGHYTAVEPKNSSGTHESNLSKTFPHCCFRSEODRNCSLCADNIECKTPEVTSNLSVF 120
DB 61 nghyetavepkfnsqthsnlskttfhccfrseqdrcnscldadniecktfvstnslyvf 120
QY 121 QOITDANMNIQCKLKGDKLKFCTYVESLFRNLFRRNRYKHLIYVPEVLDSPLYPQKGS 180
DB 121 qgidanmniqcklkgdklfcyveslfrnlfrrnrykhllyvpevledsplypqkgs 180
QY 181 PQMVHNCNSVHECCCEIVPPTAKINDTLMLCKITSGVIFOSPLMSVQPIVMKPDPP 240
DB 181 pqmvhncnsvheccceivpvtakindtlmlckitsgvifqspmlmsvqpivmkpdpp 240
QY 241 IGLHMEITDDGNLKITSMSSPPLVPPLOYOVKXSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 iglhmeitddgnlkitssmsspplvpplloyovkxsensttvireadkivsatsllvdsilp 300
QY 301 GSSYEVQVNGKRLDQPGTMSDSTRVFTQDVITYFPFKILTSVGSNNVSFHCITKKENKI 360
DB 301 gssyevqvgkrlldqpgtmsdstrvftqdvityfpfkiltsvgsnnvsfhcitrkknki 360
QY 361 VPSKEITVMNMNIAEKIPQSOYDVVSDHVSKVTFPMINERKPRGKFTYDAVVCNEHECH 420
DB 361 vpskeitvmnmniaekipqsoydvvsvdhvskvtfpminerkprgkfttydavyvcnehech 420
QY 421 RYAEELVIDVNNINISCEIDGYLTRKMTCRMSTSTIOSLAESTLQOLRYHRSLSYCDIPSIH 480
DB 421 ryaeeividvnniniscetidgyltrkmtcrmststioslaestlqolryhrslycdipsih 480
QY 481 PISEKDCYLOSDFGYECTFPPIFLSGYTMWIRLNHSIGSDSPPTCVLPDVSVKPLPP 540
DB 481 pisekdcylsdfgyectfpipflsgytmwirlnhsigsdspptcvlpdvsvkplpp 540
QY 541 SSVKAEITINIGLKLISMEKIPVEPENNIOFOIRYGLSKREVQMKVYEVYDAKSKVSILPV 600
DB 541 ssvkaeitinigllklismekipvepenniofoirylglskrevmkvyyevydaakskvsilpv 600

DB 541 ssvkaeitinigllklismekipvepenniofoirylglskrevmkvyyevydaakskvsilpv 600
QY 601 PDLCAVAVQVRCRKLDDGLGYWSNMSNPAYTVMDIKYPMRGPFRWIRINDGTMRKENY 660
DB 601 pdlcaavavqvrckrlddglgywsnmsnpaytvmdikypmrgpfrwirindgtmrkeny 660
QY 661 TLLMKPLKNDSLCSVORYVNIHHTSCNGTMSDEVGNHTKFTETLDEQAHVTVALAINSI 720
DB 661 tllmkplkndslcsvoryvnihtscngtmsdevgnhtkftetldeqahvtvalainst 720
QY 721 GASVANFNTEFPMPSKNIYOSLSAYPLNNSCVSNLSIDSVKLMWFIEEMNLNED 780
DB 721 gasvanfnfepmpskniyoslsayplnnsccvsnlsidsvklmwfieemnlnd 780
QY 781 GRKMLRISSSVKKYIHDHFPIEKYOFSLPIRMEGVKPKIINSFTODIEXHOSDA 840
DB 781 grkmlrisssvkkylidhfpieryofslpirmegvkkpkiinsftodiexhosda 840
QY 841 GLYIVLPVYISSLILGLTLISHQRMKKLFMEDVPNRKNCMAGLNFQKRETEHFI 900
DB 841 glyivlpvylsslllgltlisshqrmkklfmedvpnrkncmagslfnfqkretelhfi 900
QY 901 KHTASVTCGPLLEPETSIEDISVDTSWKNKDEMPPTVVSILSTTDLEKGSVCISDPFN 960
DB 901 khtasvtcgpillepetsiedisvdtswknkdempptvvsilstdlekgsvcisdqfn 960
QY 961 SVNFSEAEGETVYDESGROPFVYATLISNSKPSKETGEEOGLINSVTKCFSSKNPDL 1020
DB 961 svnfseaegetvtydesgropfvayatlisnskpsketgeeoqlinsvtfkssknpdl 1020
QY 1021 KDSFNSNSWEIRAOAFILISDQHPNIIISPHLTFSGLDLKLKFNFPENNDRKSTIYL 1080
DB 1021 kdsfnssnwelraqafilisdqhpniisphltfsgldlklkfnfpenndrkstiyyl 1080
QY 1081 GVTSLKRRSEGVLLTDKSRVSCFPAPCLFTDIRILOSCHSFVNNTNLGTSKRTFAS 1140
DB 1081 gvtslkrrsegvlltdksrvscfpapclftdiriloschsfvnnnlgtsskrtfas 1140
QY 1141 YMPFOFOTCSTOTHTKTMENKMDLTIV 1165
DB 1141 ympfofotcstothtktemnkmdltiv 1165

RESULT 2
AAEI2609
ID AAEI2609 standard; Protein: 1165 AA.
XX
AC AAEI2609;
XX
DT 03-JAN-2002 (first entry)
XX
DE Human Ob receptor (OBR) protein.
XX
KW Human; obese receptor; OBR; anorectic; anabolic; body weight disorder;
XX therapy; obesity; cachexia; anorexia.
OS
XX Homo sapiens.
XX
FH Key
FH Peptide 1..20
FH Protein /label- Signal_peptide 21..1165
FH Domain /label- Human_mature_OBR_protein 21..839
FH /label- Extracellular_domain 23..25
FT Modified-site /note- "Asn is N-glycosylated" 41..43
FT Modified-site /note- "Asn is N-glycosylated" 56..58
FT Modified-site /note- "Asn is N-glycosylated" 59..61
FT Modified-site /note- "Asn is N-glycosylated"

FT Modified-site 73..75 /note- "Asn is N-glycosylated"
 FT Modified-site 98..100 /note- "Asn is N-glycosylated"
 FT Modified-site 187..189 /note- "Asn is N-glycosylated"
 FT Modified-site 206..208 /note- "Asn is N-glycosylated"
 FT Modified-site 276..278 /note- "Asn is N-glycosylated"
 FT Modified-site 347..349 /note- "Asn is N-glycosylated"
 FT Modified-site 319..323 /note- "Asn is N-glycosylated"
 FT Region 397..399 /note- "Conserved motif of cytokine I receptor family"
 FT Modified-site 433..435 /note- "Asn is N-glycosylated"
 FT Modified-site 516..518 /note- "Asn is N-glycosylated"
 FT Modified-site 622..626 /note- "Asn is N-glycosylated"
 FT Region 624..626 /note- "Conserved motif of cytokine I receptor family"
 FT Modified-site 659..661 /note- "Asn is N-glycosylated"
 FT Modified-site 670..672 /note- "Asn is N-glycosylated"
 FT Modified-site 688..690 /note- "Asn is N-glycosylated"
 FT Modified-site 697..699 /note- "Asn is N-glycosylated"
 FT Modified-site 728..730 /note- "Asn is N-glycosylated"
 FT Modified-site 750..752 /note- "Asn is N-glycosylated"
 FT Modified-site 840..862 /note- "Asn is N-glycosylated"
 FT Domain /label- "Transmembrane_domain"
 FT Domain 863..1165 /label- "Cytoplasmic_domain"
 FT Domain /label- "Cytoplasmic_domain"
 PN US6287782-B1.
 PD 11-SEP-2001.
 XX 29-APR-1998; 98US-0069781.
 XX 27-NOV-1995; 95US-0562663.
 PR 04-DEC-1995; 95US-0566622.
 PR 08-DEC-1995; 95US-0569485.
 PR 11-DEC-1995; 95US-0570142.
 PR 28-DEC-1995; 95US-0583153.
 PR 22-JAN-1996; 96US-0599455.
 PR 26-APR-1996; 96US-0638524.
 PR 03-SEP-1996; 96US-0708123.
 PR 28-MAY-1997; 97US-0864564.
 XX
 PA (MILL.) MILLENNIUM PHARM INC.
 XX
 PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;
 XX
 DR WPI: 2001-624489/72.
 DR N-PSDB; AAD20509.
 XX
 PT Identifying compounds for treating body weight disorder, e.g. obesity,
 PT anorexia or cachexia, comprises contacting cell expressing mammalian Ob
 PT receptor protein, JAK2 protein and mammalian SOCS-1 protein with test
 PT compound
 XX
 PS Claim 1; Fig 3; 109pp; English.
 CC The patent discloses obese receptor (Obr) proteins and nucleic acids
 CC encoding them. Obr protein participates in the regulation of mammalian

CC body weight. The invention also relates to a method of identifying
 CC therapeutic compounds for the treatment of a body weight disorder.
 CC The method involves contacting a cell that expresses a mammalian Obr
 CC protein, a JAK2 protein and a mammalian SOCS-1 protein with a test
 CC compound. The method is useful for identifying compounds which modulate
 CC Obr gene expression and gene product activity, which can be used as
 CC agents to control body weight particularly as therapeutic agents for
 CC treating body weight disorders, including obesity, cachexia and anorexia.
 CC The present sequence is Obr protein from human.
 XX
 SQ Sequence 1165 AA;

Query Match 100.0%; Score 6254; DB 22; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLWMEFVITAFNLSVPTPMFKLSQMPNNTYVFLPALSKNTS 60
 DB 1 mtcgkfcvllwmevltatnlslpplvprfklsmpnntdyfllpagskntns 60
 QY NGHYETAVEPRFNSSGTHPSNLSKTTFHCCFSEDDRNCSLCADNIEGTFVSTNSLVF 120
 DB 61 nghyetaveprkfnsqthnskskttfhccfseqdncslcadnlegkftvstnslvf 120
 QY 121 QOIDANMNIQCMKGDLEKLFICVESLFFKNLFRNRYKVLHLLVLPVLEDSPLVPQKS 180
 DB 121 qoidanwniqcmkgdleklficveslffknlfrnykvhllvlpvlevedsplvpqks 180
 QY 181 FQWVHNCNVHSCCECLVPPVPAKNDTLMLCKITSGVIRQSPLMSQPINMKVPPDP 240
 DB 181 fgmvnncnvhscceclvppvpakndtlmlckitlsgvirlqspmsvqpinmkvppdp 240
 QY 241 LGLHMETDGMKLSWSSPPLVPPVQVRYKSESTVIREAPKIVSATSLVDSILP 300
 DB 241 lglhmeitdgmklswsspplvppvqvryksestvirleapki vsat slvdsilp 300
 QY 301 GSSYEYQVGRKLDGPGIWSDMSTPRVFTTQVYIFPPKILTSVGSNVSFHCITKKENKI 360
 DB 301 gssyeqvgrkldpgiwsdmsprvfttqvdyifppkiltsvgsnvsfhclykknk 360
 QY 361 VPSKETVMMNNAEKIPQSOQDVVSDHVSQVTFPNLNETKPRGKLTVDVAVCCNEHECH 420
 DB 361 vpsketvmmnaekipqsgdvdsdhvskvctfnlnekpqkltvdavccnehech 420
 QY 421 RYAEIYVIDVNNISCEITDGYLTMMTCRMSTSTIOSLAESTQLRHRSLYCSIDPSIH 480
 DB 421 ryaelyvldvnnisctetdgyltmctcrststiqslaestqlrhrsl ycsidpsih 480
 QY 481 PISEPKDCTLOSDFEYECIFOPIFLISGTYMMIRINHSIGSLDSPPTCYLPDSYVAKLPP 540
 DB 481 pisepkdcylsdfeyecifopiflislgytmmirinhslgsldspptcylpdsyvklpp 540
 QY 541 SSVKAEITINIGLKTSMKRPVPEPENNLOFOIRYGLSGKEVQMKV EYVDASKSVSLPV 600
 DB 541 ssvkaeitiniglktsmkrpvpepennlofoir yglsgkevqmkv eyvdasksvslpv 600
 QY 601 PDLCAVYAVOVRCRKLDSGLGWSNMSNPATVYMDIKVPMRGPPEFRIINGDTMKKEKNV 660
 DB 601 pdlcavayavovrcrkldsglgwsnmsnpatvymdikvpmrgp pefriingdtmkkeknv 660
 QY 661 TLIMKPLMKNDLSLCSYQRYVINNHHSNCGTWSGEDVGNHKKFTFLKT EOHATYVLAINSI 720
 DB 661 tllmkplmkndslslcsyqryvinnhhsncgtwsge dvgnhkkftflk t eohatyvlainsi 720
 QY 721 GASVANFNLTFSMPMSKVNIOSLSAYPLNSSCVIYSWILSPSDYKLMFIIEMKRLNED 780
 DB 721 gasvanfnltfsmppmskvniosl sayplnsscviysw ilspdyk lmfiiemkrlned 780
 QY 781 GEIKMLRISSSVKYYIHDHFIPIEKYQPSLPIFMEVGGKRIINSFTQDDIEKHQSDA 840
 DB 781 geikmlri:sssvkyyihdhfipiekyqpslpi fmevggkriinsftqddiekhqsd 840

OY	841	GUYVIVPVIILSSILLGTLTLLISQRRKKLFEMEDVPNPKNCMAOGLINOKPEFPHLFI	900
Dd	841	glyIvIvPIIIssSIlllgtlLIshqrmkklfEvedvpnpknswaglnfqdpetfehlfi	900
OY	901	KHTASVTCGPILLPEPTISEDISVDYSWMKKNDEMPITVVSLSTTDLEKGSVCISDQFN	960
Dd	901	khtasvtcgpIlllepetIsedIsvdtswnkkndemPitvvslsttdlekgsvcIsdqfn	960
OY	961	SVNSFEAGCTVTYTEDESOGOPFKKYATLTLSNKSAPETGEQGLINSVTKCFESSKNSPL	1020
Dd	961	svnfsEaGctevTyedesgqpIvKyacLLsnksApEtgeeqglInsvtkCfEssKnSpL	1020
OY	1021	KDSFSNSWEIEAOAFETILSDQHPNIISPHLTFSEGLDELKLEGNFPEENNDRKSIYYL	1080
Dd	1021	kdsfsnsweIeaGaFetiLsdqhpniiSPHltfsegldeIlkegnfpEennDrKksiYyL	1080
OY	1081	GVTSTKRKESSVLLTDKSRSCPPAPACLETDIRVLQDSCSHFVENNIMLGTSKKTRFAS	1144
Dd	1081	gvtsTkRkesvgvlltDKsrscPfPaclEtDirvlqdScshFvenniMlgtSkktRfas	1144
OY	1141	YMPQFCSTOTHKIKMNKKODLTIV	1165
Dd	1141	ympqfcstqtKhikmnkmdltiv	1165
 RESULT 3 AAM34500 ID AAN34500 standard; protein; 1220 AA. XX AC AAM34500; DT 18-MAR-1998 (first entry) XX DE Obesity receptor D protein. XX KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex; KW high blood lipid level; obesity; diabetes; high cholesterol level; KM weight loss; therapy; weight maintenance. XX OS Homo sapiens. XX XX Key Location/Qualifiers FH Misc-difference 1..1165 /note="encoded by AAT98531" FT FT Misc-difference 1166 /label="unknown FT /note-" "encoded by stop codon" FT Misc-difference 1169 /label="unknown FT /note-" "encoded by stop codon" FT Misc-difference 1187 /label="unknown FT /note-" "encoded by stop codon" FT Misc-difference 1207 /note="unknown FT /label="unknown FT Misc-difference 1..1165 /note="encoded by stop codon" FT /note-" "encoded by AAT98531" XX XX WO9725424-A1. PN PD 17-JUL-1997. XX PF 02-JAN-1997; 97MO-US00128. XX PR 31-DEC-1996; 96US-0774414. PR 04-JAN-1996; 96US-0582825. XX PA (AMGE-) AMGEN INC. XX XX Chang M, Fletcher PA, Welcher AA; XX WPI: 1997-384981/35. OR			

DR	N-PSDB;AAT98531.
XX	Obesity protein receptor(s) and related DNA - used to treat weight
PT	disorders, e.g. obesity, diabetes and high cholesterol or blood
PT	lipid levels
PS	
XX	
XX	Claim 31; Page 76; 151pp; English.
CC	This sequence represents the obesity (OB) receptor D protein. This
CC	sequence has one or more of the biological properties of naturally
CC	occurring OB receptor protein. The OB receptor proteins and OB
CC	receptor/OB protein complexes are used for the treatment of obesity,
CC	diabetes, high blood lipid levels and high cholesterol levels. The
CC	proteins may also be used to treat an individual for weight loss or
CC	weight maintenance required for purely cosmetic purposes.
SQ	Sequence 1220 AA;
Query Match	100.0%; Score 6254; DB 18; Length 1220;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1165; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MICQKFCVLLHMEFTVTAFNLSTPIITWRFKLSCEMPNSTVDYFILPAGLSKNTNS 60
Db	1 micqgfcvlllhmefiyvltafnlstpiitwrfklscompnstcydflilpaglskntns 60
OY	61 NGHYEFAVEPRKNSSGTHFSNLSKTTFPHCCFHSBDNRNCSLCADNI EGTFFSTNSLVE 120
Db	61 nghyevaveprknssgthfsmksttfphccrfsqdqrmslcadnleagctfsvsnslvf 120
OY	121 QOIDANMNITQMICKDKLFETCYVESLEFKNLFRNYKYVHLLYVPREVLDSPLYPOKS 180
Db	121 qgidanmwigcwlbgdklkificyveslfknlfrnykykhillylvpevledsplvpqks 180
OY	181 PQMWNCNSVHECCCCLVYPFPRAKINDPLMLCKLTSGVITROSPLMSQPINMKRPPR 240
Db	181 fqmwnconsvehcccclvypprakindtlmlcklitsgvtlgsplmsvqpimmkpprp 240
OY	241 IGLHMEITDDGMILKISWSSPPLVPPFLQYQVYSSENSTVIAREAKIVSATSLDVSILP 300
Db	241 lglhmeitddgmlikswsspplvppflqyvqysensstviareakivsatsildvsilp 300
OY	301 GSSTVVOVRGRKLDPGLSDMNSTPRVFETTDVITYPPKILT SVCSNVSFHCITYKENKI 360
Db	301 gssyvevyrgrklldpglswdsnstprvfetfgdvityfpkllt svqsnsvfhciylkenki 360
OY	361 VPSKLIWMNMNLAEKIRPOSQDVYSDHYSKYFEFNLENKRPGRKTPYAAYVCNGHECH 420
Db	361 vpskelivwmnmnlaea klrposqvavsdhyshkvelflnnekrgpkrtlyadvycnehech 420
OY	421 RYAEELYVIDVNINISCEDFDGYLTKKTKCWSTSTIOSLAESTOLUYNHSSLSICSDIPSIH 480
Db	421 ryaeelyvidvniniscedfdgyltkktcwststioslaestolulynhsslsicdsipsh 480
OY	481 PISEPKDCYLQSDGTYECTIFOPFIPLSGTYMTKRINHSLGSIDSRPCYLPDSVYKPLRP 540
Db	481 pisepkdcylqsdfgeyeictfipfilisgtymtkrinhslgsidsprtcvlpdvskplrpp 540
OY	541 SSVKKEITINIGLKLTSMEEKPFEPENNNOFOFRYLTSGEKVEOMKUYEUYDAKRSVSLPV 600
Db	541 ssvkkeitinigllkltsmekpfepennnqfqltyslgkevqwkmyeydakrsksvslpv 600
OY	601 PDLCADVAVOVQRCKRLDLGIYWSMNSNPAYTVVMDIKVPMRGPREFWRIINGDTMKREKNV 660
Db	601 pdlcadvavovqrckrlldglywsmsnpaytvvmidikvpmrgprefwriingdtmkkeknv 660
OY	661 TLWKMRILKKNSTCSVORVVVINHHNSCGTSESDVGNHTKFTFLMTBOAHPTYVALINSI 720
Db	661 tlwkmrkndstcsvqvryvinhhnsctsedvgnthtkftflwcgahtcvvalansi 720
OY	721 GASVANFMILTESWPMSKNNIVOSLSAAYLNSCVIVSWILSPSDKLMFYFIEMKNELMD 780

Db 721 gasvanfultfswpmksknivgsisayplnscvlsvslpsdyklymfilewknined 780
Qy 761 GEIKWLRISSVKKYKYYIDHDFPIEKYQFSLYPIEMEGVGKPKIINSPFODDIEKHQSDA 840
Db 761 geikwlriSSVKKYKYYIDHDFPIEKYQFSLYPIEMEGVGKPKIINSPFODDIEKHQSDA 840
Qy 841 GLYVIVPPIISSLTGLTLISHORMKKLPWEDVPNPKNCWAOGLNFKQKETEHLFI 900
Db 841 glyvivpviISSLTGLTLISHORMKKLPWEDVPNPKNCWAOGLNFKQKETEHLFI 900
Qy 901 KHTASVTGCPILLPEPTISEDISVDTSMKNKDEKMPVTVVSLSTDTLEKGSVCISDPFN 960
Db 901 khtasvtGCPILLPEPTISEDISVDTSMKNKDEKMPVTVVSLSTDTLEKGSVCISDPFN 960
Qy 961 SVNFSAEAGTEVYEDESOROPFVKYATLISNPKSPETGEOGLINSSVTKCFSSKNSPL 1020
Db 961 svnfseagteVYEDESOROPFVKYATLISNPKSPETGEOGLINSSVTKCFSSKNSPL 1020
Qy 1021 KDSFNSNWEIFAOAFILSDHPNITSPHLTFSGLDELKLEGNFPENNDKXSYTYL 1080
Db 1021 kdsfnsnweIfaOAFILSDHPNITSPHLTFSGLDELKLEGNFPENNDKXSYTYL 1080
Qy 1081 GVTSSIKRESGVLTIDKRSVSCFPAPCLFTDRIVLQDSCSHFVENNTNLGTSKKTFAS 1140
Db 1081 gvtssikresgvLTIDKRSVSCFPAPCLFTDRIVLQDSCSHFVENNTNLGTSKKTFAS 1140
Qy 1141 YMPQFQCSQTQHKIMENKMCULTV 1165
Db 1141 ympqfqcstqtkhimenkmcultv 1165

RESULT 4
AAEI2551 ID AAEI2551 standard; Protein; 1165 AA.
XX AAEI2551;
AC
XX
XX 03-JAN-2002 (first entry)
XX
XX Human Ob receptor (OBR) protein mutant (Y1141F).
XX DE Human; obese receptor; OBR; anorectic; anabolic; body weight disorder;
KW therapy; obesity; cachexia; anorexia; mutant; mutein.
XX OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FT Peptide 1..20
FT /label- Signal_peptide
FT /label- Signal_peptide 21..1165
FT /label- Human_mature_OBR_protein 21..839
FT /label- Extracellular_domain 23..25
FT /note- "Asn is N-glycosylated" 41..43
FT /note- "Asn is N-glycosylated" 56..58
FT /note- "Asn is N-glycosylated" 59..61
FT /note- "Asn is N-glycosylated" 73..75
FT /note- "Asn is N-glycosylated" 98..100
FT /note- "Asn is N-glycosylated" 187..189
FT /note- "Asn is N-glycosylated" 206..208
FT /note- "Asn is N-glycosylated" 276..278
FT /note- "Asn is N-glycosylated" 347..349

FT Region /note- "Asn is N-glycosylated" 319..323
FT /note- "Conserved motif of cytokine I receptor family" 397..399
FT Modified-site /note- "Asn is N-glycosylated" 433..435
FT Modified-site /note- "Asn is N-glycosylated" 516..518
FT Modified-site /note- "Asn is N-glycosylated" 622..626
FT Region /note- "Conserved motif of cytokine I receptor family" 624..626
FT /note- "Asn is N-glycosylated" 659..661
FT Modified-site /note- "Asn is N-glycosylated" 670..672
FT Modified-site /note- "Asn is N-glycosylated" 688..690
FT Modified-site /note- "Asn is N-glycosylated" 697..699
FT Modified-site /note- "Asn is N-glycosylated" 728..730
FT Modified-site /note- "Asn is N-glycosylated" 750..752
FT Modified-site /note- "Asn is N-glycosylated" 840..862
FT Domain /label- Transmembrane_domain 863..1165
FT Domain /label- Cytoplasmic_domain 1141
FT Misc-difference /note- "Wild type Tyr substituted with Phe" 1141
FT US6287782-B1.
XX 11-SEP-2001.
XX
XX 29-APR-1998; 98US-0069781.
XX
XX 27-NOV-1995; 95US-0562663.
XX 04-DEC-1995; 95US-0566622.
XX 08-DEC-1995; 95US-0569485.
XX 11-DEC-1995; 95US-0570142.
XX 28-DEC-1995; 95US-0583153.
XX 22-JAN-1996; 96US-0599453.
XX 26-APR-1996; 96US-0638524.
XX 03-SEP-1996; 96US-0708123.
XX 28-MAY-1997; 97US-0864564.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;
XX WPI: 2001-624489/72.
XX
XX Identifying compounds for treating body weight disorder, e.g. obesity, anorexia or cachexia, comprises contacting cell expressing mammalian Ob receptor protein, JAK2 protein and mammalian SOCS-1 protein with test compound
XX
XX
XX Disclosure: Page -: 109pp; English.
XX
XX The patent discloses obese receptor (OBR) proteins and nucleic acids encoding them. OBR protein participates in the regulation of mammalian body weight. The invention also relates to a method of identifying therapeutic compounds for the treatment of a body weight disorder. The method involves contacting a cell that expresses a mammalian OBR protein, a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The method is useful for identifying compounds which modulate OBR gene expression and gene product activity, which can be used as agents to control body weight particularly as therapeutic agents for treating body weight disorders, including obesity, cachexia and anorexia. The present sequence is human OBR protein mutant (Y1141F).
XX Note: This sequence is not shown in the specification but is derived

CC from the wild-type human ODR protein shown in figure 3 of the
 CC specification (AA12609).

XX Sequence 1165 AA;

Query Match 99.9%; Score 6250; DB 22; Length 1165;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MCCORCVLLHMEFYVTAFTAFNLSPYTPMRFKLSQMPNSTYDFELLPAGLSKNTS 60
DB 1 mccqfcvllhmetfvtatfnlsyplcpwfklsmpnstydfellpagslknstns 60
OY 61 NCHYETAPEPKFNSSGTHFSNLKTTFHCCFSEODRNCSLCADNTEGKFTSTVNSL 120
DB 61 nchyetapepkfnssgthfnslnskttfhccfseodrnscslcadnteegkftstvnslvf 120
OY 121 QOIDANNNTQCVLKGDLKLFICYVSLFKNLFKNLYKVLHLLVLPVLEDSPLVPQKS 180
DB 121 qoidannntqcvlkgdldklficyvslfknlfknlykvllhllvlpvleedsplvpqks 180
OY 181 FQMVHNCNSVHCCCECLVNPFTAKINDTLMLKLTSGVITQSPLMASQPINMKRDP 240
DB 181 fqmvhncnsvhccceclvnpftakindtlmlcltsgvltqspmsvqpinmkvdpdp 240
OY 241 LGIAMEITDDGNLKITSSWSSPLVPPLOQVYKSENSTVIREADKIYATSLVDSILP 300
DB 241 lgiameitddgnlkitsswssplvpploqvkyksenstvirreadkiyatstlvdsilp 300
OY 301 GSSYEVQVNGKRLDGPGLSDMSTPRVFTTQVYIYFPFKILTSVGSNNVFCITKKENKI 360
DB 301 gssyevqvgkrlldpgplsdmstprvfttqvdiyfpfkiltsvgsnsvfchlykknki 360
OY 361 VSKETIVMMNMTAEKIPQSOQDVSPSHVSKVTFEFLNTEKPKGKFFYDYDVCCNEHECH 420
DB 361 vsketivmmnmtaekipsgqdyvshdvskvtfelnetskpgkfydydvccnehech 420
OY 421 RYAEIYVIDVNNINISCEITDGYLTAKMTKRWSTSTIOSLASTIOLRYHRSSLYCSDIPSIH 480
DB 421 ryaeliyvidvnniniscetdgytlkmtcrwststioslastiolryhrsslycsdipsih 480
OY 481 PISEPKDCLQSDGFVECLFQPIFLISGTYMIRINHSGLSDSPPTCVLPSPVAKPLPP 540
DB 481 pisepkdcylqsdgfveclfqpiflisytmwirinhsghsdspptcwlpsvavkplpp 540
OY 541 SSVKAEITTNIGLKLISMEKPVFPENNLOFOJIRYGLSGEYQWKMKEVYDAKSKSVSLPV 600
DB 541 ssvkaeitnigllklsmekpvfpennlofojirysglsgewkmkewydaaksksvslpv 600
OY 601 PDLCAVYAVQVRCRRLDGLGIYWSNMSNPAYTVVMDIKYPMRGPPEFWRILNGDTMKKENV 660
DB 601 pdlcavyavqvrckrlldglgiywsnmsnpaytvvmdikypmrpgefwrilngdtmkkenv 660
OY 661 TLLMPLKMNDSLCVQORVINHHTSCNCTNSGDVGNHFKFFFLMTEQAHYTVLAINI 720
DB 661 tllmplkmnndslcvqorvinhhtscnctnsedvgnhfkffflmteqahyvtvlaini 720
OY 721 GASVANFNLTFSMPMSKVIQSLASAPYNSQVYTWILSSDYKLMFIEEMKLNED 780
DB 721 gasvanfnltfsmvmskviqslasapyntsqvyswvylssdyklymfieemklned 780
OY 781 GEIKMLRISSSVKYYIHDFPIEKYOFSLYPIFMEGEGKPKIINFTQDIEKHQSDA 840
DB 781 geikmlri:sssvkyyihdfpiekyofslypifmegygpkkliinfstqddiekhsda 840
OY 841 GLIYIVPVYIISIIILGLILSHQRMKLEWEDVPNPNRCWAGQINQKRETEHLEFI 900
DB 841 gliyivpvylisiiilglilshqrmkliwevdpnpncwagqinfqkretelhlefi 900
OY 901 KJTASVTCGPLLEPETISEDIVTSWNRKDEMMPTTVVSLSTDLKSGVCSIDQFN 960
DB 901 khtasvtcgppllepetisedivtswnkndemtpctvsvslstdlekgsvcsidqfn 960

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OY 961 SVNFSEAEGETVTEDESGQRPVYAYATLISNSKPSSETGEQGLINSVTCKFSKNSPL 1020
DB 961 svnfseaegetvteydesqrgpfvayatlinskspssetgeegllnsvtckfcsknspl 1020
OY 1021 KDSFNSNSWEITDAQAFILISDOHPNISPRLTFPSGLDELKLEKNFPENNDDKSIYTL 1080
DB 1021 kdsfnsnsweiteaqaffilisdohpnisprltpfsgldelklegnfpennddksiiyl 1080
OY 1081 GYTSIKKRRESGVLLIDKRSVSCPPAPCLETDIRVLQDSCSEHFNINILGTSKKTFFAS 1140
DB 1081 gytsikkrresgvllidkrsvscppapcletdirvldqscshfnvnnilgtskktffas 1140
OY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 fmpqfotcstqthkimenkmoldtv 1165

```

```

RESULT 5
AAV13474
ID AAV13474 standard; Protein; 1165 AA.
XX
AC AAV13474;
XX
DT 26-JUL-1999 (first entry)
DE Peptide Seq ID No: 4 of W09923493.
XX
KW Leptin; phosphorylated leptin receptor; tyrosine phosphatase ID: PTP-ID;
KW modulator; drug; weight loss; adiposity; hypertension; heart disease;
KW type II diabetes; cancer; AIDS; agriculture.
OS Homo sapiens.
PN
XX W09923493-A1.
PD 14-MAY-1999.
XX
PF 27-OCT-1998; 98WO-0522797.
XX
PR 26-OCT-1998; 98US-0178691.
PR 31-OCT-1997; 97US-0961805.
XX
PA (UTRO ) UNITV ROCKEFELLER.
PI
XX Friedman JM, Li C;
XX WPI: 1999-327025/27.
XX N-PSDB; AAX55588.
DR
PT Identifying modulators agents that modulate leptin activity
PS Disclosure; Page 77-84; 96pp; English.
XX
CC The invention provides a method for identifying modulators of binding of
CC a phosphorylated leptin receptor with tyrosine phosphatase ID PTP-ID).
CC The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin
CC receptor or its phosphorylated fragment with protein PTP-ID or its
CC fragment in the presence and absence of a candidate agent under
CC conditions in which the absence of the agent the binding of the
CC phosphorylated leptin receptor or fragment with PTP-ID or its fragment
CC can be detected; and (b) detecting the binding of the phosphorylated
CC leptin receptor and PTP ID; where an increase in binding detected in the
CC presence of the agent, indicates that the agent enhances binding, and a
CC decrease in binding in the presence of the agent indicates that the agent
CC is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin
CC receptor-dependent PTP-ID phosphorylation are useful as drugs in weight
CC loss diet regimens. The drugs identified can regulate adiposity and fat
CC content of animals, particularly in mammals. Disorders that can be
CC treated by PTP-ID modulators include obesity and its associated diseases,
CC e.g. hypertension, heart disease and type II diabetes, and weight loss
CC associated with cancer and AIDS. Additionally the agents identified may
CC be useful in agriculture where body weight of domestic animals can be

```


FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 433
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 516
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 624
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 658
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 670
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 688
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 697
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 728
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"
 FT 750
 FT Modified-site
 FT /label- Glycosylation
 FT /note- "potential N-linked glycosylation site"

W09719952-A1.

05-JUN-1997.

27-NOV-1996; 96MO-US19128.

03-SEP-1996; 96US-0708123.

27-NOV-1995; 95US-0562662.

04-DEC-1995; 95US-0566622.

11-DEC-1995; 95US-0569485.

28-DEC-1995; 95US-0570142.

22-JAN-1996; 95US-0583153.

26-APR-1996; 96US-0598455.

(MILL-) MILLENNIUM PHARM INC.

Culpepper JA, Tartaglia LA, Tepper RI, White DW.

WPI: 1997-310525/28.

N-PSDB; AAT69592.

Isolated Ob receptor genes and polypeptide(s) - useful to develop

products for diagnosis or treatment of body weight disorders, e.g.

obesity, cachexia, anorexia and bulimia

Example: Fig 3; 265pp; English.

Human Ob receptor (OBR) (AAM19116) is a novel polypeptide that

participates in the control of body weight and which is involved in

signal transduction triggered by the binding of its natural ligand,

Ob (leptin). It is a member of the class I cytokine receptor

family. Its amino acid sequence was deduced from a foetal brain

cDNA clone (AAT69592). The receptor corresponds to the long form

mouse OBR (AAM19115). OBR proteins, peptides, antibodies, agonists

and antagonists can be used in the diagnosis and treatment of body

weight disorders such as obesity, cachexia and anorexia.

Sequence 1165 AA;

Query Match 99.8%; Score 6240; DB 18; Length 1165;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTCOKFCVLLHWEFTYTAFTAFNLSPYTPWRFKISCAPPNSTYDFLLPAGLSKNTSNS 60
 1 mtcqkfcvllhweftyltalfnlsplytpwrfkiscappnstydfllpagskntns 60

QY 61 NGHYTFAVEPKFNSSGTHFSNLSKTFTHCCFSEEDRNCSCADNIEGTFVSTVNSLWF 120
 61 nghytavepkfnssgthfnskthfocfsegedrncscadniegkftvstvnslwf 120

QY 121 QOIDANWNIQCWLKDDKLFICYVESLFRNLERNRYKXVHLVLPVLEDSPLYPQGS 180
 121 qoidanwniqcwlkddklficyveslfrnlernrykxvhlvlpvledsplypqgs 180

QY 121 qgidanwniqcwlkddklficyveslfrnlernrykxvhlvlpvledsplypqgs 180
 121 qgidanwniqcwlkddklficyveslfrnlernrykxvhlvlpvledsplypqgs 180

QY 181 FOMWNCNSVHECCCLVPPVPAKLNQTLNLTSGVIRIOPSLMSVQPNMYKPP 240
 181 fomwncnsvhccclvppvpaqlnqtlntltsgviriosplmsvqpnmykpp 240

QY 181 fgmwhncnsvhccclvppvpaqlnqtlntltsgviriosplmsvqpnmykpp 240
 181 fgmwhncnsvhccclvppvpaqlnqtlntltsgviriosplmsvqpnmykpp 240

QY 241 IGLHMEITDDGNLKTISWSSPLVPFLOQYQVYSENSTTVIREADKIVSATSGLVDSILP 300
 241 iglhmeitddgnlktiswssplvpfloyqvysensttvireadkivsatsglvdsilp 300

QY 241 iglhmeitddgnlktiswssplvpfloyqvysensttvireadkivsatsglvdsilp 300
 241 iglhmeitddgnlktiswssplvpfloyqvysensttvireadkivsatsglvdsilp 300

QY 301 GSSYEVQVRGKRLDGPRTMSDMSTPRVFTODVTFPPKILTSVGSNVSFHCYKKENKI 360
 301 gssyevqvrgrldgprtgmsdmstprvftodvtfppkiltsvgsnvsfhcyykknki 360

QY 301 gssyevqvrgrldgprtgmsdmstprvftodvtfppkiltsvgsnvsfhcyykknki 360
 301 gssyevqvrgrldgprtgmsdmstprvftodvtfppkiltsvgsnvsfhcyykknki 360

QY 361 VPSKEIVMMNLAEKIPQSYDVSDHVSKYTFEFLNETKPRGKFTYDAVYCCNHECHH 420
 361 vpskeivmmnlAEKIPQSYDVSDHVSKYTFEFLNETKPRGKFTYDAVYCCNHECHH 420

QY 361 vpskeivmmnlAEKIPQSYDVSDHVSKYTFEFLNETKPRGKFTYDAVYCCNHECHH 420
 361 vpskeivmmnlAEKIPQSYDVSDHVSKYTFEFLNETKPRGKFTYDAVYCCNHECHH 420

QY 421 RYAEIYVDVNNINISCEFDGYITKMTCKMNSTIOSLAESTQLRYHRSSLYCSPISIH 480
 421 ryaeiyvdvnniniscEFDGYITKMTCKMNSTIOSLAESTQLRYHRSSLYCSPISIH 480

QY 421 ryaeiyvdvnniniscEFDGYITKMTCKMNSTIOSLAESTQLRYHRSSLYCSPISIH 480
 421 ryaeiyvdvnniniscEFDGYITKMTCKMNSTIOSLAESTQLRYHRSSLYCSPISIH 480

QY 481 PISEPKDCYLOSDFYECIFOPFIILSGTWMIRIHNLSGSDSPCTCLPSPVYKPP 540
 481 pisepkdcylosdfyeciFOPFIILSGTWMIRIHNLSGSDSPCTCLPSPVYKPP 540

QY 481 pisepkdcylosdfyeciFOPFIILSGTWMIRIHNLSGSDSPCTCLPSPVYKPP 540
 481 pisepkdcylosdfyeciFOPFIILSGTWMIRIHNLSGSDSPCTCLPSPVYKPP 540

QY 541 SSVKAEITINILKLTISWEKPVFPENNLOFQIRYGLSCGENQWQKVEYVYDANKSVSLPV 600
 541 ssvkaeitiniLkLTISWEKPVFPENNLOFQIRYGLSCGENQWQKVEYVYDANKSVSLPV 600

QY 541 ssvkaeitiniLkLTISWEKPVFPENNLOFQIRYGLSCGENQWQKVEYVYDANKSVSLPV 600
 541 ssvkaeitiniLkLTISWEKPVFPENNLOFQIRYGLSCGENQWQKVEYVYDANKSVSLPV 600

QY 601 PDLCAVYAVQVCKRLDGLIGYSNNSNPAYTYVMQIKYPMKCPERWRIINGTMMKKNV 660
 601 pdlcavYAVQVCKRLDGLIGYSNNSNPAYTYVMQIKYPMKCPERWRIINGTMMKKNV 660

QY 601 pdlcavYAVQVCKRLDGLIGYSNNSNPAYTYVMQIKYPMKCPERWRIINGTMMKKNV 660
 601 pdlcavYAVQVCKRLDGLIGYSNNSNPAYTYVMQIKYPMKCPERWRIINGTMMKKNV 660

QY 661 TLKMKPLKNDISGVORVNIHHTSCNGTMSDEDGNHFKFELTDEOAHYTVLAINSI 720
 661 tlkmpLkNDISGVORVNIHHTSCNGTMSDEDGNHFKFELTDEOAHYTVLAINSI 720

QY 661 tlkmpLkNDISGVORVNIHHTSCNGTMSDEDGNHFKFELTDEOAHYTVLAINSI 720
 661 tlkmpLkNDISGVORVNIHHTSCNGTMSDEDGNHFKFELTDEOAHYTVLAINSI 720

QY 721 GASVANFNLTFSPMKSXVNIIVOSLSAYPLNSSCVIWSILSPSDYKLMVFITEMKNLMD 780
 721 gasvanfNLTFSPMKSXVNIIVOSLSAYPLNSSCVIWSILSPSDYKLMVFITEMKNLMD 780

QY 721 gasvanfNLTFSPMKSXVNIIVOSLSAYPLNSSCVIWSILSPSDYKLMVFITEMKNLMD 780
 721 gasvanfNLTFSPMKSXVNIIVOSLSAYPLNSSCVIWSILSPSDYKLMVFITEMKNLMD 780

QY 781 GEIKWLRTISSYKRYINDHFIPIEKYQFSLYPIRMEVGRKXINSTODDIEKHQSDA 840
 781 geikwlrtissYKRYINDHFIPIEKYQFSLYPIRMEVGRKXINSTODDIEKHQSDA 840

QY 781 geikwlrtissYKRYINDHFIPIEKYQFSLYPIRMEVGRKXINSTODDIEKHQSDA 840
 781 geikwlrtissYKRYINDHFIPIEKYQFSLYPIRMEVGRKXINSTODDIEKHQSDA 840

QY 841 GLYVIVPIYIISIIILTLTILSHQMRKLFMEDVDPNPKNSCMAOGLPQRPETREHFI 900
 841 glyvivpiYIISIIILTLTILSHQMRKLFMEDVDPNPKNSCMAOGLPQRPETREHFI 900

QY 841 glyvivpiYIISIIILTLTILSHQMRKLFMEDVDPNPKNSCMAOGLPQRPETREHFI 900
 841 glyvivpiYIISIIILTLTILSHQMRKLFMEDVDPNPKNSCMAOGLPQRPETREHFI 900

QY 901 KHTASVTCGPLLEBETISEDISVDTSMKKNDEMPTVSLSTTDLEKGSVCISIDQFN 960
 901 khtasvTCGPLLEBETISEDISVDTSMKKNDEMPTVSLSTTDLEKGSVCISIDQFN 960

QY 901 khtasvTCGPLLEBETISEDISVDTSMKKNDEMPTVSLSTTDLEKGSVCISIDQFN 960
 901 khtasvTCGPLLEBETISEDISVDTSMKKNDEMPTVSLSTTDLEKGSVCISIDQFN 960

QY 961 SYNSEAEGETEYTVDESOROPFVYATLINSKSKSEFGEEOGLINSVYTKCFSSKNPL 1020
 961 synseaegeteYTVDESOROPFVYATLINSKSKSEFGEEOGLINSVYTKCFSSKNPL 1020

QY 961 synseaegeteYTVDESOROPFVYATLINSKSKSEFGEEOGLINSVYTKCFSSKNPL 1020
 961 synseaegeteYTVDESOROPFVYATLINSKSKSEFGEEOGLINSVYTKCFSSKNPL 1020

QY 1021 KDSFSSNWMETEAQAFILTSOHPNITISPHLTFSGLDELLKLEGNPEENNDRKSIYLL 1080
 1021 kdsfssnwmETEAQAFILTSOHPNITISPHLTFSGLDELLKLEGNPEENNDRKSIYLL 1080

QY 1021 kdsfssnwmETEAQAFILTSOHPNITISPHLTFSGLDELLKLEGNPEENNDRKSIYLL 1080
 1021 kdsfssnwmETEAQAFILTSOHPNITISPHLTFSGLDELLKLEGNPEENNDRKSIYLL 1080

QY 1081 GYTSIKKRESGYLLTDKRSVSCPPAPCLFTDIRVLDSCSHFVENNINLGTSKKTPTAS 1140
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 Db 1081 gvtstikkrresgylltdkrsvscppapclftdirvldscshfvennlnlgtskktfas 1140
 QY 1141 YMPQFOTGCTGTHKIMENKMDLTIV 1165
 |||||||
 Db 1141 ymqpfotgctgthkimenkmdltiv 1165
 RESULT 7
 AAM62544
 ID AAM62544 standard; protein: 1221 AA.
 AC AAM62544;
 XX 12-OCT-1998 (first entry)
 XX ob-receptor replacement mutant.
 DE Human ob-receptor replacement mutant.
 XX
 XX ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;
 KM anorexia; cachexia.
 XX
 XX Homo sapiens.
 OS
 XX MO3824881-A1.
 PN 11-JUN-1998.
 PD 26-NOV-1997; 97MO-US22165.
 PE 02-DEC-1996; 96US-0032367.
 PR (MERI) MERCK & CO INC.
 PA Fong TM, Huang RC, Van Der Ploeg L;
 PI WPI: 1998-333304/29.
 DR
 XX New mutant ob receptor(s) - used to develop products for drug
 PT screening and for gene therapy for weight control, e.g. obesity or
 PT anorexia
 PS
 XX Claim 6; Fig 2; 27pp: English.
 PS
 XX The ob-receptor (OB-R), a member of the cytokine receptor family is
 CC transcribed in the hypothalamus and is involved in obesity. The
 CC replacement mutant has had amino acids 420-496 the second CK-F3
 CC module in OB-R deleted and replaced by amino acids 500-632. The
 CC replacement mutant together with mutants lacking a functional first CK-F3
 CC module or a functional intracellular domain can be used in assays for the
 CC detection of ligands, agonists, antagonists and ligand mimetics. The
 CC leptin agonists identified can be used in situations where leptin
 CC insufficiency causes obesity, diabetes or infertility. The leptin
 CC antagonists identified can be used in the treatment of anorexia and
 CC cachexia. The mutant receptor nucleic acids can also be used in gene
 CC therapy for weight control, e.g. for treating obesity or anorexia.
 CC
 XX Sequence. 1221 AA;
 SQ

Query Match 92.9%; Score 5809; DB 19; Length 1221;
 Best Local Similarity 90.6%; Pred. No. 0;
 Matches 1110; Conservative 17; Mismatches 34; Indels 64; Gaps 8;

QY 1 MITGCFEVCVLLHMERIVITAFNLSYPTTPMRFKISCMFPNSTYDFLLPAGLSKNTS 60
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 Db 1 mtgcfcvllhmerivitaftnlsypttpmrfkiscmfpnstydfllpagskntss 60
 QY 61 NGHYTAAVEPKFNSSGTHFNSLKTTFHCCFSEODRNCSLCADNIEGKTFVSTNSLVF 120
 |||||||
 Db 61 nghytavepkfnssgthfnslnskttfhccfseodrnscslcadniegkltfvstnslvf 120

QY 121 QOIIDANNNIQCCKADKDLFLFCYVESLFRKNLFRNNRYKWHLLVLPVLEDSPLVPQKS 180
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 Db 121 qoidannniqcckadkdlflfcyveslfrknlfrnnrykwhllvlpvledsplvpqks 180
 QY 181 FOMVHCNCSVHECCCECLVPVPKALNDTLMLCKITSGGVIFQSPUNSVOPINWVKPPDP 240
 |||||||
 Db 181 fomvhcnscsvheccceclvpvpkaldtlmlckitsggvifqspunsvopinwvkppdp 240
 QY 241 LGLHMEITDDGNLKLISWSPPPLVPPLOQYVYKSENSSTTVIREADKIVSATSLVDSILP 300
 |||||||
 Db 241 lglhmeitddgnlkliswsppplvpplvpploqyvysenssttvireadkivsatslvdsilp 300
 QY 301 GSSYEVQYRGKRLDGPGLWSMDSTPRVFTTQDYITFPFKILFVSQSNVSFHCITYKKENKI 360
 |||||||
 Db 301 gssyevqyrgkrlldgpplwsdstprrvfttqdyitfpfkilfvsqsnvsfhcitykкенki 360
 QY 361 VPSKEIVMMNNIAEKIPOSQYDVSDHVSQVFNLFNFKPRGFTYDAVYCCNHECHN 420
 |||||||
 Db 361 vpskeivmmnniaekiposqydvsdhvsqvfnlfnfkprgftydavyccnhechf 420
 QY 421 RYAEI---YVIDVNINISCEIDGYL-TRKTCRWSTSTIOSL-----AESTL----- 462
 |||||||
 Db 421 qpifllsgytmwlrlnhsl---gsldspptcylpdsavvkplppssvkaeiftnlgllkis 477
 QY 463 -----QLRYHRS-----SLYCSDFSIHPISPKDCTL 490
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 Db 463 wekprfpeennlqfqlrlygsgkevqwmkyevdaksksvslpvpdlcavayav-qvrcrkrl 536
 QY 491 QSDGFY-----ECIFQPIFLISGTYMWRIRNHSIGSLDSPPCVLPSPVYKPLPP 540
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 Db 491 dqlgywsnwnspaytveclfdgplfllsgytmwlrlnhslgsldspptcylpdsavvkplpp 596
 QY 541 SSVKAETITINIGLITISMEKPYFPENNLOFQIRYGLSGKEVONKMYEVYDAKSSEVSLPV 600
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 Db 541 ssvkaetitiniglitismekpyfpennlofqiiryglsgkevqwmkyevydaakssevspv 656
 QY 597 SSVKKEITINIGLITISMEKPYFPENNLOFQIRYGLSGKEVONKMYEVYDAKSSEVSLPV 656
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 Db 597 pdlcavayavqvrckrlldgplgywsnwnspaytvmvdlkypmrgpelfrlingdtlmkкенkv 716
 QY 601 PDLCAYAVAVQVRCKRLDGLGYWSNWSNPAYTYVMVMDIKYPMRGPEFTWRITNGDTMKKENV 660
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 Db 601 tllmkpimkndslcgvorvtnhhtscngtsewdgnhkfelfmteqahntvtaianisi 720
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 QY 777 GASVANFNLTFSMPKSKVIYOSLSAYPWNSSCVTYWLLSPDYKMLWFIEMKNLND 780
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 Db 777 gasvanfnltfspmkskviyoslsaypwnsscvtywllspdykmlwfiemknlnd 836
 QY 781 GEIKMLRISSSVKRYIHDHFTPIEKYQSLPIFMEGVGKPKIINSTQDDIEKHQSDA 840
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 Db 781 gelkmlrissssvkkryihdhftpiekyqslpifmegvgkpkiiinstqddlekhgsda 896
 QY 837 GELKMLRISSSVKRYIHDHFTPIEKYQSLPIFMEGVGKPKIINSTQDDIEKHQSDA 896
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 QY 841 GELYVRVPVISSLLGLLTSHOYMKKLFMEDVNPNCNAGIINOKREFEHLPT 900
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 Db 841 gelyvrvpviisslllglltshqtmkklfmedvnpncnwaqllmqdpctehlti 956
 QY 897 GELYVRVPVISSLLGLLTSHOYMKKLFMEDVNPNCNAGIINOKREFEHLPT 956
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 Db 897 khtasvTCGPLLEPETISEDISVDTSWKNKDEMPPTYVSLSTLDEKGVCSICSDQFN 960
 QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTYVSLSTLDEKGVCSICSDQFN 960
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 Db 901 khtaavtgcgplllepetisedisvdswnkndempptyvslstldexgvcsldqfn 1016
 QY 957 KHTAAVTCGPLLEPETISEDISVDTSWKNKDEMPPTYVSLSTLDEKGVCSICSDQFN 1016
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 Db 957 synfsbaegtevytyedesogropvkvatllisnsksetgeogllnsytkcrrsknspl 1020
 QY 961 SYNFSBAEGTEVYTYEDESOGROPVKVATLLISNSKSETGEEOGLNSYTKCRRSKNSPL 1020
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 QY 1017 SVNFSEAEGLTEVYTYEDESOGROPVKVATLLISNSKSETGEEOGLNSYTKCRRSKNSPL 1076
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 Db 1017 ksfpsnssweieiaofpflisodhpnitshlfnfsegldekllegfpeenndkrsiyyL 1080
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 QY 1077 KSFPSNSSWEIEIAQAFLLISDGHPNITSHPNLCTSEGLDEKLLEGFPEENNDKRSIYYL 1136
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 Db 1077 gvtstikkrresgylltdkrsvscppapclftdirvldscshfvennlnlgtskktfas 1140
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 Db 1137 gvtstikkrresgylltdkrsvscppapclftdirvldscshfvennlnlgtskktfas 1196
 QY 1141 YMPQFOTGCTGTHKIMENKMDLTIV 1165

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Db      1197 ymptqfctstqtkhmenkmdltv 1221
|||||
RESULT 8
AAM34499
ID      AAM34499 standard; protein; 970 AA.
XX
AC      AAM34499;
XX
DE      18-MAR-1998 (first entry)
XX
DE      Obesity receptor C protein.
XX
KW      Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW      high blood lipid level; obesity; diabetes; high cholesterol level;
KW      weight loss; therapy; weight maintenance.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Misc-difference 959
FT      /label= unknown
FT      /note= "encoded by stop codon"
XX
XX      WO9725424-A1.
XX      17-JUL-1997.
XX      02-JAN-1997; 97WO-US00128.
XX      31-DEC-1996; 96US-0774414.
XX      04-JAN-1996; 960S-0582825.
XX      (AMGE-) AMGEN INC.
XX      Chang M, Fletcher RA, Welcher AA;
XX      WPI: 1997-384981/35.
XX      DR      N-PSDB; AAT98530.
XX
PT      Obesity protein receptor(s) and related DNA - used to treat weight
PT      disorders, e.g. obesity, diabetes and high cholesterol or blood
PT      lipid levels
XX
XX      Claim 2; Page 72; 151pp; English.
XX
CC      This sequence represents the obesity (OB) receptor C protein. This
CC      sequence has one or more of the biological properties of naturally
CC      occurring OB receptor protein. The OB receptor proteins and OB
CC      receptor/OB protein complexes are used for the treatment of obesity,
CC      diabetes, high blood lipid levels and high cholesterol levels. The
CC      proteins may also be used to treat an individual for weight loss or
CC      weight maintenance required for purely cosmetic purposes.
XX
SQ      Sequence 970 AA:

```

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Query Match      77.3%; Score 4831.5; DB 18; Length 970;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 904; Conservative 5; Mismatches 24; Indels 25; Gaps 3;

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OY      1 MICQRCVVLHMEFYVTAFLNSYPITPMRFKLSCMPNSTYDFLLPAGLSKNTNS 60
DB      1 mlcqfrcvllhmfeflyvtaflnslpplprfklscompnstydfllpagslntns 60
OY      61 NCHYETAPEKNSSGTFSNSKTTFFCCFSEODRNCSLCADNIEGTFVSTVNSLVE 120
DB      61 nchyetapeknsstfshnsktffccfseodrnscslcadniegtfvstvnslvf 120
OY      124 GOIDANMNQCKLKGDLKFCIFYESLFRNRYKHYLLYVPEVIEDSPVPOKGS 180
DB      124 goidanmnqcklkgdlkfcifyeslfrnrykhyllylvpeviedspvpokgs 180
DB      121 gqidaenwnqcklkgdlkfcifyeslfrnlfnykhyllylvpeviedspvpokgs 180

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OY      181 FQMVHNCNVHCCCECLVPEPTAKLNDTLMLCKITSGGVFQSPLMASVQPINMKKPDPP 240
DB      181 fgmvhncnsvhccceclvprptaklndtlmlcklitsggvifqspumsvqpinmkvkdpp 240
OY      241 LGLHMETDDGKLUKISWSSPLVPPFFLOQVQVYSEKSTTVTREADKIVATSLYDLSILP 300
DB      241 lglhmetddgnlkiswssplvpfpfqvkvysenstvlreadkivsatslydsilp 300
OY      301 GSSYEQVQVGRKRDGPGIMSDWSTPVEFTQOVYIYFPFKILTSVGSNVSFHCITKKENKI 360
DB      301 gssyeqvqvgkrlldgpgiwsdwtprvfttdqvlyfppklltsvgsnvsfnhlykknki 360
OY      361 VPSKEIYVMMNMLAEKIPQSDYDVSDHVSQVTFPFLNETKPRGKETVYAVVCCNHECHN 420
DB      361 vpskeiwmnmlaekipqsgyvdsdhvskvtfpflnetkprgkftfydavycnehechh 420
OY      421 RYAEIYVIDVNNINISGEMTGCTLKMKCRKSTSTIOSLASTIQLRYHRSLSLCSDDPSIH 480
DB      421 ryaelyvldvnnlnisctelqyltmcrcwstslqslaelstqlrshrslycsdpsih 480
OY      481 PISEPKDCYLQSDGFECIFQPIFLLSGYTMWIRINHSLSGSLDSPPCVLPSPVVKPLPP 540
DB      481 plsepkdcylqsdgfyecifqpfllsgyltmwlrlnhsldspptcvlpssvvhkplpp 540
OY      541 SSVKAEITINIGLUKISWEKVPVPENNLOPQIRYGLSGKEVQWKMYEYDAKSYSLEPV 600
DB      541 ssvkaeitiniglukswekvpvpennloqirylsgskevowkmyevdaksyslvpv 600
OY      601 PDLCAVYAAQVQRCRLDGLGYWNSNPNPAYTVVMOIKVPMRBPFRMIRINGDTMKKEKV 660
DB      601 pdlcaavyavqrcrldglgywsnspnpaytvvmdikvpmrbrpfrmirngdtmkkenv 660
OY      661 TLLMRPLMKNDSLGVSQRYVYRNHNTSCNGTWSGDVGNHTKFTFLTEQARTVTLAINSI 720
DB      661 tllmrplmkndslgsvqrvyrynhntscngtwsedvgnhtkftflteqartvtlaainsi 720
OY      721 GASVANFNLTSPMPKSKVNTIVOSLSAYPLNSSCVYSWLSLSDYKLMFTIEKKNLMD 780
DB      721 gasvanfnltspmpskvntivoslslayplnsscvyswlsldsyklmfllieknlmd 780
OY      781 GEIKMLRISSSVKRYIHHFPIREKYOSLPIFMEGVRKRIINSFODDIEKHOSDA 840
DB      781 geikmlrlsssvkryihhfpierekyslplfmevgvrkriinsfoddiekhosda 840
OY      841 GLYVIVPVISSSILLGLTILISHORMKRLFEDVPNPKNCSMAOGLNFQK-----PE 893
DB      841 glyvivpvlssslillgltilishormkrlfedvpnpknscswaoglnfok-----pe 893
OY      894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDIVDTSMKKNDKDE 933
DB      901 shhalsistqghkncgrpplhkrtdlcalylvlltllpilsydpakspavrnltge 958

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RESULT 9
AAM24052
ID      AAM24052 standard; Protein; 896 AA.
XX
AC      AAM24052;
XX
DE      17-MAR-1998 (first entry)
XX
DE      Human WSX receptor variant 6.4.
XX
KW      Human: WSX receptor; variant 6.4; identification; purification;
KW      ligand; activator; antibody; agonist; proliferation; obesity;
KW      differentiation; aneemia; treatment; neoplasia; arteriosclerosis;
KW      type II diabetes; polycystic ovarian disease;
KW      cardiovascular disease; osteoarthritis; dermatological disorder;
KW      hypertension; insulin resistance; hypercholesterolaemia;
KW      hypertriglyceridaemia; cancer; cholelithiasis.
XX
OS      Homo sapiens.

```


XX MO9725425-A1.
 PN 17-JUL-1997.
 PD 07-JAN-1997; 97MO-US00325.
 PF 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX (GETH) GENENTECH INC.
 PA Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 DR MPI: 1997-372864/34.
 N-PSDB: AAF65576.
 XX MSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 PS Claim 2; Pages 86-89; 219pp; English.
 CC The present sequence is the human MSX receptor variant 6.4,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-MSX receptor antibody can be used as an agonist to activate
 CC the MSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the MSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. MSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 CC
 XX Sequence 896 AA:
 SO

Query Match 77.2%; Score 4826; DB 18; Length 896;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEPIYVITAFNLSTPTPMFKLSMCPNPSTYDFLLPAGLSKNTSNS 60
 DB 1 mlcqlfcvllhmfeyllytatlfnlslptlprfkscmpnstydfllpagslntns 60
 QY 61 NGHYETAEPKRNSSGTHFSNLSKTTFHCCFSEODRNCSLCADNIEGTFVSTVNSLVF 120
 DB 61 ngyetavpkrnssgthfsmnlskttfhccfseodrnscslcadniegtfvstvnslvf 120
 QY 121 COIDANMNINOCILKGDILKFIQYVESLFKNLFRNRYNKHLLYLVPEVLEDSPLVPQKGS 180
 DB 121 qoidanmnigcwkldkllficyveslfnklnfrnykhlllylvpevledsplvpqkgs 180
 QY 181 FQMVHNCNSVHECCCLVVPPTAKINDTLMLKLTSGGVIFOSPLMSVQPINMKPDPDP 240
 DB 181 fgmvhncnsvheccclvvpptakindtlmlkltsggvifosplmsvqpinmkpdpdp 240
 QY 241 IGLHMEITDOGWLKTSWSSPPLVPPLOYQVYKSENSTTVIFEADKIVASATSLVDSILP 300
 DB 241 iglhmeitddgnlktswspplyvpplqykvysensttvifeadkivatsllydsilp 300
 QY 301 GSSYEVOYGRKLDGPGTMSDSTPRVFTODVIFPPKILSVGSNVSFHCITKKENKI 360
 DB 301 gssyevoygrkldgpgtmsdstprvftodvifppkilstvgsnvsfhcilykknki 360

QY 361 VPSKEIWMNLAERIPQSOQYDVVSDHVSQYTFEFLNLETNRGKFTYDAVYCCNEHECH 420
 DB 361 vpskeiwmnlaeklpsqydvvsdhvskytffnlnektprgk:tydavyccnehech 420
 QY 421 RYAEIYVIDVININISCELTGTLTKMTGCRWSTSTIOSLAESTLQLRHNSSLYCSDPISIH 480
 DB 421 ryaeliyvidvinnisceltdgltkmtcrwststioslaestlqlrhnsslycsdpsih 480
 QY 481 PISEPKDCYLOSDFECCIFQPIFLLSGYTMWIRNHSLSGSDSPPTCLPDSVYKPLPP 540
 DB 481 pisepkdcylsodfeyccifqipifllsgytmwirnhsldspptclpdsvykplpp 540
 QY 541 SSVKAEITINIGLAKISWEKVPFENNLOFOIRGLSGKEVQMKRYEYDARKSKSVSLPV 600
 DB 541 ssvkaeitinigllakiswekvpfennlofoirglsgkevqmkryeydarksksvslpv 600
 QY 601 PDLCAVYAVOYRCKRLDGLGTVSMKSNPARYVMDIKVPMKGPETWRIINDTKKKEVY 660
 DB 601 pdlcavyavoyrckrldglgvtvsmksnparyvmdikvpmkgpetwriindtkkkekny 660
 QY 661 TLWKPLKNDISLGVORRYVINHHTSCNGTSESDVGNHTKTFELMT EQAHVTVLAINSI 720
 DB 661 tlwkpdkndislgvoryvinhhtscngtsedevgnhtkftfelmt eqahvvtvlainsi 720
 QY 721 GASVANFNLTSWPMKSNKYNIVOSLSAYPLNCSGVISWILSPSDKLMYFIEMKNLND 780
 DB 721 gasvanfnltswpmksknynivoslaysplnscsvivswilspsdklnmyfiemknlned 780
 QY 781 CEIKMLRISSSVKYYIHDHFPIEKYOPSLYPTMEGVGPKKTIINSTODDIEKHQSDA 840
 DB 781 gelkmlrissvskyyihdhfpiekyopslyptmegvgpkktinstoddiekhgsda 840
 QY 841 GLYVIVPPIISSLILGLTILSHORMKMLEWEDVPNPKNCSSMAOGLNFQK 891
 DB 841 glyvivppiisslilgltilshormkmlwedvpnpknkssmawglnfqk 891

RESULT 10
 AAM24053
 ID AAM24053 standard; Proteio; 923 AA.
 XX
 AC AAM24053;
 XX
 DT 17-MAR-1998 (first entry)
 XX
 DE Human MSX receptor variant 12.1.
 XX
 KW Human; MSX receptor; variant 12.1; identification; purification;
 KW ligand; activator; antibody; agonist; proliferation; obesity;
 KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
 KW Type II diabetes; polycystic ovarian disease;
 KW cardiovascular disease; osteoarthritis; dermatological disorder;
 KW hypertension; insulin resistance; hypercholesterolaemia;
 KW hypertriglyceridaemia; cancer; cholelithiasis.
 KW
 OS Homo sapiens.
 XX
 PN MO9725425-A1.
 PD 17-JUL-1997.
 XX
 PF 07-JAN-1997; 97MO-US00325.
 PR 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX
 PA (GETH) GENENTECH INC.
 PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 DR MPI: 1997-372864/34.

XX WPI: 1997-384981/35.
 DR N-PSDB: AAT98528.
 XX
 PT Obesity protein receptor(s) and related DNA - used to treat weight
 disorders, e.g. obesity, diabetes and high cholesterol or blood
 lipid levels
 PT
 PS Claim 1; Page 64; 151pp; English.
 XX
 CC This sequence represents the obesity (OB) receptor A protein. This
 CC sequence has one or more of the biological properties of naturally
 CC occurring OB receptor protein. The OB receptor proteins and OB
 CC receptor/OB protein complexes are used for the treatment of obesity,
 CC diabetes, high blood lipid levels and high cholesterol levels. The
 CC proteins may also be used to treat an individual for weight loss or
 CC weight maintenance required for purely cosmetic purposes.
 XX
 SQ Sequence 972 AA:

Query Match 77.2%; Score 4826; DB 18; Length 972;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVLLHMERIVYITAFNLSTPTPMFKLSCMPNSTYDFLLPAGLSKNTS 60
 DB 1 micqfcvllhmerivytatfnlsptpmpfklsclmpnstydfllpagskntns 60
 QY 61 NGHYTAVEPKFNSSGTHFNSLSTKTFHCGRSEODRNCSLCADNIEGTFSTVSLVF 120
 DB 61 nghytavepknssgthfnslstktfhcgrsedrncslcadniegftstvslyvf 120
 QY 121 QOIDANMNIQCKLKDGLKLFICVSESLFRNRYKFKHLLYVPEVEDSPFLPQKGS 180
 DB 121 qoidanmniqcklkdglklficvseslfrnrykfkhllyvpevedspflpqkgs 180
 DB 121 qgidanwnlqcklkdglklficvseslfnlfrnykhllyvpevedspflpqkgs 180
 QY 181 FOMVHNCNVHECCCELVVPPTAKLNDTLMLCKITSSGCVTFQSPMLSVOPINMWKPDPP 240
 DB 181 fomvhncnvhecccelevpvtaklndtlmlckitssgcvtfqspmlsvopinmwkpdpp 240
 DB 181 fgmvhncnvhecccelevpvtaklndtlmlckitssgcvtfqspmlsvopinmwkpdpp 240
 QY 241 LGLHETDDGLKITSMSPLVPPLOVYKSSNTVTRFADKIYATSLVDSILP 300
 DB 241 lglhetddglkitsmsplvpplovykssntvtrfadtikyatslvdsilp 300
 DB 241 lglhetddglkitsmsplvpplovykssntvtrfadtikyatslvdsilp 300
 QY 301 GSSYEVQYRGKRLDGPGLMSDSTPRVFTDPVIFPPKILTSVGSNVSFHCITYKENKI 360
 DB 301 gssyevqyrgkrlldgpglmsdstprvftdpvifppkiltsvgsnvsfhcitykenki 360
 DB 301 gssyevqyrgkrlldgpglmsdstprvftdpvifppkiltsvgsnvsfhcitykenki 360
 QY 361 VPSKETVMMNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGFTYDAVYCNEHECHH 420
 DB 361 vpsketvmmnlAEKIPQSQYDVSDHVSQVTFENLNETKPRGFTYDAVYCNEHECHH 420
 DB 361 vpsketvmmnlAEKIPQSQYDVSDHVSQVTFENLNETKPRGFTYDAVYCNEHECHH 420
 QY 421 RYAEIYVDVNTNISCEDGYLTKMFCRSTIOSIAESTOLVYHRSICSDIPSH 480
 DB 421 ryaeiyvdvntniscedgyltkmtcrstiosiaestolvyrhsicSDIPSH 480
 DB 421 ryaeiyvdvntniscedgyltkmtcrstiosiaestolvyrhsicSDIPSH 480
 QY 481 PISEPKDCVLSODGFYECIFOPIFLLSGYTMIRINHSIGSDSPPTCYLPDSVYKPLPP 540
 DB 481 pisepkdcvlsodgfyecifopifllsgytmirinhsgsdspptcyLPDSVYKPLPP 540
 DB 481 pisepkdcvlsodgfyecifopifllsgytmirinhsgsdspptcyLPDSVYKPLPP 540
 QY 541 SSVKAEITINIGLKIISMEKVPFENNLOFOIRYGLSGREYQWKYEVYDAKSYSLEPV 600
 DB 541 ssvkaeitiniglkiiSMEKVPFENNLOFOIRYGLSGREYQWKYEVYDAKSYSLEPV 600
 DB 541 ssvkaeitiniglkiiSMEKVPFENNLOFOIRYGLSGREYQWKYEVYDAKSYSLEPV 600
 QY 601 PDLCAVYAVQVRCRKLDDGLGYWSNMSNPAITYVMDIKPMPREPERWRIINGTAKKEKAV 660
 DB 601 pdlcavyavqvrckrlddglgywsnmsnpaityvmdikpmpreperwriingtAKKEKAV 660
 DB 601 pdlcavyavqvrckrldggywsnmsnpaityvmdikpmpreperwriingtAKKEKAV 660
 QY 661 TLJMLPLKNDSLGSGVQRYVINHHTSCNGTWSDEDVGNHRTKFFELTMOAHTVYLAINSI 720
 DB 661 tljmlplkndslgsgvqryvinhhtscngtwsedvgnhtkffelwceqahltvYLAINSI 720

QY 721 GASVANFNLFESPMKSKVNIQVSLSAYPLNNSCVIIVSWILSPDYKLMWFIIEMKNLED 780
 DB 721 gasvanfnlftswpmkskvniqvsllsayaPLNNSCVIIVSWILSPDYKLMWFIIEMKNLED 780
 QY 781 GEIKWLRISSSVKKYIHDHPIPIKYOFSLYPIRMEGVGKPKIINSTQODIEKHQSDA 840
 DB 781 geikwlrissvkkylhdhpiPIKYOFSLYPIRMEGVGKPKIINSTQODIEKHQSDA 840
 QY 841 GLYVIVPVISSSILLTGLTSLSHORMKLFMEDVYPNPKNSMAOGLNFK 891
 DB 841 glyvivpviSSSILLTGLTSLSHORMKLFMEDVYPNPKNSMAOGLNFK 891
 DB 841 glyvivpviSSSILLTGLTSLSHORMKLFMEDVYPNPKNSMAOGLNFK 891

RESULT 12
 AAW34498
 ID AAW34498 standard; protein; 999 AA.
 XX
 AC AAW34498;
 XX
 DT 18-MAR-1998 (first entry)
 XX
 DE Obesity receptor B protein.
 XX
 KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
 KW high blood lipid level; obesity; diabetes; high cholesterol level;
 KW weight loss; therapy; weight maintenance.
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT Misc-difference 905 /label- unknown
 FT /note- "encoded by stop codon"
 FT Misc-difference 933 /label- unknown
 FT /note- "encoded by stop codon"
 FT Misc-difference 971 /label- unknown
 FT /note- "encoded by stop codon"
 FT Misc-difference 988 /label- unknown
 FT /note- "encoded by stop codon"
 FT Misc-difference 988 /label- unknown
 FT /note- "encoded by stop codon"

PN WO9725424-A1.
 XX
 PD 17-JUL-1997.
 XX
 PE 02-JAN-1997; 97WO-US00128.
 XX
 PR 31-DEC-1996; 96US-0774414.
 PR 04-JAN-1996; 96US-0582825.
 XX
 PA (AMGE) AMGEN INC.
 XX
 PI Chang M, Fletcher PA, Welcher AA;
 PI
 DR WPI: 1997-384981/35.
 DR N-PSDB: AAT98529.

PT Obesity protein receptor(s) and related DNA - used to treat weight
 PT disorders, e.g. obesity, diabetes and high cholesterol or blood
 PT lipid levels
 PS Claim 2; Page 68; 151pp; English.

XX This sequence represents the obesity (OB) receptor A protein. This
 CC sequence has one or more of the biological properties of naturally
 CC occurring OB receptor protein. The OB receptor proteins and OB
 CC receptor/OB protein complexes are used for the treatment of obesity,
 CC diabetes, high blood lipid levels and high cholesterol levels. The
 CC proteins may also be used to treat an individual for weight loss or
 CC weight maintenance required for purely cosmetic purposes.
 XX


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QY 301 GSSYEYQYRGKRLDGPGLMSDMSPTPRVPTTODVITYPPKILTSVGSNVEHCITKKEKI 360
Db 301 GSSYEYQYRGKRLDGPGLMSDMSPTPRVPTTODVITYPPKILTSVGSNVEHCITKKEKI 360
QY 361 VPSKEIYVMMMLAEKIPQSDYVSDHYSKYTPFNLTNRGKFTYDAVYCCNHECHH 420
Db 361 VPSKEIYVMMMLAEKIPQSDYVSDHYSKYTPFNLTNRGKFTYDAVYCCNHECHH 420
QY 421 RYAEIYVIVNINISCTDGYLTMTCTMSTSTIQSLAESTLQLRHRSLSYCSDDPSIH 480
Db 421 RYAEIYVIVNINISCTDGYLTMTCTMSTSTIQSLAESTLQLRHRSLSYCSDDPSIH 480
QY 481 PISEPKOCYIADSDGFYECIEIPFILSGYTMWIRINSLSGSDSEPTCVLPDSVYKPLP 540
Db 481 PISEPKOCYIADSDGFYECIEIPFILSGYTMWIRINSLSGSDSEPTCVLPDSVYKPLP 540
QY 541 SSVAKETINIGLTKISEKVPFPENNLOFOIRGLSGEKYOMKMEYEDKSKSVSLPV 600
Db 541 SSVAKETINIGLTKISEKVPFPENNLOFOIRGLSGEKYOMKMEYEDKSKSVSLPV 600
QY 601 PDLCAVYAVOYRCKRLDGLGYWMSNMPAYTVVDIKVPMRGPFEWRIINGDTMKKEKV 660
Db 601 PDLCAVYAVOYRCKRLDGLGYWMSNMPAYTVVDIKVPMRGPFEWRIINGDTMKKEKV 660
QY 661 TLLKRPILKMNOSLCSYQRYVINHTSCNGTSEEDYGNHTKFTPLTEQAHVTVLAINSI 720
Db 661 TLLKRPILKMNOSLCSYQRYVINHTSCNGTSEEDYGNHTKFTPLTEQAHVTVLAINSI 720
QY 721 GASVANFILTSPMPSKNIYQSLASAYPLNNSCVISWILSPSDYKLMYFIEMKLNED 780
Db 721 GASVANFILTSPMPSKNIYQSLASAYPLNNSCVISWILSPSDYKLMYFIEMKLNED 780
QY 781 GEIKWLRISSVKKYIHDHPIEIKYQSLYPIFMEGVGKPKIINSFTQDIEKHQSDA 840
Db 781 GEIKWLRISSVKKYIHDHPIEIKYQSLYPIFMEGVGKPKIINSFTQDIEKHQSDA 840
QY 841 GLYIVAPIISSLITGLTILSHQRMKLFMEDVPMKNSMGAGLMQR-----PE 893
Db 841 GLYIVAPIISSLITGLTILSHQRMKLFMEDVPMKNSMGAGLMQR-----PE 893
QY 894 TFEHLFIKHT-ASYVTCG-----LLEPETISHDISVDISMKKDE 933
Db 894 TFEHLFIKHT-ASYVTCG-----LLEPETISHDISVDISMKKDE 933
QY 901 SHHSLSISGKHGCGPPGPIHKTCLDCLSYLLTLPPLISYDAPKSPSVRNTE 958
Db 901 SHHSLSISGKHGCGPPGPIHKTCLDCLSYLLTLPPLISYDAPKSPSVRNTE 958

RESULT 14
AAW31911
ID AAW31911 standard; Protein: 958 AA.
XX
AC AAW31911;
XX
DT 02-FEB-1998 (first entry)
XX
DE Human OB-R leptin receptor variant.
XX
KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
XX
OS diagnosis; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT MISC-difference 85 /note= "variation from published sequence"
FT MISC-difference 109 /note= "variation from published sequence"
FT MISC-difference 223 /note= "variation from published sequence"
FT MISC-difference 223 /note= "variation from published sequence"
FT Domain 845..862
FT MISC-difference /label= Transmembrane_domain
FT MISC-difference 892..958 /note= "divergence from published sequence"
FN W09726370-A1.

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XX 24-JUL-1997.
XX
PD 17-JAN-1997: 97MO-US00570.
PF
XX 18-JAN-1996: 96US-0588190.
PR
XX (PROG-) PROGENITOR INC.
PA
XX Cioffli J, Shafer AW, Snodgrass HR, Zupancic TJ:
PI WPI: 1997-385353/35.
XX N-PSDB: AAT89193.
DR
XX
XX Claim 12; Fig 1A-E; 26pp; English.
XX
XX This polypeptide comprises a variant of the human leptin receptor
XX (OB-R). Its sequence was deduced from a contiguous cDNA (AAT89193)
XX derived from overlapping clones isolated from a human foetal liver
XX library. The sequence shows near identity to a published OB-R
XX sequence in the extracellular domain, with the exception of 3 amino
XX acids, but there is extensive diversity in the intracellular
XX cytoplasmic domain at the C-terminal end. A claimed method for
XX detection of OB-R in cells comprises extraction of RNA and testing
XX this for hybridisation to an oligonucleotide (I) derived from the
XX OB-R variant gene, especially from the region beyond nucleotide
XX 2770. Also claimed are methods of: (1) treating obesity by
XX administration of an agent that inhibits expression of the OB-R
XX variant gene; and (2) identification of a compound that can
XX supplement activity of leptin by: (1) incubating cells expressing
XX OB-R variant first with leptin and then with a test compound, and
XX (ii) comparing activation signals between cells treated and not
XX treated with the test compound. Inhibition/down-regulation of the
XX variant OB-R (found in obese people) improves response of cells to
XX weight regulation by leptin. Replacing variant OB-R by gene therapy
XX (in homozygous individuals) can be used to treat obesity. Labelled
XX probes based on the gene can be used to isolate other variant forms
XX of the receptor gene or to detect the variant gene (e.g. for
XX determining predisposition to obesity), while the OB-R gene can be
XX used to express recombinant OB-R (optionally as fusion protein) and
XX in standard hybridisation assays. The OB-R gene can also be used
XX therapeutically in cases of overexpression of functional OB-R
XX (causing loss of appetite and hypermetabolic activity). Cells
XX engineered to express variant receptor are used in method (2) to
XX screen for (ant)agonists of leptin/OB-R interaction, also to generate
XX antibodies that competitively inhibit, neutralise or enhance activity
XX of the variant receptor.
XX
XX Sequence 958 AA:
XX
XX Query Match 77.1%; Score 4819.5; DB 18; Length 958;
XX Best Local Similarity 94.1%; Pred. No. 0;
XX Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;
XX
QY 1 MICOQFCVALLHMEPIYVITAENLSYPTPMWRKISCMPPNSTYVFLIPAGLSKNTNS 60
Db 1 mtcgkfcvllhmfefiyatfnlsyptlpwrfkiscmpnstyvlilpagskntns 60
QY 61 NCHYETAVEPKRNSGTFPSNLSKTFHCPCFSSBEDRNCISLADHIEKTFYSTNSLYF 120
Db 61 ngyetavepkfnssgltfnlskalfncctfseqdrcnscadnlegtfystnslvf 120
QY 121 QOIDANMNIQCLGDLKLFICVYSLPKNLFERNYVHLLYVPEVLEDSPLVPQKGS 180
Db 121 qgidanwniqclkgdlnlficyveslfnlfrnyvnhlllyvpevleedsplvpqkgs 180
QY 181 FOMVHNCNVHCECECLVPPPTAKLNDTLMLCKITTSQGVIFQSLMSVQPINMVKPPPP 240

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Db 181 fgmhvncsbhcececllyvptacklndcllmcllksagvlftrpslmsvqplnmvkdpp 240
Qy 241 LGIHWMTDGDNLKISMSKSPPLVPLOYQVYSENSTVIREAKIYATSLDLSITP 300
Db 241 lglhmetlddgnlkkswspplpvlpdgvykysensltvreadlysatlslydsllp 300
Qy 301 GSSYEQVQGRKRLDGPGLMSDWTSPRVTQDVYIFPPKILTSVGSNVSFHCIIYKKNKI 360
Db 301 gssyevqvygkrldgplkwsdwtspvftctgdvlyfprklltsvgnsvfchlykknk 360
Qy 361 VSKKEIYVMMNIAEKIPQSQYOVSDHSAKVFENLNKPKPGKFTYDAVYCCNHECHH 420
Db 361 vpskelvwmnlaekipgsqydvadhsakvflfnlnekprgkitydvcvcsnechch 420
Qy 421 RYAEIYVDVNNINISCEGTGYLTMTKCRMTSTIOSLAESTIOLRHRASLCSDDPSIH 480
Db 421 ryaelvldvnnlnisctegtlylmtcrvstlgslaestlqlyhnslycsdpsih 480
Qy 481 PISEPKCYLQSDGFYEICIFOPIFLLSGYTMIRINHSIGSLDSPPTCVLPDSVYKPLPP 540
Db 481 pisepkdcylgsdgyfecifgplfllsgytmwlrlnhsigsldspptcvlpdsvypkplpp 540
Qy 541 SSVKAEITINILKITSWKRPYPPENNLOFQIRYGLSGKEVQWKNTEYVDASKSVSLPV 600
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Qy 601 POLCAVYAVQVQCKRLDGLGYSNMNSNPAYTVMDIKVPMRGPPEFRRIINGDTMKKEKV 660
Db 601 polcavayavqvcrlldgfygysnmsnpaytvmdikvpmrpefrlringdtmkkek 660
Qy 661 TLLMKRPLKNSLSCVQRYVNHHSNGTSEEDVGNHTKFTPLMEQAHVTVALAINSI 720
Db 661 tllmkrplmndslscvqryvnhhsngtseedvgnhtkftplmteqahvtvalainsi 720
Qy 721 GASVANFNLTFSMPKSVIYOSLSAYPLNSSCVIYSWLSSDKIMFELIEMNLND 780
Db 721 gasvanfnltfsmprkvnlyoslsayplnsscvlswlssdyklnmfliemnlnd 780
Qy 781 GEIKMLRISSSVKYYIHDFPIPIEKYOSLPYIFMEGVGKRIINSFTQDIERHOSDA 840
Db 781 gelkmlrissvskyyihdfpripiekyslpyifmegvgkriinsftqddierhgsda 840
Qy 841 GIXYVYPIYISSIILLGLTSLSHQBMKLFMEDVDPNPNKCSWAQGLNFQK-----PE 893
Db 841 gixyvypiyissillgltslshqbmklfmedvdpnpkncswagllfqklegssfyk 900
Qy 894 TFEHLFIKHT-ASVTCGP-----LLEPETISDIDISVDTSMKKNKE 933
Db 901 shhhalisstgghkncgprpgplhkttdlcslyllclppllsydpakspsvrntge 958

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FT 181 Domain /note- "variation from published sequence"
FT 241 845..862 /label- Transmembrane_domain
FT 301 Misc-difference 892..958 /note- "divergence from published sequence"
FT 361 W09726272-A1.
FT 421 24-JUL-1997.
FT 481 17-JAN-1997; 97WO-US00880.
FT 541 18-JAN-1996; 96US-0588189.
FT 601 (PROG-) PROGENITOR INC.
FT 661 Cioffi J, Shafer AM, Snodgrass HR, Zupancic TJ;
FT 721 WPI: 1997-385291/35.
FT 781 P-P5DB: AAT72649.
FT 841
FT 893
FT 900
PS 12: Fig 1A-E; 26pp; English.
XX This polypeptide comprises a variant of the human leptin receptor
XX (OB-R). Its sequence was deduced from a contiguous cDNA (AAT72649)
XX derived from overlapping clones isolated from a human foetal liver
XX library. The sequence shows near identity to a published OB-R
XX sequence in the extracellular domain, with the exception of 3 amino
XX acids, but there is extensive diversity in the intracellular
XX cytoplasmic domain at the C-terminal end, suggesting alternative
XX splicing of a common precursor mRNA. A claimed method for
XX detection of OB-R in cells comprises extraction of RNA and testing
XX this for hybridisation to an oligonucleotide (1) derived from the
XX OB-R variant gene, especially from the region beyond nucleotide
XX 2770. Also claimed are methods of: (1) treating obesity by
XX administration of an agent that inhibits expression of the OB-R
XX variant gene; and (2) identification of a compound that can
XX supplement activity of leptin by: (1) incubating cells expressing
XX OB-R variant first with leptin and then with a test compound, and
XX (1) comparing activation signals between cells treated and not
XX treated with the test compound. Inhibition/down-regulation of the
XX variant OB-R (found in obese people) improves response of cells to
XX weight regulation by leptin. Replacing variant OB-R by gene therapy
XX (in homozygous individuals) can be used to treat obesity. Labeled
XX probes based on the gene can be used to isolate other variant forms
XX of the receptor gene or to detect the variant gene (e.g. for
XX determining predisposition to obesity), while the OB-R gene can be
XX used to express recombinant OB-R (optionally as fusion protein) and
XX in standard hybridisation assays. The OB-R gene can also be used
XX therapeutically in cases of overexpression of functional OB-R
XX (causing loss of appetite and hypermetabolic activity). Cells
XX engineered to express variant receptor are used in method (2) to
XX screen for (ant)agonists of leptin/OB-R interaction, also to generate
XX antibodies that competitively inhibit, neutralise or enhance activity
XX of the variant receptor.
XX
XX Sequence 958 AA:
XX
XX Query Match 77.1%; Score 4819.5; DB 18; Length 958;
XX Best Local Similarity 94.1%; Pred. No. 0;
XX Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;
Qy 1 MICOKFCVLLHWEFIYVITAFNLSTPTTPWRFKLSCHPPNSTYDYFLPAGLSKNTS 60
Db 1 mlcokfcvllhweifyltafnlsypttpwrfklschppnstydyfllpaglskntns 60
Qy 61 NGHETAVEPKFNSSGRTFHSNLSTTTHFCRSEQDRKCSLCADNIIEKTVSTVNSLVF 120

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Db 121 qgidanwniqcwlkgdliklfcyveslfnklfrnynkvhllylvpevledsplyvpqkgs 180
QY 181 FOMVHCNCSVHECECECLVPVPFPAKINDTLMLCKLITSGGVTFOSPMSVQPINWVKPDP 240
Db 181 fgmwhcnscsvhecececlvpvptaklndtlmlcklitsgsvlfrspmsvqpinmwkpdpp 240
QY 241 LGLHMETDDGNLTKISWSSPPLVPPLOYOVKYSENSSTVIREAKIYSATSLLYDSTLP 300
Db 241 lglhmetddognlkwsspsplvpfpplqyvkysensstvirreakivsatsllvdsllp 300
QY 301 GSSYEYVGRKRLDGPJMSDMSTPRVFTQDVIYFPFKILTSVGSNVSFHCITYKKENKI 360
Db 301 gssyevgvgrkrlldgpgjmsdmsprvfttqdvlyfppkiltsvgsnvsfncitykknki 360
QY 361 VPSKEIYVMMNLAEKIPQSDYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 vpskeiyvmmnlaekipqsgdvvsdhsqvtffnlnetkprgkftdydavyccnehechh 420
QY 421 RYAEIYVADVNIINTSCFEDGLTKMTCRWSTSTIOSLAESTLOLRHRSLLYCSDPISIH 480
Db 421 ryaeliyvadvnintscfedgltkmtcrwststioslaestlqlrhrsllycsdpisih 480
QY 481 PISEPKDCYLQSDGFYECEIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 pisepkdcylqsdgfyecelfqipifllsgytmwirinhslgsldspptcvlpdsvvkplpp 540
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Db 541 ssvkaeltiniglkwiswekvpfennlqfiryglsgkevqwkmyevydaaksksvslpv 600
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Db 601 polcavyavoyrcrldglgywmsnmpaytyvmdikvpmrgpelfrriingdtmkkeknv 660
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Db 841 glyvivpyi:issll:llgl:tlshormkll:fwe:devn:pnknc:maogl:npo:k:-----pe 893
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDIVSTWKNKDE 933
Db 901 shhhalisestqghkncgprpgplhnrktrdclcalyltltiprlisydpakspsvrntge 958
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Search completed: May 18, 2002, 06:52:53
Job time: 5693 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 06:47:52 ; Search time 230.02 Seconds

(without alignments)
1782.703 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254

Sequence: 1 MICQKRCVLLHWEFIYIT.....QTCSTQTHKIMKMDLTV 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/PCUTS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6254	100.0	1165	9	US-08-570-142D-4
2	6254	100.0	1165	9	US-08-583-153A-4
3	6254	100.0	1165	9	US-08-585-005-2
4	6254	100.0	1165	10	US-08-638-524B-4
5	6254	100.0	1165	10	US-08-667-197-2
6	6254	100.0	1165	11	US-08-708-123D-4
7	6254	100.0	1165	11	US-08-779-457-2

8	6254	100.0	1165	11	US-08-780-562-2	Sequence 2, Appl1
9	6254	100.0	1165	14	US-09-094-410-4	Sequence 4, Appl1
10	6254	100.0	1165	15	US-09-137-132-4	Sequence 4, Appl1
11	6254	100.0	1165	23	US-09-950-149-4	Sequence 4, Appl1
12	6254	100.0	1216	11	US-08-774-414-7	Sequence 7, Appl1
13	6254	100.0	1216	20	US-09-671-049-7	Sequence 7, Appl1
14	6247	99.9	1167	23	US-09-948-933-284	Sequence 284, App
15	6247	99.9	1167	23	US-09-948-947-87	Sequence 948, App
16	6246	99.9	1165	9	US-08-599-974C-56	Sequence 56, Appl
17	6246	99.9	1165	11	US-08-713-296-11	Sequence 11, Appl
18	6246	99.9	1165	13	US-08-961-809-4	Sequence 4, Appl1
19	6246	99.9	1165	15	US-09-178-691-4	Sequence 4, Appl1
20	6246	99.9	1165	21	US-09-700-813-10	Sequence 10, Appl
21	6246	99.9	1165	23	US-09-948-933-256	Sequence 256, App
22	6246	99.9	1165	23	US-09-948-947-73	Sequence 73, Appl
23	6246	99.9	1165	24	US-10-095-929-11	Sequence 11, Appl
24	6240	99.8	1165	9	US-08-583-153-4	Sequence 4, Appl1
25	6240	99.8	1165	9	US-08-599-455A-4	Sequence 4, Appl1
26	6240	99.8	1165	10	US-08-638-524A-4	Sequence 4, Appl1
27	6240	99.8	1165	11	US-08-708-123C-4	Sequence 4, Appl1
28	6240	99.8	1165	12	US-08-864-564A-4	Sequence 4, Appl1
29	6240	99.8	1165	24	US-10-079-625-4	Sequence 4, Appl1
30	6236	99.7	1165	9	US-08-570-142B-4	Sequence 4, Appl1
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32	6172	98.7	1165	9	US-08-589-915A-11	Sequence 11, Appl
33	6032	96.5	1137	9	US-08-569-918-4	Sequence 4, Appl1
34	5809	92.9	1221	13	US-08-982-825-5	Sequence 2, Appl1
35	4831.5	77.3	969	9	US-08-582-825A-5	Sequence 5, Appl1
36	4831.5	77.3	969	9	US-08-582-825B-5	Sequence 5, Appl1
37	4831.5	77.3	969	11	US-08-774-414-5	Sequence 5, Appl1
38	4831.5	77.3	969	11	US-08-774-414-6	Sequence 6, Appl1
39	4831.5	77.3	969	20	US-09-671-049-6	Sequence 5, Appl1
40	4831.5	77.3	969	20	US-09-671-049-6	Sequence 6, Appl1
41	4826	77.2	896	9	US-08-582-825-1	Sequence 1, Appl1
42	4826	77.2	896	9	US-08-582-825A-1	Sequence 1, Appl1
43	4826	77.2	896	9	US-08-585-005-3	Sequence 3, Appl1
44	4826	77.2	896	10	US-08-667-197-3	Sequence 3, Appl1
45	4826	77.2	896	11	US-08-779-457-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1

US-08-570-142D-4

Sequence 4, Application US/08570142D

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING

TITLE OF INVENTION: OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/570,142D

FILING DATE: 11-DEC-1995

PRIOR APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meikie John, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/014001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1165 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-570-142D-4

Query Match 100.0%; score 6254; DB 9; length 1165;
 Best local similarity 100.0%; Pred. No. 0:
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MICQKRCVLLHWEFTYVITAFNLSTPTPWRFKLSMPNNTYDYFLLPAGISKNTS 60
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 DB 61 NGHYETAVPEKPNSSGTHSNLSKTFHCCEFEEDORNSLADNTEGTFVTSVSLVF 120
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 DB 121 QQIDAMNINQCMWLGDKLFTICVESLFRNLFNRYKYLHYLVLEVEDSPLVPQKS 180
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 DB 181 FQWVHCNCSYHECCCELVPPYPAKLNDTLMLCKITSGVIFOSPLMSVQPINMKRDP 240
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 DB 241 LGHMEITDGNLKIEMSSPPLVPFLOYOVKSENSTVIRADYVATSLVSLV 300
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 DB 301 GSSYEYQVGRKRLDGPIMSDSTPRVFTTQDYIYPPKILTSVGSNVSFHCYKKNKI 360
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 DB 661 TLLMKPLMKNDSICSVQRYVINHTSCNGTWSDEVGNTKFTFLMTEQAHYTVLAINSI 720

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 DB 721 GASVANFNLTFSWPMKRNIVOSLSAYPLNSSCVIWSMILSPSDYKLMYFIEMKNLND 780
 QY 781 GEKWLRISSSKYKYYIHHPFPIEKYQFSLPIFMEGKGRKINSFQODIEKHQSDA 840
 DB 781 GEKWLRISSSKYKYYIHHPFPIEKYQFSLPIFMEGKGRKINSFQODIEKHQSDA 840
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 DB 841 GLYVIYVYIISSSILLGLTLISHSORMKLFMEDVNPNCMSAOGINFQKPEFELFI 900
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 DB 901 KHTASVTCGPLLEPTEISEDISVDTSMKNKDEMPYVSLSTDLKSGVCSIDQPN 960
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 DB 1081 GYTSIKKRESGVLLDKNVSCPPAPCLFTDIRVLQDSCSHFVENNTLGTSSKKTFS 1140
 QY 1141 YMPQFOTCSTQTHIKIMENKMDLTV 1165
 DB 1141 YMPQFOTCSTQTHIKIMENKMDLTV 1165

RESULT 2

US-08-583-153A-4
 Sequence 4, Application US/08583153A

GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.
 APPLICANT: Culpepper, Janice A.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
 NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
 CITY: Boston

STATE: MA
 COUNTRY: US

ZIP: 02110-2804
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/583,153A

FILING DATE: 28-DEC-1995
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Meikie John, Anita L.

REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/016001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELE: 200154
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1165 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-583-153A-4

Query Match 100.0%; Score 6254; DB 9; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 241 LGLHMEITDDGNLKLKISWSSPLVPPLOYVKSSENSTVIREADKIVATSILVDSILP 300
 DB 241 LGLHMEITDDGNLKLKISWSSPLVPPLOYVKSSENSTVIREADKIVATSILVDSILP 300
 QY 301 GSSYEYQVNGKRLDGFGLISDMSTPRVPTTQDYIYFPFKILTSVGSNVGFHCYKKENKI 360
 DB 301 GSSYEYQVNGKRLDGFGLISDMSTPRVPTTQDYIYFPFKILTSVGSNVGFHCYKKENKI 360
 QY 361 VSKETVYMMNLAERKIPQSDYVSDHVSQVTFENLNETKPKGKFTYDVAVCCNEHECH 420
 DB 361 VSKETVYMMNLAERKIPQSDYVSDHVSQVTFENLNETKPKGKFTYDVAVCCNEHECH 420
 QY 421 RYAEVLVIDVNNISCEIDGYLTAKTCRMSSTIOSIAESTIQLRYHRSILVCSIDPSIH 480
 DB 421 RYAEVLVIDVNNISCEIDGYLTAKTCRMSSTIOSIAESTIQLRYHRSILVCSIDPSIH 480
 QY 481 PISEKDCYLGSDGFYECIFQPIFLISGYTMMIRINHSIGSLDSPPTCYLPDSVAKPLPP 540
 DB 481 PISEKDCYLGSDGFYECIFQPIFLISGYTMMIRINHSIGSLDSPPTCYLPDSVAKPLPP 540
 QY 541 SSVKAEITINIGLTKISWKPVPENNLQFOIRYLSGKEVQMKMEYDASKSISLVP 600
 DB 541 SSVKAEITINIGLTKISWKPVPENNLQFOIRYLSGKEVQMKMEYDASKSISLVP 600
 QY 601 PDLCAVYAVQVCKRLDGLGYSWMSNPAYTYVMIDIKVPMRGPEFWRINNGDTMKKEKNV 660
 DB 601 PDLCAVYAVQVCKRLDGLGYSWMSNPAYTYVMIDIKVPMRGPEFWRINNGDTMKKEKNV 660
 QY 661 TLLMKPLMKNDSICSVQRYVINHHTSCNGTWSGSDVGNHTKFTFLMTEQAHYTVLAINSI 720
 DB 661 TLLMKPLMKNDSICSVQRYVINHHTSCNGTWSGSDVGNHTKFTFLMTEQAHYTVLAINSI 720
 QY 721 GASVANFNLTFSMPKSVNIQSLAVPLNNSGVISWILSPDYLMTFETEMKLNLD 780
 DB 721 GASVANFNLTFSMPKSVNIQSLAVPLNNSGVISWILSPDYLMTFETEMKLNLD 780
 QY 781 GEIKMLRISSSVKYYIHDHFIPIEKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
 DB 781 GEIKMLRISSSVKYYIHDHFIPIEKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840

QY 841 GLYIVPVISSILLGLTLLISHORAKKLEWEDVNPKNCSWAGLNFQKPETEHFLI 900
 DB 841 GLYIVPVISSILLGLTLLISHORAKKLEWEDVNPKNCSWAGLNFQKPETEHFLI 900
 QY 901 KHTASVTCGPLLEPTESEDISVDTSMKNKDEMPPTVYSLISTDLEKGSVCISDPN 960
 DB 901 KHTASVTCGPLLEPTESEDISVDTSMKNKDEMPPTVYSLISTDLEKGSVCISDPN 960
 QY 961 SVNFESEGETEYEDESORQPFVYATLISNKSSETGEODGLINSVTKCFSSKNPFL 1020
 DB 961 SVNFESEGETEYEDESORQPFVYATLISNKSSETGEODGLINSVTKCFSSKNPFL 1020
 QY 1021 KDSFNSSWIEBAQAFILSDQHPNISPHTFSGDLDELKLEGNFPEENNDKSIYYL 1080
 DB 1021 KDSFNSSWIEBAQAFILSDQHPNISPHTFSGDLDELKLEGNFPEENNDKSIYYL 1080
 QY 1081 GVTSTIKKRESGVLLTDKSVSCPPAPCFETDIRVLDQSCSHVENNINLGTSSKKTAS 1140
 DB 1081 GVTSTIKKRESGVLLTDKSVSCPPAPCFETDIRVLDQSCSHVENNINLGTSSKKTAS 1140
 QY 1141 YMPQFOTCSTQTHKIMENKCDLTV 1165
 DB 1141 YMPQFOTCSTQTHKIMENKCDLTV 1165

RESULT 3

US-08-585-005-2
 ; Sequence 2, Application us/08585005

GENERAL INFORMATION:

APPLICANT: Matthews, William

APPLICANT: Bennett, Brian

TITLE OF INVENTION: WSX RECEPTOR

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/585,005

FILING DATE: 08-Jan-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0986

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-585-005-2

Query Match 100.0%; Score 6254; DB 9; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYITAFNLSTPIPMRFKLSGMPNSTYDYFLPAGLSKNTS 60
 DB 1 MICQKFCVLLHMEFIYITAFNLSTPIPMRFKLSGMPNSTYDYFLPAGLSKNTS 60

```

QY 61 NGHYEFAVEPRKNSGTHFSNLKTTFHCCFNSSEODRNCSLCADNIEGTFVSTVNSLVE 120
DB 61 NGHYEFAVEPRKNSGTHFSNLKTTFHCCFNSSEODRNCSLCADNIEGTFVSTVNSLVE 120
QY 121 QOQIDAMNINOCMLKGDGLKLFICVVESELFKNLPNNYKXHLLYVLEPEVLEDSPLVPOKGS 180
DB 121 QOQIDAMNINOCMLKGDGLKLFICVVESELFKNLPNNYKXHLLYVLEPEVLEDSPLVPOKGS 180
QY 181 FQWVHCNCSVHECCLECLVPTAKLNDTLMLCLITSGGVIFQSPPLMSVOPIMVAPDP 240
DB 181 FQWVHCNCSVHECCLECLVPTAKLNDTLMLCLITSGGVIFQSPPLMSVOPIMVAPDP 240
QY 241 LGIHMETDGNLKSISWSSPPLVPPLOQVQKXSENVSTVIREADKIVATSILVDSILP 300
DB 241 LGIHMETDGNLKSISWSSPPLVPPLOQVQKXSENVSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEVOVGKRLDGPJMSDMSPTPVFTODVYFPPILTSVGSNVSFHCYKKEKNT 360
DB 301 GSSYEVOVGKRLDGPJMSDMSPTPVFTODVYFPPILTSVGSNVSFHCYKKEKNT 360
QY 361 VPSKEIYVMMNLAERIPQSOYDVSDHVSQVTFPNLNETKPRGKFYDAVCCNEHECHH 420
DB 361 VPSKEIYVMMNLAERIPQSOYDVSDHVSQVTFPNLNETKPRGKFYDAVCCNEHECHH 420
QY 421 RYAEIYDVNINISCEVDGYLTMTCRMSTTQSLAESTLQLRHRSLSYCDIPSIH 480
DB 421 RYAEIYDVNINISCEVDGYLTMTCRMSTTQSLAESTLQLRHRSLSYCDIPSIH 480
QY 481 PISEPDXYLOSGEYECIFOPFLLSGYTMIRINHSIGSLDSPCTVCLPVSVPRLP 540
DB 481 PISEPDXYLOSGEYECIFOPFLLSGYTMIRINHSIGSLDSPCTVCLPVSVPRLP 540
QY 541 SSVKAEITINIGLKISMEKPVFPENNLOFOIRYGLSGKEVQMKMEVDAKSKSVLEP 600
DB 541 SSVKAEITINIGLKISMEKPVFPENNLOFOIRYGLSGKEVQMKMEVDAKSKSVLEP 600
QY 601 PDLCAVYAVOVCKRDLGJGYSNMSNPAYVYMDIKVMPRGPEFRIINGDTMKKEKNV 660
DB 601 PDLCAVYAVOVCKRDLGJGYSNMSNPAYVYMDIKVMPRGPEFRIINGDTMKKEKNV 660
QY 661 TLLMKRPLKNDLSQVORVYVNHHTSCNGTWSBDVGNHRTFPLMTEQAHYTVLAINSI 720
DB 661 TLLMKRPLKNDLSQVORVYVNHHTSCNGTWSBDVGNHRTFPLMTEQAHYTVLAINSI 720
QY 721 GASVANFLTFSPMSKVNIVOSLAVPLNNSCVIYMWILSPDYKLMFIIEMKMLND 780
DB 721 GASVANFLTFSPMSKVNIVOSLAVPLNNSCVIYMWILSPDYKLMFIIEMKMLND 780
QY 781 GEIKWLRISSVAKKYIHDFPIEKEYOPLPIEMEGVGPRIINSFTQDDIEKHQSDA 840
DB 781 GEIKWLRISSVAKKYIHDFPIEKEYOPLPIEMEGVGPRIINSFTQDDIEKHQSDA 840
QY 841 GLVYIYVYIISILLGLTLLISHOMKRLFMEDVNPNCMAOGLNOKETEPHEHFT 900
DB 841 GLVYIYVYIISILLGLTLLISHOMKRLFMEDVNPNCMAOGLNOKETEPHEHFT 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSKKNKDEMPPTVVSILSTJDLKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLEPETISEDISVDTSKKNKDEMPPTVVSILSTJDLKSGVCSIDQFN 960
QY 961 SVNFSABETEVYEDESOROPFVKATYATLINSKSETEGEGLINSSYTKCFSSKNSPL 1020
DB 961 SVNFSABETEVYEDESOROPFVKATYATLINSKSETEGEGLINSSYTKCFSSKNSPL 1020
QY 1021 KQSFSSMEIEAOAFIISDOHNTISPHLTFSEGLDLELLLEGFPENNNDKSIYLL 1080
DB 1021 KQSFSSMEIEAOAFIISDOHNTISPHLTFSEGLDLELLLEGFPENNNDKSIYLL 1080
QY 1081 GVTSIKRRSGVLLTDKSHVSCPPAPCLFTDIRVLQDSCSHFVENNINILGTSKKTFS 1140
DB 1081 GVTSIKRRSGVLLTDKSHVSCPPAPCLFTDIRVLQDSCSHFVENNINILGTSKKTFS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

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DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
RESULT 4
US-08-638-524B-4
Sequence 4, Application US/08638524B
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpeper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
TITLE OF INVENTION: CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,524B
FILING DATE: 26-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: MeikieJohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-638-524B-4
Query Match 100.0%; Score 6254; DB 10; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQFCVLLHMERITYITAFNLSYPTTPMRFKLSCHPNSSTYRFLPAGLSKNTSNS 60
DB 1 MICQFCVLLHMERITYITAFNLSYPTTPMRFKLSCHPNSSTYRFLPAGLSKNTSNS 60
QY 61 NGHYEFAVEPRKNSGTHFSNLKTTFHCCFNSSEODRNCSLCADNIEGTFVSTVNSLVE 120
DB 61 NGHYEFAVEPRKNSGTHFSNLKTTFHCCFNSSEODRNCSLCADNIEGTFVSTVNSLVE 120

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QY 121 QOIDANNMIQCMKGLDKLFCYVESLFRNFRNRYKVVHLLYLPEVLEDSPLVPQKGS 180
Db 121 QOIDANNMIQCMKGLDKLFCYVESLFRNFRNRYKVVHLLYLPEVLEDSPLVPQKGS 180
QY 181 FOMVHNCNSVHCCCECLVPPPAKINDTLMLCKLITSGGVIFQSPMLASQPIINMVKPDP 240
Db 181 FOMVHNCNSVHCCCECLVPPPAKINDTLMLCKLITSGGVIFQSPMLASQPIINMVKPDP 240
QY 241 LGLHMEITDDGNLKITSMSPPLVPPLOYQVYKSENSSTVIREADKIVATSILVDSILP 300
Db 241 LGLHMEITDDGNLKITSMSPPLVPPLOYQVYKSENSSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEVQVGRKLDGPGIWSMDSTPRVFTTODVIFYPPKILTVSGSVNSVSHCIYKKNKI 360
Db 301 GSSYEVQVGRKLDGPGIWSMDSTPRVFTTODVIFYPPKILTVSGSVNSVSHCIYKKNKI 360
QY 361 VPSKELIVMMNLAEKIPQSDYVSDHVKYTFENLNEKPRGKITYDAVYCCNEHECH 420
Db 361 VPSKELIVMMNLAEKIPQSDYVSDHVKYTFENLNEKPRGKITYDAVYCCNEHECH 420
QY 421 RYAEIYVIDVININISCEIDGVLTKMTCRMSSTIOSLAESTLQLYHRSSLYCSDIPSIH 480
Db 421 RYAEIYVIDVININISCEIDGVLTKMTCRMSSTIOSLAESTLQLYHRSSLYCSDIPSIH 480
QY 481 PISEKRCOYLQSDGFYECLTQPIFLSLGTYTMTIRINHSIGSDSPPTCVLPDSVYKPLRP 540
Db 481 PISEKRCOYLQSDGFYECLTQPIFLSLGTYTMTIRINHSIGSDSPPTCVLPDSVYKPLRP 540
QY 541 SSVKKEITINILKTIKISWKPYEPENNLOFOIRYGLSGKEVOYMKRYEYDASKSVSLPV 600
Db 541 SSVKKEITINILKTIKISWKPYEPENNLOFOIRYGLSGKEVOYMKRYEYDASKSVSLPV 600
QY 601 PDLCAVYAVQVCKRLDGLGYWMSNMPAYTVYMDIKYPMRGPPEFIRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVCKRLDGLGYWMSNMPAYTVYMDIKYPMRGPPEFIRIINGDTMKKEKNV 660
QY 661 TLLMTPMLKNDLSQVQRYVINHHTSCNGTSEEDVGNHTKFTFLTEQAHYTVLAINSI 720
Db 661 TLLMTPMLKNDLSQVQRYVINHHTSCNGTSEEDVGNHTKFTFLTEQAHYTVLAINSI 720
QY 721 GASVANFNLTFSMPKSVKIVIOSLAPLNSSCVIVSLLSPDSQKLYMFTIEMKNLND 780
Db 721 GASVANFNLTFSMPKSVKIVIOSLAPLNSSCVIVSLLSPDSQKLYMFTIEMKNLND 780
QY 781 GRIKMLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGKRIINSFTODDIEKHQSDA 840
Db 781 GRIKMLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGKRIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVIISSILLGLTLLISHORMKLEWEDVNPKNCSMAOGLNFQKPETFEHLFT 900
Db 841 GLYVIVPVIISSILLGLTLLISHORMKLEWEDVNPKNCSMAOGLNFQKPETFEHLFT 900
QY 901 KHTASVTCGRLLEPTEIEDI SVTSMKNKDEMPYTVVLSLTTDLKSGVICIDQCN 960
Db 901 KHTASVTCGRLLEPTEIEDI SVTSMKNKDEMPYTVVLSLTTDLKSGVICIDQCN 960
QY 961 SYNFAEAGTEVYTEDSROFPVKYATLINSKSPETGEEOGLINSVTKCFSSKNSPL 1020
Db 961 SYNFAEAGTEVYTEDSROFPVKYATLINSKSPETGEEOGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIQAQAFILSDQHPNIIISPHLTFSEGLDELLEGNPRENNDRKSIYYL 1080
Db 1021 KDSFNSSSWEIQAQAFILSDQHPNIIISPHLTFSEGLDELLEGNPRENNDRKSIYYL 1080
QY 1081 GYTSIKKRSGVLLDKSVSCFPAPCLFTDIRVLQDSCSHFVENNINMGTSISKTFAS 1140
Db 1081 GYTSIKKRSGVLLDKSVSCFPAPCLFTDIRVLQDSCSHFVENNINMGTSISKTFAS 1140
QY 1141 YMPQOTCTQTHKIMENKCDLTV 1165
Db 1141 YMPQOTCTQTHKIMENKCDLTV 1165

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RESULT 5
US-08-667-197-2
: Sequence 2, Application US/08667197
: GENERAL INFORMATION:
: APPLICANT: Matthews, William
: TITLE OF INVENTION: USES FOR MSX LIGANDS
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/667,197
: FILING DATE: 20-Jun-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/585005
: FILING DATE: 01/08/96
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: P-40,378
: REFERENCE/DOCKET NUMBER: P0386P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
US-08-667-197-2

Query Match 100.0%; Score 6254; DB 10; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIOQKCVYLLHMEFYVTAFLNSYPIPMWRKLSQMPNSTYDYELLPAIGSKNTS 60
Db 1 MIOQKCVYLLHMEFYVTAFLNSYPIPMWRKLSQMPNSTYDYELLPAIGSKNTS 60
QY 61 NGHYETAVERPFNSGTHSNLSKTFPHCCFNSQODRNCSLCADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAVERPFNSGTHSNLSKTFPHCCFNSQODRNCSLCADNIEGTFVSTVNSLVF 120
QY 121 QOIDANNMIQCMKGLDKLFCYVESLFRNFRNRYKVVHLLYLPEVLEDSPLVPQKGS 180
Db 121 QOIDANNMIQCMKGLDKLFCYVESLFRNFRNRYKVVHLLYLPEVLEDSPLVPQKGS 180
QY 181 FOMVHNCNSVHCCCECLVPPPAKINDTLMLCKLITSGGVIFQSPMLASQPIINMVKPDP 240
Db 181 FOMVHNCNSVHCCCECLVPPPAKINDTLMLCKLITSGGVIFQSPMLASQPIINMVKPDP 240
QY 241 LGLHMEITDDGNLKITSMSPPLVPPLOYQVYKSENSSTVIREADKIVATSILVDSILP 300
Db 241 LGLHMEITDDGNLKITSMSPPLVPPLOYQVYKSENSSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEVQVGRKLDGPGIWSMDSTPRVFTTODVIFYPPKILTVSGSVNSVSHCIYKKNKI 360
Db 301 GSSYEVQVGRKLDGPGIWSMDSTPRVFTTODVIFYPPKILTVSGSVNSVSHCIYKKNKI 360
QY 361 VPSKELIVMMNLAEKIPQSDYVSDHVKYTFENLNEKPRGKITYDAVYCCNEHECH 420

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Db 361 VPSKEIWMNNLAEKIPQSOYDVSDHVSQVTEFNLNETKPRGKFTYDAVYCNEHECHH 420
QY 421 RYRELVIYDVNINISCEITDGLTKMCRWSTSTIOSLAESTLQDLYRHSRLYC6DIPSIH 480
Db 421 RYRELVIYDVNINISCEITDGLTKMCRWSTSTIOSLAESTLQDLYRHSRLYC6DIPSIH 480
QY 481 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSYKAEITINIGLKTSMEKRPVPENNLOQIRYGLSGKEVOKMKEVYDAKRSKSLPV 600
Db 541 SSYKAEITINIGLKTSMEKRPVPENNLOQIRYGLSGKEVOKMKEVYDAKRSKSLPV 600
QY 601 PDLCAVYAVOVRCKRDLGCLGYSMNSNPATYVMDIKVPRGPEFRRIINGDMKKEKNV 660
Db 601 PDLCAVYAVOVRCKRDLGCLGYSMNSNPATYVMDIKVPRGPEFRRIINGDMKKEKNV 660
QY 661 TLLMKPLMKNDLSQSVQRYVINHTSCNGTWSQVGNHRTFTPLMTEQAHVTYVLAINST 720
Db 661 TLLMKPLMKNDLSQSVQRYVINHTSCNGTWSQVGNHRTFTPLMTEQAHVTYVLAINST 720
QY 721 GASVAPNPLTFSPMKNKVNVOVSLAVPLNSCVIYSWILSPSDYKLMFTEKMLNED 780
Db 721 GASVAPNPLTFSPMKNKVNVOVSLAVPLNSCVIYSWILSPSDYKLMFTEKMLNED 780
QY 781 GEIKMPLRISSVKKYIHDHFIEKYOFSLYIFEMEGVGRPKIINSFODDIEKHQSDA 840
Db 781 GEIKMPLRISSVKKYIHDHFIEKYOFSLYIFEMEGVGRPKIINSFODDIEKHQSDA 840
QY 841 GLYIYVPIVSISSILLGLTLLSHQMKKLFMEDVNPKNCSAQCUNFOKPFTEHLEP 900
Db 841 GLYIYVPIVSISSILLGLTLLSHQMKKLFMEDVNPKNCSAQCUNFOKPFTEHLEP 900
QY 901 KHTASVTCGPLEPETISDISVDTSMKKNKDEMPYVSLSTDLDEKGSICIDOFN 960
Db 901 KHTASVTCGPLEPETISDISVDTSMKKNKDEMPYVSLSTDLDEKGSICIDOFN 960
QY 961 SVNFSAEGETEYTEDESQRPVYATYLLSNSKPSETGEQGLINSSVTKCHSKNSPL 1020
Db 961 SVNFSAEGETEYTEDESQRPVYATYLLSNSKPSETGEQGLINSSVTKCHSKNSPL 1020
QY 1021 KDSFSSSWMEIEAOAFPIISDQHPNIIISPLTSEGLDELKLEGNPEENNDRKSIYVL 1080
Db 1021 KDSFSSSWMEIEAOAFPIISDQHPNIIISPLTSEGLDELKLEGNPEENNDRKSIYVL 1080
QY 1081 GYSIKKREGVLLTJDKSRVSCPAPACLETDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
Db 1081 GYSIKKREGVLLTJDKSRVSCPAPACLETDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

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RESULT 6
US-08-708-123D-4

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: Sequence 4, Application us/08708123D
: GENERAL INFORMATION:
: APPLICANT: Tartaglia, Louis A.
: APPLICANT: Tepper, Robert I.
: APPLICANT: Culpepper, Janice A.
: APPLICANT: White, David W.
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
: TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: US

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: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/708,123D
: FILING DATE: 03-SEP-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/638,524
: FILING DATE: 26-APR-1996
: APPLICATION NUMBER: 08/599,455
: FILING DATE: 22-JAN-1996
: APPLICATION NUMBER: 08/583,153
: FILING DATE: 28-DEC-1995
: APPLICATION NUMBER: 08/570,142
: FILING DATE: 11-DEC-1995
: APPLICATION NUMBER: 08/569,485
: FILING DATE: 08-DEC-1995
: APPLICATION NUMBER: 08/566,622
: FILING DATE: 04-DEC-1995
: APPLICATION NUMBER: 08/562,663
: FILING DATE: 27-NOV-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Melkielejohn, Ph.D., Anita L.
: REGISTRATION NUMBER: 35,283
: REFERENCE/DOCKET NUMBER: 07334/019001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-542-5070
: TELEFAX: 617-542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: Protein
: FRAGMENT TYPE: Internal
: US-08-708-123D-4

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Query Match 100.0%; Score 6254; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICOKFCVLLHMEFYITVTAENLSYPTIPMPRKLSCMPNPNSTYDFLLPAGLSKNTSNS 60
Db 1 MICOKFCVLLHMEFYITVTAENLSYPTIPMPRKLSCMPNPNSTYDFLLPAGLSKNTSNS 60
QY 61 NGHYETAVERPKFNSSGTHESNLSKTFHCCFNSQDORNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVERPKFNSSGTHESNLSKTFHCCFNSQDORNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANMNIOQWKLKDLKLFICYVESLFKNLPNNYKWHLLYVLEVEDSPLVPQKGS 180
Db 121 QOIDANMNIOQWKLKDLKLFICYVESLFKNLPNNYKWHLLYVLEVEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCCECLVVPYPAKLNDTLLMCLKITSGGVIFOSPLMSQPINMVAPDP 240
Db 181 FQWVHCNCSVHECCCECLVVPYPAKLNDTLLMCLKITSGGVIFOSPLMSQPINMVAPDP 240
QY 241 LGLHMEITDGNLKIWSMSSPPLVPPLOQVYKXSENSTVIREADKIVATSILVDSILP 300
Db 241 LGLHMEITDGNLKIWSMSSPPLVPPLOQVYKXSENSTVIREADKIVATSILVDSILP 300
QY 301 GSYEYQVGRKLDGPGIWSMSTPRVFTTODYIYFPPKILISVGSNVSFHCITYKKENKI 360
Db 301 GSYEYQVGRKLDGPGIWSMSTPRVFTTODYIYFPPKILISVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIWMNNLAEKIPQSOYDVSDHVSQVTEFNLNETKPRGKFTYDAVYCNEHECHH 420
Db 361 VPSKEIWMNNLAEKIPQSOYDVSDHVSQVTEFNLNETKPRGKFTYDAVYCNEHECHH 420

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QY 421 RYLLAYIVDNINISCEFTOGYILTKMKCRNSTSTIOSLAEFTLOLRHSSXYCSDIPB 480
Db 421 RYALAYIVDNINISCEFTOGYILTKMKCRNSTSTIOSLAEFTLOLRHSSLYCSDIPB 480
QY 481 PISEPKKCYLOSQGFECIEFOPIFLLSGYTMIRINHSHGSLDSEPTCVLPDSVVKPLPP 540
Db 481 PISEPKKCYLOSQGFECIEFOPIFLLSGYTMIRINHSHGSLDSEPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKITSWEKVPENNNLOFOIRYGLSGKEVOMKWEYVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKITSWEKVPENNNLOFOIRYGLSGKEVOMKWEYVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVOVRCKRLDGLGYSNMSNPAVYVMMIDKVPMBRPEFWRIRINDPTMKKEKNV 660
Db 601 PDLCAVYAVOVRCKRLDGLGYSNMSNPAVYVMMIDKVPMBRPEFWRIRINDPTMKKEKNV 660
QY 661 TLLMKPLMKNDLSVCYORVYVNNHSTSCNGTWSDEDVGNHTRKFTLWTEQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSVCYORVYVNNHSTSCNGTWSDEDVGNHTRKFTLWTEQAHVTVLAINSI 720
QY 721 GASVANNLTFSPMBSKVNIVOSLSAVPANSFCYVSHLSSDYKLMVFTIEMKNLNE 780
Db 721 GASVANNLTFSPMBSKVNIVOSLSAVPANSFCYVSHLSSDYKLMVFTIEMKNLNE 780
QY 781 GEIKWILRISSSVKRYIYIHHFIPRIEKYOPSLVPIFMEGVGRKIIINSFTODDIEKHSDA 840
Db 781 GEIKWILRISSSVKRYIYIHHFIPRIEKYOPSLVPIFMEGVGRKIIINSFTODDIEKHSDA 840
QY 841 GLVYIVPVITISSIILLGTLTLLSHQBKKLFMEDVVPNPKNSMAOGLNFORKETEPEHFI 900
Db 841 GLVYIVPVITISSIILLGTLTLLSHQBKKLFMEDVVPNPKNSMAOGLNFORKETEPEHFI 900
QY 901 KHTASVYCGLLLEPERISBDISVOTSMKNKDEMPPTYVSLSTTDLKSGVCISDOFN 960
Db 901 KHTASVYCGLLLEPERISBDISVOTSMKNKDEMPPTYVSLSTTDLKSGVCISDOFN 960
QY 961 SVNSSEAEGETEYVYEDESQOPFVKATATILNSKPSETEEOGLINSSVYKCFSSKN SPL 1020
Db 961 SVNSSEAEGETEYVYEDESQOPFVKATATILNSKPSETEEOGLINSSVYKCFSSKN SPL 1020
QY 1021 KDSFSSNSWEIEAOAFITISDOHPNITISPLTFSEGLDELKLEBNPRENNKDKSIYLL 1080
Db 1021 KDSFSSNSWEIEAOAFITISDOHPNITISPLTFSEGLDELKLEBNPRENNKDKSIYLL 1080
QY 1081 GVTSIKKREGVILITOKSRSCFPAACLETDIRVLQDSCSHFVNNNTNLGTSKKRTAS 1140
Db 1081 GVTSIKKREGVILITOKSRSCFPAACLETDIRVLQDSCSHFVNNNTNLGTSKKRTAS 1140
QY 1141 YMPQFQCTQTFHKIMENKMCDELTV 1165
Db 1141 YMPQFQCTQTFHKIMENKMCDELTV 1165

RESULT 7
US-08-779-457-2
: Sequence 2, Application US/08779457
: GENERAL INFORMATION:
: APPLICANT: Carter, Paul J.
: APPLICANT: Chiang, Nancy Y.
: APPLICANT: Kyung, Jin Kim
: APPLICANT: Matthews, William L.
: APPLICANT: Rodrigues, Maria L.
: TITLE OF INVENTION: MSX RECEPTOR AGONIST ANTIBODIES
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:

```

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/779,457
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/667197
 FILING DATE: 06/20/96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585005
 FILING DATE: 01/08/96
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0986P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/925-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1165 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

QY	601	PDLCAVAVVOYRCRBLDGLGYMSWMSNPATYVMDIKVPMRGPENRRIINGDTMRKEKV	660
QY	601	PDLCAVAVVOYRCRBLDGLGYMSWMSNPATYVMDIKVPMRGPENRRIINGDTMRKEKV	660
Db	601	PDLCAVAVVOYRCRBLDGLGYMSWMSNPATYVMDIKVPMRGPENRRIINGDTMRKEKV	660
QY	661	TLLMKPRLKNDJSLCSVORYVYVNHHTSCNGTWSEDEVDGNHKTFTLMTAEQATVVLANSI	720
Db	661	TLLMKPRLKNDJSLCSVORYVYVNHHTSCNGTWSEDEVDGNHKTFTLMTAEQATVVLANSI	720
QY	721	GASVANFULTSMWSKXVNIYQSLSATPLANSICYISMILSPBDYKLMFTIEMKULND	780
Db	721	GASVANFULTSMWSKXVNIYQSLSATPLANSICYISMILSPBDYKLMFTIEMKULND	780
QY	781	GEIKMLRISSSVKKYYIHDHPIPLEKQFSLYPIFMGVGKPKIINSFTODDIEMHQSDA	840
Db	781	GEIKMLRISSSVKKYYIHDHPIPLEKQFSLYPIFMGVGKPKIINSFTODDIEMHQSDA	840
QY	841	GLYVIVPYIISSSILLGTLTLISHQRKKLFMEDVDPNPKKCSMAOGLNFOKPEPHELP	900
Db	841	GLYVIVPYIISSSILLGTLTLISHQRKKLFMEDVDPNPKKCSMAOGLNFOKPEPHELP	900
QY	901	KHTAVTCGPIILPEPISDIYDTSWKNKDEMPPTVYSLSTDDLEKGSVCISDOJN	960
Db	901	KHTAVTCGPIILPEPISDIYDTSWKNKDEMPPTVYSLSTDDLEKGSVCISDOJN	960
QY	961	SVNFEAGTEVYTEDESQORPEFYATVTLINSKPSPTGEQGLINSVTKCPSKNSPL	1020
Db	961	SVNFEAGTEVYTEDESQORPEFYATVTLINSKPSPTGEQGLINSVTKCPSKNSPL	1020
QY	1021	KDSESNSSWEIEAOAFPLISDQHPNITSPLHTSEGLDELLKGNPPEBNDRKSIYYL	1080
Db	1021	KDSESNSSWEIEAOAFPLISDQHPNITSPLHTSEGLDELLKGNPPEBNDRKSIYYL	1080
QY	1081	GVTSTKRRSEGVLLTDKSRVSCPAPCLTDDIRVLDDSCSHFVENNINLGTSSKRTFS	1140
Db	1081	GVTSTKRRSEGVLLTDKSRVSCPAPCLTDDIRVLDDSCSHFVENNINLGTSSKRTFS	1140
QY	1141	YMPQFOTCSTQTHKIMENKMDLTV	1165
Db	1141	YMPQFOTCSTQTHKIMENKMDLTV	1165
RESULT 8			
US-08-780-562-2			
: Sequence 2, Application US/08780562			
: GENERAL INFORMATION:			
: APPLICANT: Matthews, William			
: TITLE OF INVENTION: WSX RECEPTOR			
: NUMBER OF SEQUENCES: 45			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Genentech, Inc.			
: STREET: 460 Point San Bruno Blvd			
: CITY: South San Francisco			
: STATE: California			
: COUNTRY: USA			
: ZIP: 94080			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: WinPatIn (Genentech)			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/780,562			
: FILING DATE:			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: 08/585005			
: FILING DATE: 01/08/97			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: 60/			
: FILING DATE: 01/08/97			
: ATTORNEY/AGENT INFORMATION:			

:	NAME:	Lee, Wendy M.
:	REGISTRATION NUMBER:	40.378
:	REFERENCE/DOCKET NUMBER:	P0986K1
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE:	415/225-1994
:	TELEFAX:	415/952-9881
:	TELEX:	910/371-7168
:	INFORMATION FOR SEQ ID NO:	2
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH:	1165 amino acids
:	TYPE:	Amino Acid
:	TOPOLOGY:	Linear
:	US-08-780-562-2	

Query Match	100.0%	Score 6254	DB 11	Length 1165
Best Local Similarity	100.0%	Pred. No. 0	Mismatches 0	Indels 0
Matches 1165	Conservative 0	Gaps 0		
Oy	1	MICQFCVLLHMEIYYTTAFNLSYPIPMWFKLSCMPNSTYDFLLPAGLSKNTS	60	
Db	1	MICQFCVLLHMEIYYTATFNLSYPIPMWFKLSCMPNSTYDFLLPAGLSKNTS	60	
Oy	61	NGHYETAPEPKNSSGTHRSNLSTKTTHCCCFSESDRNCSCADNIEGTFYSTNSLYE	120	
Db	61	NGHYETAPEPKNSSGTHRSNLSTKTTHCCCFSESDRNCSCADNI EGTFTYSTNSLYE	120	
Oy	121	GOIDANMNIOCLAKDMLKEIFYESLFKNLPFRNYKYHLLYLVPEVLDESPLVPQKS	180	
Db	121	GOIDANMNIOCLAKDMLKEIFYESLFKNLPFRNYKYHLLYLVPEVLDESPLVPQKS	180	
Oy	181	FQMWHCNCSVECCELVPPPAKLNDTLMLCKITTSGGVIFOSPMSYQPIIMWKPDPP	240	
Db	181	FQMWHCNCSVEHCCELVPPPAKLNDTLMLCKITTSGGVIFOSPMSYQPIIMWKPDPP	240	
Oy	241	LGLHMEITDDGDLKISWSSPPLPFPLOYQVYSENSTVIIEADKIYSATSLVDLSILP	300	
Db	241	LGLHMEITDDGDLKISWSSPPLPFPLOYQVYSENSTVIIEADKIYSATSLVDLSILP	300	
Oy	301	GSSYEVOVGKRRLDPGISMDWSTPRVFETTDVIFYPPKILTVSGSNVSFHCIYKKENKI	360	
Db	301	GSSYEVOVGKRRLDPGISMDWSTPRVFETTDVIFYPPKILTVSGSNVSFHCIYKKENKI	360	
Oy	361	VPSKETIVMMNLAEIKIPSOYDVYSDHKYKFEFLNTERKPGSKTYAAVVCNHECHH	420	
Db	361	VPSKETIVMMNLAEIKIPSOYDVYSDHKYKFEFLNTERKPGSKTYADVVCNHECHKH	420	
Oy	421	RVAELYVIDVINISCEFDGYLTLMKTCRMSTISTIOSLAESTIQLELYHRSSLYCSDIPSIIH	480	
Db	421	RVAELYVIDVINISCEFDGYLTLMKTCRMSTISTIOSLAESTIQLRXHRSSLYCSDIPSIIH	480	
Oy	481	PISEKDCYLOSDBGYECIFOPFIPLSGTYMIRINHSLGSJDSPTCYLPDSYVKPLRP	540	
Db	481	PISEKDCYLOSDBGYECIFOPFIPLSGTYMIRINHSLGSJDSPTCYLPDSYVKPLRP	540	
Oy	541	SSVKREITINIGLKISWEKPYEPENNLOFOPTYGLSGKEYOMKMYEYDAKSKSVSLPV	600	
Db	541	SSVKREITINIGLKISWEKPYEPENNLOFOPTYGLSGKEYOMKMYEYDAKSKSVSLPV	600	
Oy	601	PDLCAVAVAOVRCKRLDGLGYWSNMSNPAITYVMIDIKVPMRGPEFWRIINGDTMKKEKNV	660	
Db	601	PDLCAVAVAOVRCKRLDGLGYWSNMSNPAITYVMIDIKVPMRGPEFWRIINGDTMKKEKNV	660	
Oy	661	TLLMKPELKNKNSICGVORYVINHHHTSCGJTSEDGNHTKFFELMTBOAHVTYVAINSI	720	
Db	661	TLLMKPELKNKNSICGVORRYVINHHHTSCGJTSEDGNHTKFFELMTBOAHVTYVAINSI	720	
Oy	721	GASVANFMULTSPWPSKKNIVOSLSAYLUNSCSVIYSWLBSBDVKLWFYFIEMKNLMD	780	
Db	721	GASVANFMULTSPWPSKKNIVOSLSAYLUNSCSVIYSWLBSBDVKLWFYFIEMKNLMD	780	
Oy	781	GEIKWLRTISSVKKYYIHDFPIEKYOPSLEYPIFMECVGKPKIINSTODDIIEKHOSDA	840	

DB 781 GELKMLRISSVKKYYIHDFIPIEKYOSLYPIFMEGVGPKKIINSFQDDIEKHQSDA 840
QY 841 GLXVYVPIVITSSILLLGLTLLISHORMKLEWEDVNPKNCSMAOGLNFOKPEFHEHLEI 900
DB 841 GLXVYVPIVITSSILLLGLTLLISHORMKLEWEDVNPKNCSMAOGLNFOKPEFHEHLEI 900
QY 901 KHTASTGCPILLEPTISEDISVDTSMKNKDEMPYVSLSTLTDLEKGSVCISIDQDN 960
DB 901 KHTASTGCPILLEPTISEDISVDTSMKNKDEMPYVSLSTLTDLEKGSVCISIDQDN 960
QY 961 SYNFSEAEETVTEDESQROFPVKATLINSKPSSETGEEOGLINSVTKCFSSKNSEPL 1020
DB 961 SYNFSEAEETVTEDESQROFPVKATLINSKPSSETGEEOGLINSVTKCFSSKNSEPL 1020
QY 1021 KDSFNSNSWEIBAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKRSIYYL 1080
DB 1021 KDSFNSNSWEIBAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKRSIYYL 1080
QY 1081 GYTSIKRKRSVLLDNRKSVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
DB 1081 GYTSIKRKRSVLLDNRKSVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPOTCTSTQTHKIMENKCDLTV 1165
DB 1141 YMPOTCTSTQTHKIMENKCDLTV 1165

RESULT 9
US-09-094-410-4
Sequence 4, Application US/09094410
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OR RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
SERIES: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,410
FILING DATE: 09-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/369,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Weikiejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: Protein
FRAGMENT TYPE: Internal
US-09-094-410-4
Query Match 100.0%; Score 6254; DB 14; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFTYVTAENLSYPTIPWPRKLSOMPNSIYDVELLPAGISKNTNS 60
DB 1 MICQKFCVLLHWEFTYVTAENLSYPTIPWPRKLSOMPNSIYDVELLPAGISKNTNS 60
QY 61 NGHYETAVEPEKFNSSGTHFSNLSKTFPHCCFRSEQDRNCSICADNIEGTFVSTVSLVE 120
DB 61 NGHYETAVEPEKFNSSGTHFSNLSKTFPHCCFRSEQDRNCSICADNIEGTFVSTVSLVE 120
QY 121 QOIDANMNIOQWLKGLKLFICYBSLFKNLFRNYKYKHLVLPVELDESLVYQKGS 180
DB 121 QOIDANMNIOQWLKGLKLFICYBSLFKNLFRNYKYKHLVLPVELDESLVYQKGS 180
QY 181 FQWVHNCVSHECCBLVPPPTAKINDTLMCLKITSGGYIFQSIPLMSYQPIWVVPDP 240
DB 181 FQWVHNCVSHECCBLVPPPTAKINDTLMCLKITSGGYIFQSIPLMSYQPIWVVPDP 240
QY 241 LGLHMETDGNLKIWSMSPPLVPLQYQVKSNSSTYIRADKIVASITSLVDSILP 300
DB 241 LGLHMETDGNLKIWSMSPPLVPLQYQVKSNSSTYIRADKIVASITSLVDSILP 300
QY 301 GSSYEYQVRGKRLDGGIMSDMSTPRVFTTQDYIYPPKILTSVGSVNSFHCYKKEKNI 360
DB 301 GSSYEYQVRGKRLDGGIMSDMSTPRVFTTQDYIYPPKILTSVGSVNSFHCYKKEKNI 360
QY 361 VPSKEIYVMMNLAELIPQSOYDVAVSDHVSQVTFENLNETKPRKFTYDAYCCNEHCHH 420
DB 361 VPSKEIYVMMNLAELIPQSOYDVAVSDHVSQVTFENLNETKPRKFTYDAYCCNEHCHH 420
QY 421 RYAEIYVIDNINISCETDGYLTKMTCRMSSTTQSLAESTLQDKYHRSLSYCSIDPSIH 480
DB 421 RYAEIYVIDNINISCETDGYLTKMTCRMSSTTQSLAESTLQDKYHRSLSYCSIDPSIH 480
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRIHNSLGSLSPPCYVDPDYYVPLPP 540
DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRIHNSLGSLSPPCYVDPDYYVPLPP 540
QY 541 SSVKAEITINIGLKIISMEKPVPEENNLOFQIRYVSGKGVQKKNIEVDYAKSKSLPV 600
DB 541 SSVKAEITINIGLKIISMEKPVPEENNLOFQIRYVSGKGVQKKNIEVDYAKSKSLPV 600
QY 601 PDLCAVAVOVRCKRLDGLGYSNMSNPATVVMIDKVPARGELPKIINGDMKKREKNV 660
DB 601 PDLCAVAVOVRCKRLDGLGYSNMSNPATVVMIDKVPARGELPKIINGDMKKREKNV 660
QY 661 TLIAKPLMKNDLSQVQRYVINHTSCNGWSEDVGNHRTFTLRTQATTVVLAINSI 720
DB 661 TLIAKPLMKNDLSQVQRYVINHTSCNGWSEDVGNHRTFTLRTQATTVVLAINSI 720
QY 721 GASVANFNLTFSWPMGKVNIVOSTLSAYPLNSSCVIYSWILSPEDYKLMFPIEMKMLNED 780
DB 721 GASVANFNLTFSWPMGKVNIVOSTLSAYPLNSSCVIYSWILSPEDYKLMFPIEMKMLNED 780

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QY 781 GEIKWLRISSVKKYYIHDFPIEYQPSLYPIEMEGVKKPIINSFTODIEKHQSDA 840
DB 781 GEIKWLRISSVKKYYIHDFPIEYQPSLYPIEMEGVKKPIINSFTODIEKHQSDA 840
QY 841 GLVYIYVPISSILLGLTLLSHQMKKLFMEDVNPKNCSAOLNOKPETHLFI 900
DB 841 GLVYIYVPISSILLGLTLLSHQMKKLFMEDVNPKNCSAOLNOKPETHLFI 900
QY 901 KHTASVTCPLLEPTIEDISVDTSMKNDKEMPTVYVSLSTDLKSGVCSIDQFN 960
DB 901 KHTASVTCPLLEPTIEDISVDTSMKNDKEMPTVYVSLSTDLKSGVCSIDQFN 960
QY 961 SVNFSEAECTEYVEDESGROPFVKYATLISNSKPSETGEOGLINSVTKCFSSKNSPL 1020
DB 961 SVNFSEAECTEYVEDESGROPFVKYATLISNSKPSETGEOGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFSSMSWEIEQAFILSDQHPNLSPLTSEGLDELKLEGNFPENNDRKSIYLL 1080
DB 1021 KDSFSSMSWEIEQAFILSDQHPNLSPLTSEGLDELKLEGNFPENNDRKSIYLL 1080
QY 1081 GYTSIKRRSGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNIMLGTSKKTFAS 1140
DB 1081 GYTSIKRRSGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNIMLGTSKKTFAS 1140
QY 1141 YMFQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMFQFOTCSTQTHKIMENKMDLTV 1165

RESULT 10
US-09-137-132-4
Sequence 4, Application US/09137132
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137.132
FILING DATE: 18-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622

```

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FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-09-137-132-4

```

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Query Match 100.0%; Score 6254; DB 15; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MICQKRCVVLHMEFIYVITAFNLSTPTPRPKLSCMPNSTYVFLPAGLSKNTSNS 60
DB 1 MICQKRCVVLHMEFIYVITAFNLSTPTPRPKLSCMPNSTYVFLPAGLSKNTSNS 60
QY 61 NGHYEFAVEPKNSGTHFSNLSTKTFHCCFSSBODRNCSLCADNIECKTFSTNSLVE 120
DB 61 NGHYEFAVEPKNSGTHFSNLSTKTFHCCFSSBODRNCSLCADNIECKTFSTNSLVE 120
QY 121 QOIDANMNIOCKLKGDLKFLICYVESLFKNLFRNNYKVLHYVLEVLDSPLVPQKS 180
DB 121 QOIDANMNIOCKLKGDLKFLICYVESLFKNLFRNNYKVLHYVLEVLDSPLVPQKS 180
QY 181 FQMVHNCNVHCCBCLVVPAPKANDTLMLCKITSGVITQSLVLSYQPINMKPDP 240
DB 181 FQMVHNCNVHCCBCLVVPAPKANDTLMLCKITSGVITQSLVLSYQPINMKPDP 240
QY 241 LGLHMEITDGNLKTSSWSPPLVPLOYQVYSENSTVIREAKIYATSLVDSTLP 300
DB 241 LGLHMEITDGNLKTSSWSPPLVPLOYQVYSENSTVIREAKIYATSLVDSTLP 300
QY 301 GSSYEYQVGRKLDGPGIWSMSTPRVFTTQDVYIFPRKILTSVVSNSVFCIYKKNKI 360
DB 301 GSSYEYQVGRKLDGPGIWSMSTPRVFTTQDVYIFPRKILTSVVSNSVFCIYKKNKI 360
QY 361 VPSKEIWMNMNLAEKIPQSQDYVSDHVSQVTFPNLNETKPRGKIYDAVYCNEHECH 420
DB 361 VPSKEIWMNMNLAEKIPQSQDYVSDHVSQVTFPNLNETKPRGKIYDAVYCNEHECH 420
QY 421 RYAEIYVDVNTINISCEDGYLTKMCRWSTSTQSLAESTQLVYHRSLSLCSIPSH 480
DB 421 RYAEIYVDVNTINISCEDGYLTKMCRWSTSTQSLAESTQLVYHRSLSLCSIPSH 480
QY 481 PISEPKDCYLOSDGYECIFQPIFLSGTYMIRINHSLSGSDSPPTCVLPDSVYKPLP 540
DB 481 PISEPKDCYLOSDGYECIFQPIFLSGTYMIRINHSLSGSDSPPTCVLPDSVYKPLP 540
QY 541 SSVKAEITINIGLKTISWEKPVFPENNLOFOIRYGLSGKEVQWKVEYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLKTISWEKPVFPENNLOFOIRYGLSGKEVQWKVEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVCKRDLGIGYSNMSNPAYTVVMDIKVPMRGPPEPPIINGDTMKKENV 660
DB 601 PDLCAVYAVQVCKRDLGIGYSNMSNPAYTVVMDIKVPMRGPPEPPIINGDTMKKENV 660
QY 661 TLAMPPLKNDLSGVQRYVINHTSCNGTSESDGNHTKFFLATEQAHYTVYLAINSI 720
DB 661 TLAMPPLKNDLSGVQRYVINHTSCNGTSESDGNHTKFFLATEQAHYTVYLAINSI 720

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QY 721 GASYANNTLFSPMSKYNIVOSIAFPLANSSCYIVSMILSPSDYKIMYFIENKLNED 780
DB 721 GASYANNTLFSPMSKYNIVOSIAFPLANSSCYIVSMILSPSDYKIMYFIENKLNED 780
QY 781 GETKWLBISSVKRYTHDHFPIEKYOFSLYPIFMEGVGPKIINSTODDIEKHSDA 840
DB 781 GETKWLBISSVKRYTHDHFPIEKYOFSLYPIFMEGVGPKIINSTODDIEKHSDA 840
QY 841 GLVYIVPVIISSILLGLTLLISHQRMKLFWEDEVNPNKNSMAOGLNFOKPEFHEHFI 900
DB 841 GLVYIVPVIISSILLGLTLLISHQRMKLFWEDEVNPNKNSMAOGLNFOKPEFHEHFI 900
QY 901 KHTASVTCGILLPEPFISEDIVDTSMKNKDEMPPTVVSLLSTTDEKGSVCISDOFN 960
DB 901 KHTASVTCGILLPEPFISEDIVDTSMKNKDEMPPTVVSLLSTTDEKGSVCISDOFN 960
QY 961 SVNPSSEAGTEVYEDSOPRFKYATLINSKSPSEGEGLINSVTCFESKSNPL 1020
DB 961 SVNPSSEAGTEVYEDSOPRFKYATLINSKSPSEGEGLINSVTCFESKSNPL 1020
QY 1021 KDSFNSNSWEIEAOAFILSDQHNIISPHLTFEGELDELKLEGNPEENNDRKSIYLL 1080
DB 1021 KDSFNSNSWEIEAOAFILSDQHNIISPHLTFEGELDELKLEGNPEENNDRKSIYLL 1080
QY 1081 GYVSIKRESQVLLTDKSRVSCPPAPCLFTDVIYLODSCHSEVENNINIGTSKKTFFAS 1140
DB 1081 GYVSIKRESQVLLTDKSRVSCPPAPCLFTDVIYLODSCHSEVENNINIGTSKKTFFAS 1140
QY 1141 YMPOFOTCSOTHKIMENKMODLTV 1165
DB 1141 YMPOFOTCSOTHKIMENKMODLTV 1165

RESULT 11
US-09-950-149-4
: Sequence 4, Application US/09950149
: GENERAL INFORMATION:
: APPLICANT: Tartaglia, Louis A.
:           Tepper, Robert I.
:           Culpepper, Janice A.
:           White, David W.
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
:                   THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
:                   INCLUDING OBESITY AND CACHEXIA
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Fish & Richardson, P.C.
:   STREET: 225 Franklin Street
:   CITY: Boston
:   STATE: MA
:   COUNTRY: US
:   ZIP: 02110-2804
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Diskette
:   OPERATING SYSTEM: Windows95
:   SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/950,149
:   FILING DATE: 10-Sep-2001
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 09/069,781
:   FILING DATE: <Unknown>
:   APPLICATION NUMBER: US 08/708,123
:   FILING DATE: 03-SEP-1996
:   APPLICATION NUMBER: US 08/638,524
:   FILING DATE: 26-APR-1996
:   APPLICATION NUMBER: US 08/599,455
:   FILING DATE: 22-JAN-1996
:   APPLICATION NUMBER: US 08/583,153
:   FILING DATE: 28-DEC-1995
:   APPLICATION NUMBER: US 08/570,142
:   FILING DATE: 11-DEC-1995

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: APPLICATION NUMBER: US 08/569,485
: FILING DATE: 08-DEC-1995
: APPLICATION NUMBER: US 08/566,622
: FILING DATE: 04-DEC-1995
: APPLICATION NUMBER: US 08/562,663
: FILING DATE: 27-NOV-1995
: ATTORNEY/AGENT INFORMATION:
:   NAME: MelkeJohn, Ph.D., Anita L.
:   REGISTRATION NUMBER: 35,283
:   TELEPHONE: (617) 542-5070
:   TELEFAX: (617) 542-8906
:   TELETYPE: 200154
: INFORMATION FOR SEQ ID NO: 4:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 1165 amino acids
:     TYPE: amino acid
:     TOPOLOGY: unknown
:     MOLECULE TYPE: protein
:     FRAGMENT TYPE: internal
:     SEQUENCE DESCRIPTION: SEQ ID NO: 4:
: US-09-950-149-4

```

```

Query Match      100.0%; Score 6254; DB 23; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MICQKFCVYLLHMEFIYITAFNLSYPTTPWRFKLSCHPNNSTYDFLLPALSNTS 60
DB 1 MICQKFCVYLLHMEFIYITAFNLSYPTTPWRFKLSCHPNNSTYDFLLPALSNTS 60
QY 61 NGHYTAVEPKFNSGTFHNSLKTFFHCCFSEEDRNCSCADNIEGTFEYNSLVE 120
DB 61 NGHYTAVEPKFNSGTFHNSLKTFFHCCFSEEDRNCSCADNIEGTFEYNSLVE 120
QY 121 QOIDANNNIQCWLKGLDLKFLICYVESLFKNLEFRNRYKAVHLLYLPEVLDSPLVPQKS 180
DB 121 QOIDANNNIQCWLKGLDLKFLICYVESLFKNLEFRNRYKAVHLLYLPEVLDSPLVPQKS 180
QY 181 FOMVHCNSVHECCCLVPPVPAKINDLMLCKITTSQGVIFOSPLNSQPIINMKRPP 240
DB 181 FOMVHCNSVHECCCLVPPVPAKINDLMLCKITTSQGVIFOSPLNSQPIINMKRPP 240
QY 241 LGLHMEITDDGNLKISWSSPLVPPLOYVYSENSTVIREAKIVSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKISWSSPLVPPLOYVYSENSTVIREAKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKRLDGPGLMSDSTPRVFTQDVIYFPPKILTSVGSNVSFHCITYKENKI 360
DB 301 GSSYEVOVGRKRLDGPGLMSDSTPRVFTQDVIYFPPKILTSVGSNVSFHCITYKENKI 360
QY 361 VPSKEITVMMNIAEKIPOSQDVVSDHYSKYTFENLNKTRPGKITYDAVYCCNHECH 420
DB 361 VPSKEITVMMNIAEKIPOSQDVVSDHYSKYTFENLNKTRPGKITYDAVYCCNHECH 420
QY 421 RYAEIYVIDVININISCEDGYLTAKTCRMTSTIOSLAESTIQLRHRHSILCSDIPSI 480
DB 421 RYAEIYVIDVININISCEDGYLTAKTCRMTSTIOSLAESTIQLRHRHSILCSDIPSI 480
QY 481 PISEPKDYLQSDGFYECIFQPIFLISGYTMMIRINHSIGSLDSPICVLPDSVYKPLPP 540
DB 481 PISEPKDYLQSDGFYECIFQPIFLISGYTMMIRINHSIGSLDSPICVLPDSVYKPLPP 540
QY 541 SSVKAEITINIGLKLISWEKPYFPENNLOFOIRYGLSGEYVWKRYEYVDASKSVSLPV 600
DB 541 SSVKAEITINIGLKLISWEKPYFPENNLOFOIRYGLSGEYVWKRYEYVDASKSVSLPV 600
QY 601 PDLCAVYAVOVACKRLDGLGYSNNSNPAYTYVMDIKYPMRGPETPRIRITNGTMMKKNV 660
DB 601 PDLCAVYAVOVACKRLDGLGYSNNSNPAYTYVMDIKYPMRGPETPRIRITNGTMMKKNV 660

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QY 661 TLKMPKLNKNSLCSVQRYVYVNHHTSCNGTMSDEVGNHTKFTFLTEQAHVTVLAINSI 720
DB 661 TLKMPKLNKNSLCSVQRYVYVNHHTSCNGTMSDEVGNHTKFTFLTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSPMSKKNVIVOSLSAYPLNSCIVVSNLSPSDYKLMFYIEMKNLMD 780
DB 721 GASVANFNLTFSPMSKKNVIVOSLSAYPLNSCIVVSNLSPSDYKLMFYIEMKNLMD 780
QY 781 GEIKWLRISSSVKKYYIHDFPIEIKYQSLYPIFMEGVGKPKIINFTODDIEKHQSDA 840
DB 781 GEIKWLRISSSVKKYYIHDFPIEIKYQSLYPIFMEGVGKPKIINFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSILLTGLTLLISHQRMKLMEDVPNPKNSWAGLNFQKRETFEHLFI 900
DB 841 GLYVIVPVISSILLTGLTLLISHQRMKLMEDVPNPKNSWAGLNFQKRETFEHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDIVTSKKNDEMPPTVSVLSTTDLKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLLEPETISEDIVTSKKNDEMPPTVSVLSTTDLKSGVCSIDQFN 960
QY 961 SVNFSSEAGTEVYEDESQROPFYVATLISNKSKEPTEGEGGLINSVTCFSSKNSPL 1020
DB 961 SVNFSSEAGTEVYEDESQROPFYVATLISNKSKEPTEGEGGLINSVTCFSSKNSPL 1020
QY 1021 KDSFSNNSWEIIPAQAFLLSDQHPNIIISPHLTFSGLDELKLEGNFPEENDKKSIYYL 1080
DB 1021 KDSFSNNSWEIIPAQAFLLSDQHPNIIISPHLTFSGLDELKLEGNFPEENDKKSIYYL 1080
QY 1081 GVTSTKRESGVLLTDKRSVCPFPAPCLFTDIRVLQDSCSHFVNNINLIGSSKKTAS 1140
DB 1081 GVTSTKRESGVLLTDKRSVCPFPAPCLFTDIRVLQDSCSHFVNNINLIGSSKKTAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 12
US-08-774-414-7
Sequence 7, Application US/08774414
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: WELCHER, ANDREW A.
TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,414
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER: A-382-A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1216 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-774-414-7
Query Match 100.0%; Score 6254; DB 11; Length 1216;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQFVCVLLHMEFIYITAFNLISYPTTPMRFKLSKMPNNTYVFLPAGLSKNTSNS 60
DB 1 MICQFVCVLLHMEFIYITAFNLISYPTTPMRFKLSKMPNNTYVFLPAGLSKNTSNS 60
QY 61 NGHYETAEPKFNSSGTFHSNLKTTFHCCFRSEDRNCSLCADNLEGTFTYSTNSLVF 120
DB 61 NGHYETAEPKFNSSGTFHSNLKTTFHCCFRSEDRNCSLCADNLEGTFTYSTNSLVF 120
QY 121 OQIDANMNIQCKLKDGLKLFICYVESLFNLFRRNRYKHLLYVPEVLEDSPLVPQKGS 180
DB 121 OQIDANMNIQCKLKDGLKLFICYVESLFNLFRRNRYKHLLYVPEVLEDSPLVPQKGS 180
QY 181 FQMVHNCNSVHECCCECLVVPVPAKLNDPLMLCLKITSQGVIFQSPLSVOPINMVKPPDP 240
DB 181 FQMVHNCNSVHECCCECLVVPVPAKLNDPLMLCLKITSQGVIFQSPLSVOPINMVKPPDP 240
QY 241 LGLHMETIDGKMLKISWSSPPLVPPLOQYKYSNSTTVTREAKEYSATSLYDLSILP 300
DB 241 LGLHMETIDGKMLKISWSSPPLVPPLOQYKYSNSTTVTREAKEYSATSLYDLSILP 300
QY 301 GSSYEVQYGRKRDGPGJMSDMSPPRVFTTODVYIFEPKILTSVGSNVSFHCITYKENKI 360
DB 301 GSSYEVQYGRKRDGPGJMSDMSPPRVFTTODVYIFEPKILTSVGSNVSFHCITYKENKI 360
QY 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPGKLTJYDAVYCCNHECHH 420
DB 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPGKLTJYDAVYCCNHECHH 420
QY 421 RYAEIYVIDVNNINISCEFDGYLTAKTCRMNSTTOSLAESTLOLKHSSSLYCSIPSIH 480
DB 421 RYAEIYVIDVNNINISCEFDGYLTAKTCRMNSTTOSLAESTLOLKHSSSLYCSIPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMWIRLNHSGSLDSPPCYLPDSVYKPLPP 540
DB 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMWIRLNHSGSLDSPPCYLPDSVYKPLPP 540
QY 541 SSVKAETITINIGLAKISWEKPFYPPENNLOFOIRYGLSGKEVQWKYEVYDAKRSVSLPV 600
DB 541 SSVKAETITINIGLAKISWEKPFYPPENNLOFOIRYGLSGKEVQWKYEVYDAKRSVSLPV 600
QY 601 PDLCAVYAVQYRCKRLDGLGYWSMNSNPAYIVYMIDIKVPMRQPEFWRRIINGTMRKENV 660
DB 601 PDLCAVYAVQYRCKRLDGLGYWSMNSNPAYIVYMIDIKVPMRQPEFWRRIINGTMRKENV 660
QY 661 TLKMPKLNKNSLCSVQRYVYVNHHTSCNGTMSDEVGNHTKFTFLTEQAHVTVLAINSI 720
DB 661 TLKMPKLNKNSLCSVQRYVYVNHHTSCNGTMSDEVGNHTKFTFLTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSPMSKKNVIVOSLSAYPLNSCIVVSNLSPSDYKLMFYIEMKNLMD 780
DB 721 GASVANFNLTFSPMSKKNVIVOSLSAYPLNSCIVVSNLSPSDYKLMFYIEMKNLMD 780
QY 781 GEIKWLRISSSVKKYYIHDFPIEIKYQSLYPIFMEGVGKPKIINFTODDIEKHQSDA 840
DB 781 GEIKWLRISSSVKKYYIHDFPIEIKYQSLYPIFMEGVGKPKIINFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSILLTGLTLLISHQRMKLMEDVPNPKNSWAGLNFQKRETFEHLFI 900
DB 841 GLYVIVPVISSILLTGLTLLISHQRMKLMEDVPNPKNSWAGLNFQKRETFEHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDIVTSKKNDEMPPTVSVLSTTDLKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLLEPETISEDIVTSKKNDEMPPTVSVLSTTDLKSGVCSIDQFN 960
QY 961 SVNFSSEAGTEVYEDESQROPFYVATLISNKSKEPTEGEGGLINSVTCFSSKNSPL 1020
DB 961 SVNFSSEAGTEVYEDESQROPFYVATLISNKSKEPTEGEGGLINSVTCFSSKNSPL 1020

Db 961 SVNFSEABGTEVYDEDSOROPFVKYATLISNSKPSFTEGGLINSSVTYKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPENNDDKSIYYL 1080
Db 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPENNDDKSIYYL 1080
QY 1081 GVTISIKKRESGVLLTDKSRVSCPPAPCLFTDINVLQDSCHFEVENNINIGTSSKTFAS 1140
Db 1081 GVTISIKKRESGVLLTDKSRVSCPPAPCLFTDINVLQDSCHFEVENNINIGTSSKTFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165

RESULT 13

US-09-671-049-7
; Sequence 7, Application US/09671049
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; FLETCHER, ANDREW A.
; FLETCHER, FREDERICK A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/671,049
; FILING DATE: 27-Sep-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,414
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382-A
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1216 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-671-049-7

Query Match 100.0%; Score 6254; DB 20; Length 1216;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVLLHMEFIYITAFNLSYPTPWRFKLSKMPNSTYDFLLPAGLSKNTSNS 60
Db 1 MICQFCVLLHMEFIYITAFNLSYPTPWRFKLSKMPNSTYDFLLPAGLSKNTSNS 60
QY 61 NGHETAVEEPFNSSGTHFSLSTTFHCRCRSDRNCSCADNIEKTFVSYNSLVF 120
Db 61 NGHETAVEEPFNSSGTHFSLSTTFHCRCRSDRNCSCADNIEKTFVSYNSLVF 120
QY 121 QQIDANNIQCWLKGLDLFLICYVESLFLKNLFRNRYKVHLLYVLEVLDPSPVPOKGS 180
Db 121 QQIDANNIQCWLKGLDLFLICYVESLFLKNLFRNRYKVHLLYVLEVLDPSPVPOKGS 180

QY 181 FOMVHCNSVHECCCELVVPPTAKINDTLMLCKLTSGGVIFQSLPLMSVQPIINMKPDP 240
Db 181 FOMVHCNSVHECCCELVVPPTAKINDTLMLCKLTSGGVIFQSLPLMSVQPIINMKPDP 240
QY 241 LGINHEITDDGTLKISWSSPLVPPFLQYQVYSENSTTVIEAKIYSATSLVDSILP 300
Db 241 LGINHEITDDGTLKISWSSPLVPPFLQYQVYSENSTTVIEAKIYSATSLVDSILP 300
QY 301 GSSYEVQYRGKRLDPGILMSDSTPRVFTQDVIYFPPKILTSVGSNVSFHCITYKENKI 360
Db 301 GSSYEVQYRGKRLDPGILMSDSTPRVFTQDVIYFPPKILTSVGSNVSFHCITYKENKI 360
QY 361 VPSKEIYVMMNIAEKIPOSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
Db 361 VPSKEIYVMMNIAEKIPOSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
QY 421 RFAELVYDVNINISCEFDGYLTAKMTCRSTQSIASESTOLVHRSLSKCSPIPSH 480
Db 421 RFAELVYDVNINISCEFDGYLTAKMTCRSTQSIASESTOLVHRSLSKCSPIPSH 480
QY 481 PISEPKDCYLOSDGFYECCIFQPIFPLSGYTMIRINHSLSGSDSPCYLPDPSVYKPLPP 540
Db 481 PISEPKDCYLOSDGFYECCIFQPIFPLSGYTMIRINHSLSGSDSPCYLPDPSVYKPLPP 540
QY 541 SSVKAEITINIGLKIISWEKVPFENNLOFQIRYGLSGKEVQWAKTEVYDAKSYSVLPV 600
Db 541 SSVKAEITINIGLKIISWEKVPFENNLOFQIRYGLSGKEVQWAKTEVYDAKSYSVLPV 600
QY 601 PDLCAVYAVOVCKRDLGIGYWSNNSPAYTVYMDIKVMBRPFMRIRINGTMRKEKV 660
Db 601 PDLCAVYAVOVCKRDLGIGYWSNNSPAYTVYMDIKVMBRPFMRIRINGTMRKEKV 660
QY 661 TLLMKPLKNDLSGVQRYVINHHTSCNGTSEDVGNHRTFELTEQAHVTVLAINSI 720
Db 661 TLLMKPLKNDLSGVQRYVINHHTSCNGTSEDVGNHRTFELTEQAHVTVLAINSI 720
QY 721 GASVANFNLTSPWMSKKNIVOSLSAYPLNSSCVIYSWILSPDYKIMYFIEMKNLND 780
Db 721 GASVANFNLTSPWMSKKNIVOSLSAYPLNSSCVIYSWILSPDYKIMYFIEMKNLND 780
QY 781 GEIKMLRITSSSVKYYIHDFPIEKYQSLPIFMEGVGKRIINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRITSSSVKYYIHDFPIEKYQSLPIFMEGVGKRIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSSILGLTILSHQRMKRIFWEDVNPKNCSMAQGLNFKETPEHLP 900
Db 841 GLYVIVPVISSSILGLTILSHQRMKRIFWEDVNPKNCSMAQGLNFKETPEHLP 900
QY 901 KHTASVTCGPLLEPETSIEDISVDTSMKNKDEMPFTYVSLSTLDEKGSVCISDPN 960
Db 901 KHTASVTCGPLLEPETSIEDISVDTSMKNKDEMPFTYVSLSTLDEKGSVCISDPN 960
QY 961 SVNFSEABGTEVYDEDSOROPFVKYATLISNSKPSFTEGGLINSSVTYKCFSSKNSPL 1020
Db 961 SVNFSEABGTEVYDEDSOROPFVKYATLISNSKPSFTEGGLINSSVTYKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPENNDDKSIYYL 1080
Db 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPENNDDKSIYYL 1080
QY 1081 GVTISIKKRESGVLLTDKSRVSCPPAPCLFTDINVLQDSCHFEVENNINIGTSSKTFAS 1140
Db 1081 GVTISIKKRESGVLLTDKSRVSCPPAPCLFTDINVLQDSCHFEVENNINIGTSSKTFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165

RESULT 14

US-09-948-933-284
; Sequence 284, Application US/09948933
; GENERAL INFORMATION:

```

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; FILE REFERENCE: C1000787
; CURRENT APPLICATION NUMBER: US/09/948, 933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Human
US-09-948-933-284

```

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Query Match      99.9%; Score 6247; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MICQKFCVLLHMERIYITAFNLSTPTPMPFKLSCMPNSTYDFLLPAGLSKNTS 60
Db 3 MICQKFCVLLHMERIYITAFNLSTPTPMPFKLSCMPNSTYDFLLPAGLSKNTS 62
Qy 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCFSRSEDORNSCLADNIEGTFSTVNSLVE 120
Db 63 NGHYETAEPKFNSSGTHFSNLSTKTFHCFSRSEDORNSCLADNIEGTFSTVNSLVE 122
Qy 121 QOIDANMNIQCKLKDGLKLFICYVESLFKNLFERNYKXVHLLYLPEVLEDSPLVPQKS 180
Db 123 QOIDANMNIQCKLKDGLKLFICYVESLFKNLFERNYKXVHLLYLPEVLEDSPLVPQKS 182
Qy 181 FOMVHCNCSVHECCCLVLPVPTAKLNDTLMLCKITSGVIRFQSPPLMSVQPINMKPDP 240
Db 183 FOMVHCNCSVHECCCLVLPVPTAKLNDTLMLCKITSGVIRFQSPPLMSVQPINMKPDP 242
Qy 241 LGLHMEITDDGKLIKISWSSPLVPPLOYQVYKSENSSTVIREADKIYATSLLVDSILP 300
Db 243 LGLHMEITDDGKLIKISWSSPLVPPLOYQVYKSENSSTVIREADKIYATSLLVDSILP 302
Qy 301 GSSYVQVGRKRLDGPJMSMSSTPRVFTQOVITYFPKILTSVGSNNSFHCIYKKEKI 360
Db 303 GSSYVQVGRKRLDGPJMSMSSTPRVFTQOVITYFPKILTSVGSNNSFHCIYKKEKI 362
Qy 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSKEYFFNLNETKPRGKFTYDAVYCCNHECHH 420
Db 363 VPSKEIYVMMNLAEKIPQSOYDVSDHVSKEYFFNLNETKPRGKFTYDAVYCCNHECHH 422
Qy 421 RYAEIYVDVININISCEFDGYLTAKTCRWSTSTIOSLAESTYQLRYHNSSLYCSIPSIH 480
Db 423 RYAEIYVDVININISCEFDGYLTAKTCRWSTSTIOSLAESTYQLRYHNSSLYCSIPSIH 482
Qy 481 PISEPKDCYLOSDFYECIFQPIFLSGYTMIRINHSIGSDSPPTCLPDSVAKPLRP 540
Db 483 PISEPKDCYLOSDFYECIFQPIFLSGYTMIRINHSIGSDSPPTCLPDSVAKPLRP 542
Qy 541 SSVKAEITINIGLTKISWEKPYFPENNLOFOIRYGLSGEYQMKMYEYVDAKSVSILPV 600
Db 543 SSVKAEITINIGLTKISWEKPYFPENNLOFOIRYGLSGEYQMKMYEYVDAKSVSILPV 602
Qy 601 PDLCAVYAVOVRCKRLDGLIGTWSNNSNPAYTVVMDIKVPMRGPPEFRIRIINGDTMKKENY 660
Db 603 PDLCAVYAVOVRCKRLDGLIGTWSNNSNPAYTVVMDIKVPMRGPPEFRIRIINGDTMKKENY 662
Qy 661 TLLMPELMMKNISCSVOXRVYINHHSTSCNGTWSBDYGNHTKFTFLTEQAHYTVYLAINSI 720
Db 663 TLLMPELMMKNISCSVOXRVYINHHSTSCNGTWSBDYGNHTKFTFLTEQAHYTVYLAINSI 722
Qy 721 GASVANFNLTSWPMKSNIVIOSLSAYPLNNSCVIVSWILSPSDKLMFYIEMKNLMD 780
Db 723 GASVANFNLTSWPMKSNIVIOSLSAYPLNNSCVIVSWILSPSDKLMFYIEMKNLMD 782

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Qy 781 GEIKMLRISSSVKKYIYHDFPIEKYQSLPIFMEGKPKIINSFTQODIEKHQSDA 840
Db 783 GEIKMLRISSSVKKYIYHDFPIEKYQSLPIFMEGKPKIINSFTQODIEKHQSDA 842
Qy 841 GLYIVPVYISSLILGLTLLISHQAMKLEEDVDPNPKNSAQLNOKQETPEPHLEI 900
Db 843 GLYIVPVYISSLILGLTLLISHQAMKLEEDVDPNPKNSAQLNOKQETPEPHLEI 902
Qy 901 KHTASTGCPILLEPETSIEDISVPTSMKNKDEMPPTVYSLSTDLCKGVCISDQPN 960
Db 903 KHTASTGCPILLEPETSIEDISVPTSMKNKDEMPPTVYSLSTDLCKGVCISDQPN 962
Qy 961 SYNFSAEGETEYTEDESQROPFVYKATLISNKSKEETGEQGLINSVYTKCFSSKNPL 1020
Db 963 SYNFSAEGETEYTEDESQROPFVYKATLISNKSKEETGEQGLINSVYTKCFSSKNPL 1022
Qy 1021 KDSFNSSWIEIAQAFILSDQHPNISPHTFSEGLDELKLEINFPENNDRKSIYLL 1080
Db 1023 KDSFNSSWIEIAQAFILSDQHPNISPHTFSEGLDELKLEINFPENNDRKSIYLL 1082
Qy 1081 GVTSIKRESGVLLDCKSVSCFPAPCLFTDIRVLDSCSHFVNNIMAGTSKKTFFAS 1140
Db 1083 GVTSIKRESGVLLDCKSVSCFPAPCLFTDIRVLDSCSHFVNNIMAGTSKKTFFAS 1142
Qy 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1143 YMPQFOTCSTQTHKIMENKMDLTV 1167

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RESULT 15

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US-09-948-947-87
; Sequence 87, Application US/09948947
; GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; FILE REFERENCE: C1000786
; CURRENT APPLICATION NUMBER: US/09/948, 947
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Human
US-09-948-947-87

```

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Query Match      99.9%; Score 6247; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MICQKFCVLLHMERIYITAFNLSTPTPMPFKLSCMPNSTYDFLLPAGLSKNTS 60
Db 3 MICQKFCVLLHMERIYITAFNLSTPTPMPFKLSCMPNSTYDFLLPAGLSKNTS 62
Qy 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCFSRSEDORNSCLADNIEGTFSTVNSLVE 120
Db 63 NGHYETAEPKFNSSGTHFSNLSTKTFHCFSRSEDORNSCLADNIEGTFSTVNSLVE 122
Qy 121 QOIDANMNIQCKLKDGLKLFICYVESLFKNLFERNYKXVHLLYLPEVLEDSPLVPQKS 180
Db 123 QOIDANMNIQCKLKDGLKLFICYVESLFKNLFERNYKXVHLLYLPEVLEDSPLVPQKS 182
Qy 181 FOMVHCNCSVHECCCLVLPVPTAKLNDTLMLCKITSGVIRFQSPPLMSVQPINMKPDP 240
Db 183 FOMVHCNCSVHECCCLVLPVPTAKLNDTLMLCKITSGVIRFQSPPLMSVQPINMKPDP 242
Qy 241 LGLHMEITDDGKLIKISWSSPLVPPLOYQVYKSENSSTVIREADKIYATSLLVDSILP 300

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Db 243 LGLHMEITDDGNLKIWSWSSPLVPPLOVQVYSENSTVIREADK IVSATSLLVDSILP 302
QY 301 GSSYEVOYRGRLDGPJMSDMSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
Db 303 GSSYEVOYRGRLDGPJMSDMSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 362
QY 361 VPSKEIYVMMMLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYVMMMLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVADVNIINISCEFDGYLTKMTCRWSSTIOSLAESTLOLRHRSLSLXCDIPSIH 480
Db 423 RYAEIYVADVNIINISCEFDGYLTKMTCRWSSTIOSLAESTLOLRHRSLSLXCDIPSIH 482
QY 481 PISEBKDCYLOSDFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCYLPDSVYKPLRP 540
Db 483 PISEBKDCYLOSDFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCYLPDSVYKPLRP 542
QY 541 SSVKAEITINIGLKIISWEKEVPFENNLOFOIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLKIISWEKEVPFENNLOFOIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 602
QY 601 PDLCAVYAVOYRCRKLDELGYWMSNPNATYVMDIKYPMRGPEFRITNGDTMKREKNV 660
Db 603 PDLCAVYAVOYRCRKLDELGYWMSNPNATYVMDIKYPMRGPEFRITNGDTMKREKNV 662
QY 661 TLLMKPLKNDSLCSVQRYVINHTSCNGTWSDEDVGNHTKFTFLTEQAHVTVLAINSI 720
Db 663 TLLMKPLKNDSLCSVQRYVINHTSCNGTWSDEDVGNHTKFTFLTEQAHVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKSVNIQVSLASVPLNSSCVIWSLTSIDYKLMYFIEMKNLNE 780
Db 723 GASVANFNLTFSWPMKSVNIQVSLASVPLNSSCVIWSLTSIDYKLMYFIEMKNLNE 782
QY 781 GEIKMLRISSSVKKYIINDHFPIEIKYQPSLYPRIMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKMLRISSSVKKYIINDHFPIEIKYQPSLYPRIMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYVIVPVIISILLTLLSHORMKLEFEDVNPKNCSMAOGLNFOKPEFELFI 900
Db 843 GLYVIVPVIISILLTLLSHORMKLEFEDVNPKNCSMAOGLNFOKPEFELFI 902
QY 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 960
Db 903 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 962
QY 961 SVNFESEAGTEYTYDESOQROPFVYATLINSKSPSETEGEOGLINSSYTKCFSSKNSPL 1020
Db 963 SVNFESEAGTEYTYDESOQROPFVYATLINSKSPSETEGEOGLINSSYTKCFSSKNSPL 1022
QY 1021 KDSFNSSSWEIQAQAFILISDQHPNISPHLTFSEGLDELKLEGNFPEENNDKKSIIYL 1080
Db 1023 KDSFNSSSWEIQAQAFILISDQHPNISPHLTFSEGLDELKLEGNFPEENNDKKSIIYL 1082
QY 1081 GVTSLKKRESGYLLTDKRSVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1083 GVTSLKKRESGYLLTDKRSVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1142
QY 1141 YMPQOTCSTQTHKIMENKMDLTV 1165
Db 1143 YMPQOTCSTQTHKIMENKMDLTV 1167

Search completed: May 18, 2002, 06:59:12
Job time: 680 sec

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Db      504 EWMAEAMALGAVTSDHINFDVYKVKNDPNNLS--VINSEELSLIKLWTPNSIKS 560
      562 -VEFNNFOQIRYGLSGKEVQMKMYEYDAKSKSVSLPVPDL--CAVYAVOVCKRLDQ 618
      561 VILIKYNIQYRKQKQST-----WSQIPREDASTSSFTVODLAKFTEYVFIRCKMEQG 615
      619 LGYWSMSPATVYVMDIKVPARGPEFRIRINGDTMKREKNVTLMLKPLMKNDLSQVOR 678
      616 KGYWDMSEASGLTYEDR-PSKAPSFMYKIDPSHOGYRTVOLWKTLPPEANGKILD 674
      679 YVINHTSCNGWSEDVGNH-----TKFTFLWTEQAHVTVLAINSIGASVANFNLFPSNP 734
      675 YEVT-----LFRKSHLQNTYVNAKTLVNLNDRYLATLVRLNVLGSDAVALTIPAD 729
      735 MSKVINIYOSLAVPLNNSCVIYMWILSPDYKLMYFIEMKNLNDEGE--IKMLRISSSV 792
      730 FOATHPVMDLAKFP-KDMLMAYEWMTTPRESVY--KYILEMCLSDKACITDMOEDGIV 786
      793 KKYIYHDFPIEYKQSLYPIEMEGVKPKIINSFTODDIEKHOSDAGLYVIVPIIIS 852
      787 HRTYLRGNLAESKCYLITVTVPYADGPGSPESIKAY-----LKOAPPSKG-----PTV--- 834
      853 SILLIGTLLISHQBMK-----LFMEDVPRKNCMAOGLN-FQKP-----ETFEHLFI 900
      835 -----RTKKYKKNBAVLEMDOLPYDVONGFIRNTTYIRITIGETAVNDS 881
      901 KHT-----ASVTCGPLLEPETISEDISVTSWKNKDEMPATVVSLLSTDEKS--- 952
      882 SHTEVTLSSLSIDLTM-----VRMAAYTDEGKDGPEFTFT--PKFAGELIESGDKTH 935
      935 ---VCISQF-----NSVNFSEAGTEVTEDESQROPYKIVATLI----- 990
      936 TCPPAPABELLGGPSVFLPPKPKDTLMSRPEVTCVAVVDVSHDEPEKFMVYDGEV 995
      991 -SNSKPE-----TGEQGLINSVTKCFSSKY---SPLKDSFNSNSWEIE 1032
      996 HNAKTKPEEOYNSTYRVAVSVLTJLHOMLNKEYCKVSKALDAPLEKTISSAKGQPR 1055
      1033 AQAFFILSDQHNIISPHLTFSS--EGL--DELLKLEGNFPEENN-----DKSIY 1078
      1056 EPOVATLPPSRDELTKNOVSLCLVKGFPYSDIAVEMESNGPENNYTTPPVLDSDGSF 1115
      1079 YLGVTISIKRESGVLLTDKSR-----VSCPPAPCLFTDIRVLQDSC-SHEVENNINL 1130
      1116 FL-----YSKLTVDKSRMOQGNVFSK-----SYMHEALHNHTQKSLSI 1154

RESULT 2
US-09-935-868-24
: Sequence 24, Application US/09935868
: GENERAL INFORMATION:
: APPLICANT: Regeneron Pharmaceuticals, Inc
: TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
: FILE REFERENCE: REG 203D
: CURRENT APPLICATION NUMBER: US/09/935, 868
: PRIOR FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: PCT/US99/22045
: PRIOR FILING DATE: 1999-09-22
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 24
: LENGTH: 1168
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-935-868-24

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Query Match 6.0%; Score 376; DB 5; Length 1168;
 Best Local Similarity 19.6%; Pred. No. 4,76-18;
 Matches 213; Conservative 177; Mismatches 445; Indels 254; Gaps 51;

QY 196 CLYPPVPAKLNDELTL-MCLKITSQGVIFQSPLSMVQPINMKYKPDPLGLHMEIT--DDGN 252

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Db      176 COLAYPEGDSSEFYIVSMCAVSSGSKF--SKYTQTOGCGILQDPPANTTVAAVAPNPM 233
      253 LKISWSSPP-----LVFPLOYOYKYSENST--VIREADKIVASATSLVOSILPGSSY 304
      234 LSVTQODPHSNMSSRYRLRFLRYAREKSKITFTTMVKRDLQ-----HCYIHDAWSGLRH 288
      305 EVQVGRKRLDQPGIWSDMSTPRVFTTODVYFPP-----KILTSVG 345
      289 VYOLBAQEEFGGGESEMSPEAMGTPTWESRSPAPAEVNEVSTPMTGAPSAQLELLDPCG 348
      346 -----SNVSFHCITYK--ENKIYPSKEIYMMNLALEKIPQOQYVYVSDHYVK 390
      349 YISPSPPVQLHNSPTACVLEKCKMDFFHVANAYVMKTN-HFTIPKQYITINRTAS 407
      391 VTFPNLNETPRKGFYTDVAYCCNEHECHRRYAEIVDY-----NINIS-ETDGY 441
      408 VTFETL-----ASLNQLCNILITFQQLDQNYGIIITISGLPREKKNLSCLYNEG- 458
      442 LTKMTCRMSTSTIOSLAESTLOLRHYRSSLYCSDPSIHPISEPKDCYLOSQGEFCT-- 499
      459 -KMKRCMDGG-----RETHLETNFTLKEEMAT-----HKFA--DCKAKRDTPTSCYVD 504
      500 PQPIILLSGYTMWIRINHSLSLSDSPPTCVLPDSYKPLPSPSVKAEITIN----IGLKK 555
      505 YSTVFVN-IEVWAEAMALGAVTSDHINFDVYKVKNDPNNLS--VINSEELSLIK 560
      556 ISMERP-----VEFNNFOQIRYGLSGKEVQMKMYEYDAKSKSVSLPVPDL--CAVYA 608
      561 LWTNPSTIKSVIILKYNIOYRKQKST-----WSQIPREDASTSSFTVODLAKFTEYV 615
      609 VOYCKRLDGLCYWSMSPATVYVMDIKVPARGPEFRIRINGDTMKREKNVTLMLKPLM 668
      616 FPIRCKMEKEDGQWDMSEASGLTYEDR-PSKAPSFMYKIDPSHOGYRTVOLWKTLP 674
      669 KNDISCSQORYIINHTSCNGWSEDVGNH-----TKFTFLWTEQAHVTVLAINSIGASV 724
      675 PREANGKILDEVT-----LFRKSHLQNTYVNAKTLVNLNDRYLATLVRLNVLGKSD 729
      725 ANFNLTFSWPMKVINIYOSLAVPLNNSCVIYMWILSPDYKLMYFIEMKNLNDEGE-- 782
      730 AAVLTIIPADQFATHPVMDLAKFP-KDMLMAYEWMTTPRESVY--KYILEMCLSDKAPCI 786
      783 IKMLRISSSVKKYIYHDFPIEYKQSLYPIEMEGVKPKIINSFTODDIEKHOSDAGL 842
      787 TDMOEDGTVHRTYLRGNLAESKCYLITVTVPYADGPGSPESIKAY-----LKOAPPSKG- 841
      843 YVIVPVIISSILLIGTLLISHQBMK-----LFMEDVPRKNCMAOGLN-FQKP-- 892
      842 -----PTV-----RTKKYKKNBAVLEMDOLPYDVONGFIRNTTYIRITII 881
      893 --ETFEHLFIKHT-----ASVTCGPLLEPETISEDISVTSWKNKDEMPATVVSLLSTT 946
      882 GNETAVNVDSSHTVETLSSLSIDLTM-----VRMAAYTDEGKDGPEFTFT--PKFAG 935
      947 DLEKS-----VCISQF-----NSVNFSEAGTEVTEDESQROPYK 985
      936 EIESGDKTHTCPPAPABELLGGPSVFLPPKPKDTLMSRPEVTCVAVVDVSHDEPEVK 995
      986 YATLI-----SNSKPE-----TGEQGLINSVTKCFSSKN---SPLKD 1022
      996 FMVYDGEVHNAKTKPREEOYNSTYRVAVSVLTJLHOMLNKEYCKVSKNALDAPLEK 1055
      1023 SFSNSWEIEAQAFFILSDQHNIISPHLTFSS--EGL--DELLKLEGNFPEENN----- 1072
      1056 TISKAKGQPREQVYTLTPPSRDELTKNOVSLCLVKGFPYSDIAVEMESNGPENNYKTT 1115
      1073 ---DKSIYIYLGVTISIKRESGVLLTDKSR-----VSCPPAPCLFTDIRVLQDSC-S 1121
      1116 PVLVDSDGSFLL-----YSKLTVDKSRMOQGNVFSK-----SYMHEALHN 1155
      1122 HEVENNINL 1130
      : : : : :

```

Db 1156 HYOKSLSL 1164

RESULT 3
US-09-853-180-4
Sequence 4, Application US/09853180
GENERAL INFORMATION:
APPLICANT: Chirica, Madeline
APPLICANT: Parham, Christl L.
APPLICANT: Kastelein, Robert A.
APPLICANT: Moore, Kevin W.
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
FILE REFERENCE: DX01074
CURRENT APPLICATION NUMBER: US/09/853,180
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,426
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 918
TYPE: PRF
ORGANISM: Homo sapiens
US-09-853-180-4

Query Match 5.5%; Score 345.5; DB 5; Length 918;
Best Local Similarity 19.8%; Pred. No. 4,4e-16;
Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;

QY 337 PPKILTSVGSNVSFHCYK--ENKIVPSKEIYMMNLAKEIPQSYDVVSDHVSQVTF 393
Db 33 PESPVOVQHSNFTAVCYLKEKCMDFHVNANAYIWKTN-HFTIPKEQYTIINRTASSVTF 91
QY 394 FNLNETPRGKFTDAYAVCCNEHCNHRVLAELYIDV-----NINISC-ETDGYLTK 444
Db 92 TDI-----ASLNIQLTCNLTILFGOLEQNVYGIITISGLPPEKPKMLSCIVNKG--KK 141
QY 445 MTCRMSTIQLASTIQLRHRSSLYCSDIPSIHPISSEPCDCLSDGFECEI--FQP 502
Db 142 MRCMDG-----RETHLETNFTLKEWAT-----HKFA--DCKAKRDTPTSCIVDYST 188
QY 503 IFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPPSSVKAETTN----IGLLKISW 558
Db 189 YVFVN-IEVWAEANALGKVTSDHINFDPVYKVPKPNPHNLS---VINSELSILKLTW 244
QY 559 EKP-----VPPENNIQFOIRGLSGKEVQWKYEVYDAKSKSVLPVDL--CAVYANOV 611
Db 245 TNPISIKSVIILKYNIOYRTKDAST-----WSQIPEDTASTRSSFTYODLKPFTEYVERI 299
QY 612 RCKRLDGLGYMSNNSNPAYTVMDIKVPMRGPEFMRILNGDTMKKEKNVTLMKPLMKND 671
Db 300 RCMKEDGKGYMSDSEASGITYEDR-PSKAPSPMYKIDPSHTQGYRVOVLWKTLPPPE 358
QY 672 SLCSVQIRVINHTSCNGTWSDEVGNH---TKFTFLMTEQAHVTYLAINSIGASVANF 727
Db 359 ANGKILDEYV-----LTRMKSHLQNTYVNAKTLVNLFTNDRYATLTVRLNLYGSDAAV 413
QY 728 NLTRSWPMKSNIVQSLSAVPLNSSCVIYVSWILSPSDYKLMYFIIEKNLNEDGE--IKW 785
Db 414 LTIAPACFOATHPMDLKAFP-KDNMLMVEWTTTPRESYK--KYILEWCVLSDKACPIDTW 470
QY 786 LRISSVKYYIHDHFIPIEKYQFSLYPIEMEGYKPKII-----NSFTODIEKHSDAGLY- 825
Db 471 QOEDGTVHRTYLRGNLAESKCYLITVTPYVADGSPESIAAYLKQAPSPGPIVRYTKV 530
QY 826 -----NSFTODIEKHSDAGLY- 843
Db 531 GKNEAVLEMDQLPYDVONGEIRNYTIFRYTLIGNETAVNVSHTYEYLSLTSDT-LYM 589
QY 844 -----VIYVYIISSI-LLIGLLLSHOR--MKK 869
Db 590 VRMAAYTDEGKGDPEFTTTPPKAOGIEAIVAVPCIAFLITLILGLVLCFCKNRKDLIK 649

QY 870 LFWEDEVNPKNCNMAOGINPQKPFTEHFLIKHTASVTCGPLLEPETISEDIVSTSMK 929
Db 650 HWPVNDPSPKSHLAQWSPHPP-----RH-----NFN 677
QY 930 NKDEMPPTVVLSTLDLEKGSVCISDQNSVNSFEAGTEVYEDESQKPF---VKY 986
Db 678 SKDOM-----YSDGNETDVSVEIEAND--KKPFPEDLKS 710
QY 987 ATLISNKPSETGEGGLINSVYKCPSSKSNPLKDSFNS 1028
Db 711 LDLFKEKINTEGHSSGIGSS---CMSSSRPSISSDENE 749

RESULT 4
US-09-935-868-7
Sequence 7, Application US/09935868
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 859
TYPE: PRF
ORGANISM: Homo sapiens
US-09-935-868-7

Query Match 4.9%; Score 309.5; DB 5; Length 859;
Best Local Similarity 19.6%; Pred. No. 1.3e-13;
Matches 178; Conservative 145; Mismatches 378; Indels 209; Gaps 42;

QY 337 PPKILTSVGSNVSFHCYK--ENKIVPSKEIYMMNLAKEIPQSYDVVSDHVSQVTF 393
Db 33 PESPVOVQHSNFTAVCYLKEKCMDFHVNANAYIWKTN-HFTIPKEQYTIINRTASSVTF 91
QY 394 FNLNETPRGKFTDAYAVCCNEHCNHRVLAELYIDV-----NINISC-ETDGYLTK 444
Db 92 TDI-----ASLNIQLTCNLTILFGOLEQNVYGIITISGLPPEKPKMLSCIVNKG--KK 141
QY 445 MTCRMSTIQLASTIQLRHRSSLYCSDIPSIHPISSEPCDCLSDGFECEI--FQP 502
Db 142 MRCMDG-----RETHLETNFTLKEWAT-----HKFA--DCKAKRDTPTSCIVDYST 188
QY 503 IFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPPSSVKAETTN----IGLLKISW 558
Db 189 YVFVN-IEVWAEANALGKVTSDHINFDPVYKVPKPNPHNLS---VINSELSILKLTW 244
QY 559 EKP-----VPPENNIQFOIRGLSGKEVQWKYEVYDAKSKSVLPVDL--CAVYANOV 611
Db 245 TNPISIKSVIILKYNIOYRTKDAST-----WSQIPEDTASTRSSFTYODLKPFTEYVERI 299
QY 612 RCKRLDGLGYMSNNSNPAYTVMDIKVPMRGPEFMRILNGDTMKKEKNVTLMKPLMKND 671
Db 300 RCMKEDGKGYMSDSEASGITYEDR-PSKAPSPMYKIDPSHTQGYRVOVLWKTLPPPE 358
QY 672 SLCSVQIRVINHTSCNGTWSDEVGNH---TKFTFLMTEQAHVTYLAINSIGASVANF 727
Db 359 ANGKILDEYV-----LTRMKSHLQNTYVNAKTLVNLFTNDRYATLTVRLNLYGSDAAV 413
QY 728 NLTRSWPMKSNIVQSLSAVPLNSSCVIYVSWILSPSDYKLMYFIIEKNLNEDGE--IKW 785
Db 414 LTIAPACFOATHPMDLKAFP-KDNMLMVEWTTTPRESYK--KYILEWCVLSDKACPIDTW 470
QY 786 LRISSVKYYIHDHFIPIEKYQFSLYPIEMEGYKPKIINSFODJIEKHSDAGLYI 845
Db 471 QOEDGTVHRTYLRGNLAESKCYLITVTPYVADGSPESIAAY---LKQAPSPKG--- 522

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QY 846 PVIISSSILLGLTLLISHORMK-----LMEVDENPNKMSAOGLN-FQK-----E 893
Db 523 -PTV-----RTKKYKKEANVLEMDQLEVDVYONGFIRNYTTFYRIITNE 565
QY 894 TFEHLFIKHT--ASVTCGPLLEPETISBIDSVTSMKNKDEMPYTVSLSTDBLE 949
Db 566 TAVNVDSHTEYTLISLSDTLYM---VRMAAYHDEGKGOPETFTT--PKFQGELE 619
QY 950 KGSVCISIOF-----NSVNSEAEETEVYTEDESOROPV 984
Db 620 SGEPRKSCDKHTCPRCAPABELLGGPSVELFPKKPADTLMISTREVTVVVDVSHEDEV 679
QY 985 KYATLI-----SNKSPSE-----TGEEOGLINSVYTKFSSKN---SPLK 1021
Db 660 KFNMTVDGEVYNMAATKREDEOYNSTYVVSYLVLHODMLNGKTYCKKVSXKALPAPE 739
QY 1022 DSFNSSSWEIEAOAFFLISDHPNIIISPLTFS---EGL--DELLKEGNEPREEN-- 1072
Db 740 KTISAKQKPREPOVYTLPRSRDELTKNQVSLTCLVKFKFYSFDIADVENESNGQPRENNKT 799
QY 1073 -----DKSIIYLGVTSLKKREGVLLTDKSR-----VSCPFPARCLFTDIRVLQDSC- 1120
Db 800 TPVVLDSGSGFFL-----YSKLTVDKSRMOOGINFFSC-----SVXHEALH 839
QY 1121 SHFEVNNINL 1130
Db 840 NHYTOKSLSL 849

```

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: RESULT 5
: US-09-935-868-9
: Sequence 9, Application US/0935868
: GENERAL INFORMATION:
: APPLICANT: Regeneron Pharmaceuticals, Inc
: TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
: FILE REFERENCE: REG 203D
: CURRENT APPLICATION NUMBER: US/09/935,868
: PRIOR APPLICATION NUMBER: 2002-04-11
: PRIOR FILING DATE: 1999-09-22
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 9
: LENGTH: 951
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-935-868-9

```

```

Query Match 4.9% Score 308.5 DB 5 Length 951:
  . Beat Local Similarity 22.4% Pred. No. 1.7e-13:
  Matches 117: Conservative 92: Mismatches 24: Indels 73: Gaps 22:

QY 337 PKILTVGSVSNVSPFCIVKK---ENKIYPSKEITVMNMLAEKIPQSOYVVSQSHVKNF 393
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 33 PESPVYQLHSNFTAVCAVLCCKMDYFHYVANTIVKTN-HFTLPKQYITINFTASSVTF 91
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 394 ENLNETPKRGKRTYDAVYCCNEHCCHRYAEYLVIDY-----NINIS-ETDGYLTK 444
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 92 TDI-----ASLIQIOLTCNLITFGGLEQNYGIIITISGLPPEKRNKLSCLVNEG--KK 141
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 445 MTCANSTSTIOSLAESTQLRLYHRSLSVCSIDIPSHIPSEPKCYLQSDGYECT--FQP 502
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 MRCEWDGG---RETHLETNFTLSEKMAT-----HKFA--DCKAKRDTPTSCVLDYST 188
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 503 IFLLSGYIMMIRINISLSDSPPTCVLPDSVYKCLDPSSVAAEITIN---IGLIKISM 558
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 VYFVN-IEVWVEAEALAKVTSDHINPDPVYVKKPNPNNLS--VINSEELSLIKLTW 244
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 559 EKP-----VFPENNIOQPIRLGLSKREYQWKMYEYDAKSKSVSLPVDL--CAVYANOV 611
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 TNPSIKSVIILKNIQYTRKDAST-----WSQIIPEDTASTRSSFTYDOLKFTTEVEFPI 299
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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[illegible]

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RESULT 6
US-09-853-180-5
: Sequence 5, Application US/09853180
: GENERAL INFORMATION:
: APPLICANT: Chirica, Madaline
: APPLICANT: Parham, Christi L.
: APPLICANT: Kastelein, Robert A.
: APPLICANT: Moore, Kevin W.
: TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods
: FILE REFERENCE: DX01074
: CURRENT APPLICATION NUMBER: US/09/853,180
: CURRENT FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: 60/203,426
: PRIOR FILING DATE: 2000-05-10
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 862
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-853-180-5

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	Query Match	Similarity	3.5%; Score 220.5; DB 5; length 862;
	BEST Local	Similarity	19.8%; Pred. No. 2e-07;
	Matches	182; Conservative	129; Mismatches 322; Indels 265; Gaps 49.
Dy	332	DVYIEPKILTSVGNSVFHCI-----YKKNKIIVPSKEIWMNMNLAEKIFQSQYD	382
	: : :	: : :	: : :
Dd	32	DVTAKPASHVL-TGSTVNITCSLKPRQGCFHRSRRNKLTLYK-----FD	74
Oy	363	-VVSSH-----VSRTFFNLNETKRGRGFTFYAAVCCNHEDCHHYAELEY---IDVIN	433
	: : : :	: : : :	: : : :
Dd	75	RRIHHSHSLNSOYTGLPLGTTLFVCIA-----CINSEDIQIGAELEFVAABQPON	129
Oy	434	IISCEFDGYLTKMTCKWSTSTIOSL-AEETILORHARSSLY--CAIDIPSHPISEPKDC-	488
	: : :	: : :	: : :
Dd	130	LSCIQKGOGTYACMGWRGDTHLTXYTLOJSGRKNLTWKQCDI-----YCD	179
Oy	489	YLSDGETECIEFOPIFLLSGTMYMRINSGLSDDPPCLVDPSVKPELPSSKAEL-	547
	: : :	: : :	: : :
Dd	180	YLD----RGINLTPESPESPENFTAKYTAANSSLSSTPTFFDLIVRLPWMDIRIKQ	235
Oy	548	TINIGLLTWMEKVAFEPENNLOFORIGYSCKEYOVMKYEEVDAKSVALSVDPDICAY	607
	: : :	: : :	: : :
Dd	236	KASVASRCILIYMDEQLVLLN---RLRTSPSNSRL-WNNVNYTKAAGRIDLDLKKFP-IEX	290
Oy	608	AVOVBCRKRLDIGLVGVSNMNSNPATVYMDIKVPMBGP---EFWRINGDTMKK-----EK	658
	: : :	: : :	: : :
Dd	291	EFGISSKLHLXKGSMDSES-----LRAQTFEBEPTGMALDYW-----YMKRHIDYSHQ	339
Oy	659	NVTLLMKRLPMKNDISCASQRYVIYNHTSCNG-TASEEDGNKHFKTFPLMETQH-NITYULA	716
	: : :	: : :	: : :
Dd	340	QISTFWKMNIYSEAGAUKLIHVYOTLQDELTGCGAMTONIGHTSWTTTVIPRTGGNAVAAASA	399
	: : :	: : :	: : :

QY 717 INSTGASVANENLTFMSMKNVNI-----QSLSAYPLNNSCVISVITLSPSD-Y 765
DB 400 ANSGSSLP-----TRINIMNCEAGLAPROVSANSEGMDNLTVMQPPRKDPS 449
QY 766 KLMFIIEKMLNEDGE-----IKMLR-----ISSVKKYIHD-----799
DB 450 AVQEVYVEMRLHGGDQVPLNMLRSRPYVNSALISINIKSYCELRVVALSDQGC 509
QY 800 -----HFIPIEKYQFSL--YPIF--MEGVGRP 822
DB 510 SSILGNSKHKAPLSGRHINATEEKSILISMSNIPVQEQGCLLHYLTKMERDPSNQ 569
QY 823 KI-----INS-----FTQDDIKH-----QSDAGLYIYIPV 848
DB 570 QLCIEIPRVNSNHPINSLQPRVYVLMVMTALTAGESSHGEREFCLOGKNMMAFVAP 629
QY 849 IISISILLGTLISHQMKLF-----W--EDVPNPKNSMAOGLNQKQET-- 894
DB 630 SICIALIMWG-IFSTHYQQAQVYVLLALRQWCSREIIPDRANSTCAKKYPAEKTOLP 688
QY 895 FEHLFIKHTASVTCGPLLEPETISEDISVDT-----SMKNKDEMPPTVVSLLST 945
DB 689 LDRLLIDMPT-----PEDEPLVISEVLHQYTPVFRHPPCSNMPOREK-----731
QY 946 TDLKGSVCISDOFNSVNF-----EAGTEVY--YE-----DESOROPFYKATLI 990
DB 732 -GIGHQASERKDMHMSASPPPRALQAESRQLDVLYLESRGSDPRENACPWYLP 790
QY 991 SNKRPEFGEQGLINSVTCFSSKNSPLKDSFNSMEIFAQ-----AFILSDQHPNI 1046
DB 791 AGDLP-----HDGILPNSIDD-LPSHEAPLADSL-----ELEPHOISLSVFSSSLHP-- 839
QY 1047 ISPHLTSESG-----LDEL 1060
DB 840 -----LTFSCGDKLTLDOQL 853

RESULT 7
US-10-119-480-92
; Sequence 92, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Collin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-92

Query Match 3.5%; Score 218.5; DB 6; Length 582;
Best Local Similarity 20.4%; Pred. No. 1.6e-07;
Matches 118; Conservative 100; Mismatches 243; Indels 117; Gaps 28;

QY 433 NISCTDGLYLRKMCNMTSTRTIOSLAESTLQLRHRSLSY--CSDIPSIHPISPEKCYL 490
DB 59 NISC-VYYRRNLNLTCTWSPCKETSTQYTVKRTYAFGEKHDNCTNNS-----105

QY 491 QSDGFYECIF--QPIFILSGITMTIRINHSLSLSDSPPTCVLPDSVYKRLPPSSVKAET 548
DB 106 TSENKASCSFLLPRTTIPDNYTIEVEAENGDDVYKSHMTYMRLENLAKPEPRIFEVKPV 165
QY 549 INI-GLKLTSMKPEVP--ENNIOFOIRYGLSGKEVQMKMEYVADKSKSVSLPVDLCA 605
DB 166 LGIKMKIOEMKRLPELAPSSDLKTLRF-RVYNSISW--MEVNPKNKDKDNQTYNLNG 222
QY 606 V-----YAVQVCKRLDGLGYMNSNPATYVMDIKYPMRGPEPWRITNGTMMKKNV 660
DB 223 LQPFTEYVALRCAYKES-KFMSDMSQEKMGMTDE-EAPC-GLELMKRYLKPAPADGRBY 279
QY 661 TLKRLPKANDSLCSVQRYVINHHTSCN-----GTMSDEYGNHTKFTFLTEQAHYV 713
DB 280 RLIMKARCAPLEKTLGGINIYEPESNTNLTETMTNTTQOELHLGSEFW-----VS 333
QY 714 VLAISIGASVANFNLTFSMPMSKVIN-----VOSLSAYPLNNSCV-----IYSMLSPSD 764
DB 334 MYSYSLGKS-----PVATLRIPAIOEKSHOCIEYMOACVADOLVYKMOSSALD 383
QY 765 YALMTFIIEM--KNLEDGEIKMLRISSSVKRYIHDHPIEKVQFSLYPIFMGVGRP 822
DB 384 VNT--WMIEFDPDVSEPTTLMSVESQATNMTIQQDKLPFCYNISYVPMHLDRKVEP 441
QY 823 KIINFTQDDIEKHQSDAGLYIVPYITISSILLGTLISHQMKLMEDVNPKN-- 880
DB 442 YSIQVYAKGVSSEGE-----TKVENIGVKTYT-----ITWKEIPEKSERG 483
QY 881 --CSMAQGLNFQKPEFHEHLFIKHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPT 938
DB 484 IICNTI--IFYQABEGKG-FCKHNS-----IPEKNKRPQIDANDRP 522
QY 939 VVSL--STTDLKGSVCISDOFNSVNFSEAGTEVY 974
DB 523 VYGMAPPSSHCDLQPG-----MNLASLNLSE-NGAKSTH 555

RESULT 8
US-09-935-868-10
; Sequence 10, Application US/09935868
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-10

Query Match 3.1%; Score 191.5; DB 5; Length 332;
Best Local Similarity 23.2%; Pred. No. 5.5e-06;
Matches 77; Conservative 56; Mismatches 140; Indels 59; Gaps 17;

QY 337 PKIILTVSGNSVNFHCITYK--ENKIVPSKEIYMMNLAEKIPQSDYDVSDHVSQVTF 393
DB 33 PESPVQULHSNFTAVCLKEKCMQDYHVNAVNYVMKTN-HFTIPKQYIILNRTASSVTF 91

QY 394 FNUNEKPRGKTYDVAVYCCNEHECHRYAELVIDV-----NINISC-ETDQYLRK 444
DB 92 TDI-----ASLNLQLTQNLITFGQLEQONYGIGITISGLPENXNNSCIYNEG--KK 141

QY 445 MTCNMTSTRTIOSLAESTLQLRHRSLSYCSDPISHPISPEKDCY--QSDGFYECI--FOP 502
DB 142 MNCENDG-----RETHLETLNFTLKSEMAT-----HKFA--DCAKAKROTPIPSCTYDIYST 188


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; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1148
; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1148

Query Match      2.8%; Score 172.5; DB 1; Length 1461;
Best Local Similarity 19.6%; Pred. No. 0.00094;
Matches 218; Conservative 151; Mismatches 407; Indels 339; Gaps 54;

Qy 48 LIPAGL-----SKNTSNSNGHYE--TAYE-----PKFNS-----SG 76
Db 103 LIPDGLFISNVVHSHKHKPDEGYOCVATVESLGTIISRTAKLIYAGLPRTSQPEPSS 162
Qy 77 THFSNLSTTFFHC-----CFRSEODRNCSLCADNI-----EGKTFVSTVNSLVFQOID 124
Db 163 VYAGN--NAILNCEVNAIDLVPFVRWEONQOPLLLDDRYIKLPSGMLVYSNAT----- 212
Qy 125 ANMNIOCMKGLDKLFTICVESLFRNLFRNRYKVHLLVYL--PEVLED-----SPLVP 176
Db 213 -----EGGGGLYRCVYES---GGPKKYSDVELKVLPPPEVYISDLVFLKQSPPLVR 260
Qy 177 QKGSFQWVHCNSVHECCCLVVPVPTAK-----LNDTLMLCLKITSGVIFQSPILMSV 229
Db 261 VAGQVNLPCVASG-----LPPTIKMKMKNEALDPTSSRLVILAGS-----SL 305
Qy 230 QPINWKKPDPPLGLMEITDDGNLKISWSSPPLVPPLOQYKYSNSTTV--IREADKTY 288
Db 306 EISDVTEDD--AGTYFCIADNGNETIEAOA---ELTVQAOPEELKQPTNIYAHESMDIV 359
Qy 289 SATSLIYVDSILPSSYEVOYRGKRLDGPQIWSDMSTPRY--FTTQVLT-----YFP----- 337
Db 360 -----FEECVTKG-----PPTVKKWKNKNGDMVLPISDYFKIYKEH 393
Qy 338 -PKILTVGSNVSFH-CIYKKEKNIYPSKEIYVMMNLAE-----KIPOSQYDVVSDHVS 389
Db 394 NLOVGLVYKSDSGFYQCI--AENDVGNAGAGAOIILIEHAPRTGPIPARPDVVASLVS 451
Qy 390 KVFENLNETKFRKGFYTDAYCCNEHECHHRYAELIYVIDVININISCTEDGYLTJKTCRW 449
Db 452 -TRFTKLWTRP-----ASDPHGDNLTYSVFYETKEGJAREVENTSHRGEQV-- 498
Qy 450 STSTQSLAESLLOLRHNSSLYCSDIPSIHPISEPKOCYLOSOGYEICIPQIFILSGY 509
Db 499 ---TTONLMPATVYL-----F----- 511
Qy 510 TMMIRINSLGSLDPPICVLDPDVAVKPLPSSVKAELITINIGLKISWEKVPPENNIO 569
Db 512 RYMAANKHSGSSAPLARETOPVQLPBPANLRA--YASTSTIYVIMETVYSGNGEIQ 570
Qy 570 -FOIRIGLSGKAVQMKMEYVDAKSKSVSLPVDLCAYAVOYRCKRLDGLGYWSMNSP 628
Db 571 NKTLTYMEGTEKE---QDVVSSHSYTINGLKKYTEYSFRVAVANKHGPV---STP 622
Qy 629 ATTYVMDIKVPRGPPEFMIINGDTMKKEKNYTLMLKPKMKDLSLCSQRYVYINHH--TSC 687
Db 623 DVAVVTLDVPSAAPONISL---EYRNSKSTIMHOPAPAPATONGQITGYAIRKKASR 678
Qy 688 NGTWSEVDGNHTKFTFL-----WTEQATTVYVLAINSIGASVAMFNLT--TFSPMPKSVMI 740
Db 679 KSDVETELVSGTQOLIEGLDRGTENFRVALITINGCAPTDMLSATFEESDDETRIV 738
Qy 741 VO---SLSAVPLNSSCVIYSWILSPSD-----YKLMYFI-----IEMKNLINED 780

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Db 739 PEVPSLHVRPLVTS--IVSW--TPPENQNIYVRGAIYIGISGPHAOITIKVDYK----- 790
Qy 781 GEIKMLRISSYKKYIHHFIPIEKYQSLYPIFMEVGKPKIINSFQODDIEKHQSDA 840
Db 791 -----QRYTTIENLDPSHHYITTLKAFNNVGGCITPLIYSAVTRPHD--TSEV 836
Qy 841 GLVYT-----VPVISSSIILAGTLILSHORMKLLWEDVYPRNKNCSMAOG 886
Db 837 DLEVINAPYTPVDPDPLPMPMPVGVQASIL-----SHDTI-RITWADNSLPKH----- 882
Qy 887 LNFQKPEFTEHLEFIKHTASVTCGPLLEPETISEDIVSTSKNKNDENMPTTVYSLSTT 946
Db 883 ---QKITDSRYTYVRW-----KTNIPATKYKNMNAATLLSLYVLGDKPN 923
Qy 947 DLEKSCVICIDQFNVSVNF--EAGTFEYTEDESQROPEFYKATLLNSKRPSET----- 998
Db 924 TLXESVWMTKGRRSYTWMTAHT--TRELVPITSP--KDVTVSKKEKPRITIIYNMQP 979
Qy 999 -GEEOGLINSVYTKCFSSKNKSPDKDSFNSMSWEIE 1032
Db 980 PSEANGKITGYITIIYSTDVNAEIHID-----WVIE 1008

RESULT 11
PCT-US02-10824-189
; Sequence 189, Application PC/TUS0210824
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Prostate Cancer Expression Profiles
; FILE REFERENCE: 9U 206 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/10824
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/281,732
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/281,731
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 189
; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-10824-189

Query Match      2.7%; Score 170.5; DB 1; Length 1461;
Best Local Similarity 19.6%; Pred. No. 0.0013;
Matches 218; Conservative 151; Mismatches 407; Indels 339; Gaps 54;

Qy 48 LIPAGL-----SKNTSNSNGHYE--TAYE-----PKFNS-----SG 76
Db 103 LIPDGLFISNVVHSHKHKPDEGYOCVATVESLGTIISRTAKLIYAGLPRTSQPEPSS 162
Qy 77 THFSNLSTTFFHC-----CFRSEODRNCSLCADNI-----EGKTFVSTVNSLVFQOID 124
Db 163 VYAGN--GAILNCEVNAIDLVPFVRWEONQOPLLLDDRYIKLPSGMLVYSNAT----- 212
Qy 125 ANMNIOCMKGLDKLFTICVESLFRNLFRNRYKVHLLVYL--PEVLED-----SPLVP 176
Db 213 -----EGGGGLYRCVYES---GGPKKYSDVELKVLPPPEVYISDLVFLKQSPPLVR 260
Qy 177 QKGSFQWVHCNSVHECCCLVVPVPTAK-----LNDTLMLCLKITSGVIFQSPILMSV 229
Db 261 VAGQVNLPCVASG-----LPPTIKMKMKNEALDPTSSRLVILAGS-----SL 305
Qy 230 QPINWKKPDPPLGLMEITDDGNLKISWSSPPLVPPLOQYKYSNSTTV--IREADKTY 288
Db 306 EISDVTEDD--AGTYFCIADNGNETIEAOA---ELTVQAOPEELKQPTNIYAHESMDIV 359
Qy 289 SATSLIYVDSILPSSYEVOYRGKRLDGPQIWSDMSTPRY--FTTQVLT-----YFP----- 337
Db 360 -----FEECVTKG-----PPTVKKWKNKNGDMVLPISDYFKIYKEH 393

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0Y 338 -PKLITSGVNVSPH-CIYKKNKIVYSKELVMMNLAE-----KIPQGYVVDHVS 389
Db 334 MLOYGLVKSDEGFQCI--AENDVGNAGAOQLITLLEHAPATPGPLSPAPRVNVLVS 451
0Y 390 KVFPELNETPRGKFTYDAVAYCCNEHCHRRHAEVLIVDINIISCETGYLVTKTCRW 449
Db 452 -TRFKLTWRPR-----ASDPHGDNLTYEVFTKGLAREYRENTSHPGEMQV-- 498
0Y 450 STSTQSLAEETLQLRHRSLSYCSOPLSIHPISEPDCYLOSDFECLFOPILFLSG 509
Db 499 --TTONMPATVYI-----F 511
0Y 510 TMMIRINSLSLSPPTCVLPDSVVRPLPSSVAKETITNIGLKISMEKPYFENLQ 569
Db 512 RYMGNKRGSESSAPLREYQPEVQLGRAPNIRA-YAASPSITVYTWPTVPSGNEIQ 570
0Y 570 -FOIRYGLSGKEVOMKMEYVDAKSKSVSLPBDLCANVAVOYCRKLDGLGYWSMKNP 628
Db 571 NYKLTVMKGTDKDE---QDVADVSHSYITNGLKRYEYFRRVAVYKKBHPGV---STP 622
0Y 629 AYTVMDKIVMRGGEFWRIRINGDTMKKEKVTLMKPLKNDLSLGVQVYVYINH-TSC 667
Db 653 DYAVATLSDVSAAPONISL-----EVRNKSIMTHQPPAPAPATONGITGKIRKASR 678
0Y 668 NGTMSDEVGNHTKFTFL-----WTEQAHTVYVLAINSIGASVANFNL-TFSWPMKSVNI 740
Db 679 KSDVTELVISGTOISLEIGDRCTEYFNRYAALLTINGTPATDMLSAETFEEDLDETRV 748
0Y 741 VO--SLTSAVPLNSCIVVSLSPD-----YKLMFI-----IEKKNINED 780
Db 739 PEVSSLSHVRPLVS-IYVSH--TPPEQONIVAGVIAIGISGPHAQITKIVYK----- 790
0Y 781 GEIKMLRISSVKKYYIHDPPIPIEKYQFSLYPIEMGVGVPKPIINSFTODDIEKHQSDA 840
Db 791 -----QRYTLENLDPSSHVYITLKAPNNVGEPILEYSAVTRPHD--TSEV 826
0Y 841 GLHYV-----VYIISSTLLGLTILSHQMKKLPWVDVYPRKNCMAQ 886
Db 837 DLEVYADYPPPTPMPMPVPGVQASL-----SHDTI-RTWADNSLPJH----- 862
0Y 887 LNFQPEPFEHLFIKHTASVYCGPLLEPETISEDISVDTSMKKNDMPJTVVSLSTT 946
Db 883 ---QKTTDSRYTYRW-----KTNIDANKRYKANANTLSYLTGTGKPN 923
0Y 947 DIEKSVSISQFNVSNF-EAEGTBYTYEDESOROPFYATILISKRSSEF----- 998
Db 924 TLYEFSVWVTGRRSSTSMHAGT--TFELVPTSP--KDVYVSKGPKTIYVNOQ 979
0Y 999 -GEEGLINSVATCFSSKNSPLLDSPNSNSMWE 1032
Db 980 PSEANGKITGYIIYITDVNAEIID-----WYLE 1008

RESULT 12
PCT-US02-09671-1147
Sequence 1147, Application PC/TUS0209671
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/336,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04

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: PRIOR APPLICATION NUMBER: 60/358,965
: PRIOR FILING DATE: 2002-02-20
: NUMBER OF SEQ ID NOS: 2041
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1147
: LENGTH: 1461
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US02-09671-1147

```

```

Query Match      2.7%  Score 170.5:  DB 1:  Length 1461;
Best Local Similarity 19.6%:  Pred No 0.0013;
Matches 218:  Conservative 151:  Mismatches 407:  Indels 339:  Gaps

Oy 48 LIPAGL-----SKMTSNSNGHYE--TAVE-----PKNSS-----SG 76
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 103 LLPDSLFISNVSHSKHKPDGEYGVCAVATESIGTIISRTAKLYAGLPRFSOEPS 162
Oy 77 THFSMLKTHC-----CFRSBDRNCSLCAADI-----EGKTVSYRNSLVYQQID 124
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 163 VYAGN--GALLNCEVNAIDLVPFVMEONRPLLLDDHVIKLPSSGMLVISNAT----- 212
Oy 125 ANNMIOCLMKDGLKLFICYSESLKFNLFIRNYKIVHLLYL--DEVLED-----SPLVP 176
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 213 -----BEDGGLKRYVES-----GGPRKYSDBVELKLPDEVISDLYFLKQPSVLR 260
Oy 177 OKGSFQWYHNCNSVHECCCECLVPVPAK-----LNDLLMLCKITSGGVIFQSPLMY 229
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 261 VIGDQVLPVCVASG-----LPPTTKMKMBEALDESSERLVLLAGG-----SL 305
Oy 230 QPINWVKRDPPLGLHMETDGNLKISMSSPPLVPFPLOYGVYSENSTV--IREADKIY 288
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 306 EISDTEDD--AGTYFCLADNGNTIEQA---ELTVQAPEFLKQPTIYAHESMDIV 359
Oy 289 SATSLVDSILPGSSYEVQVNGKRLDGPIMSDWSTPRV--FTTQDVI---YFP----- 337
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 360 -----FEECEVTK-----PRTYKWKMKNGDVAIVSDYFKIYKEH 393
Oy 338 -PKLITSVGSNVSH--CLYKKEKNIYSKELVYMMNLAE-----KIPQOQVYSDHYS 389
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 394 NLQVYGLVKSDEGGYQCI--AENVQNAQAQOLILIEHAPATTGPIPSAPROVYASVLS 451
Oy 390 KVFTEFNLETKPRKFTYDAVAYCCNEHECHRRYAEVLVIDVINISCEPTGYLTKTTCRW 449
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 452 -TRFIKLWVRP-----ASDPHGMNLTYSVFRTKGIARERENSHRGENQV-- 498
Oy 450 STSTQSLAESTLQLRHRSLSYCSDIPSIHPISEPKCYLOSDCRTECIQPIPLSGY 509
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 499 --TQNLMPTAVYI-----F 511
Oy 510 TMMIRINISGSLSDPCTCVLPDSVYAPLPSSVKAEITINIGLKISMEKVPVPENNIO 569
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 512 RYMAONKRGSESSAPLRVETQPEVOLGPPAPNDIA--YAASPTSLTYWTTPVSGMGEIO 570
Oy 570 -FOIRYGLSGREYQMKWMEYVDAKSKSVSLPVPDLCAVAVAVQRCRKLQSLGYWMSMNP 628
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 571 NTKLYLMMKGGDKR-----QDDVDSHSHYTINGLKKIYEYSFRVAVANKHBPQV----- 622
Oy 629 AYTVMMDIKYMRGPFEWRJINSDTMKKEKNVTLLMKPLMKNDLSLCSVQRYVINHH--TSC 687
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 623 DVAVRTLSDVSPAPOMLST---EVNSKRSIMIHQPPAPATQOQICGYKIRYRKASR 678
Oy 668 NGTMSDEGVNHTKTFYL-----WTEBAHYVYVLAINISIASVANNNL--TFSPMRSKVIN 740
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 679 KSDVETLVSGTQSLQLEGLDRGTEVNFRAVALLTNGTAPADWLJAETFEESDLDETR 738
Oy 741 VQ---SLAYPLNNSCVIYSWILSPSD-----YKLWFI-----IEKMLNLED 780
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 739 PEVSSSLHVRLLVYS--IYNSH--TPPENQNIYVRGVALIGIGISLPHAQITKVDYK----- 790
Oy 781 GEIKWLRISSVKKRYIYLDHDEPIEKYQFSLYPIFMEGVKPKIINSFTQDIDIEKHQSA 840
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```


Db 791 -----QRYTIENTLDPSSHVYTLKAFNNVGGIPLYESAVTRPHD--TSEV 836
Qy 841 GLYVI-----VPYIISSILLGLTLLISHORMKLFMEDVDPNPKNSMAOG 886
Db 837 DLFVINAPTVPDPPTPMMPVGVQASIL-----SHDTI-RITWADNSLPKH----- 882
Qy 887 LNFQRPETFEHLEFIKHTASVTCGPLLEPETISEDIVTSKKNKDEMPPTVVSILSTT 946
Db 883 ---QKITDSRYTVRW-----KTNPANTKRYKNNATLSTLYVGLKPN 923
Qy 947 DLEKSVCSIDQFNVSFNS-FAEGTEVTEDESQROPFKYATLLISNKSPEF----- 998
Db 924 TLYESVMTTKGRSSSTWSMTAHGT--TFELVPTSP--KDVTVSKESKPKTIIVNMOP 979
Qy 999 -GEOGLINSVTKCFSSKNSPLKDSFNSMSWEIE 1032
Db 980 PSEANGKITGYIIYYSTDVNAEIH-----WYIE 1008

RESULT 13

PCT-US02-09671-1149
Sequence 1149, Application PC/TUS0209671
GENERAL INFORMATION:
APPLICANT: Zycoos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1149
LENGTH: 1461
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09671-1149

Query Match 2.7%; Score 170.5; DB 1; Length 1461;
Best Local Similarity 19.6%; Pred. No. 0.0013;
Matches 218; Conservative 151; Mismatches 407; Indels 339; Gaps 54;

Qy 48 LIPAGL-----SKTNSNGHYE--TAVE-----PKMS-----SG 76
Db 103 LIPDGLSFLSNVYHSHKMPDGGTQCAVTVESLGTIISRTAKLIVAGLPREFSQPEPS 162
Qy 77 TRSNLSKTTFRG-----CFRSEDRNCSICADNI-----EGKTFVSTVNSLVEQID 124
Db 163 VYAGN--GAILNCEVADLVPRVMEQNNQPLLLDDRVKILPSGMLVISAT----- 212
Qy 125 AMNNIOCMKGLDKLEFCYVESLEKMLFRNYTKVHLVYL-PEVIED-----SPLVP 176
Db 213 -----EGDGLRYCVES---GGPRKYSDEVELKVLPPREVISDLVFLKQSPSLVA 260
Qy 177 OKGSPQWVHNCNSVHCCCLVVPVTK-----LNDTLMLKTKTSGVIRQSLMSV 229
Db 261 VIGQDVVLCVAGS-----LPTPIKMKKNEALDTSESEPLVILAGS-----SL 305
Qy 230 QPINWKKPPPLGLMEITDDGMLKISWSPPLVPPLOYOVKVSNSSTTV-TREADKIV 288
Db 306 EISDVTEED--AGTYFCIADNGNETIEAQA-----ELTVQAQPPFLKOPTNIIVAHESMDIV 359

Qy 289 SATSLVDSITLGCSSSEVVOYRGKRLDGPGLWSDMSTRV--FTQDVI-----YFP----- 337
Db 360 -----FECEVTG-----PPTVKKVKNMGDMVLPDSYFKIVK 393
Qy 338 -PKILTSVGSNSFPH-CIYKKEKIKVPSKEIWMNMLAE-----KIPSOYDVSDHS 389
Db 394 NLQVLGLVKSDBGTYOCT--AENDVGNQAQGLILLEAPATTGCLPSAPRQVVASLVS 451
Qy 390 KVFENLNETKPRGKFTYDAVYCCNEHECHNRYAELVIVDVINISCEFDGVLTKMTCRW 449
Db 452 -TRFIKLTWRTP-----ASDPHGNDLNVSVYETMEGLAREVENTSHGEGQV-- 498
Qy 450 STSTIOSLAESTLQLRHYHNSLYCSDIPSIHPISEPKDCYLOSOGFYECIFOPFILSST 509
Db 499 -----TTONLMPATVYI-----F 511
Qy 510 TWMIRINSLGSLDSPPTCVLPDSYVKKPLPSSVKAETITNIGLKISMEKPYEPENNLO 569
Db 512 RYMAQKKHSGESSAPLRETOPEVOLPGPAPNLR--YAASPTSTVETETVSGNGEIQ 570
Qy 570 -FOIRYGLSGKEYOWKMYEVYDAKSKVSLPVPOLCAYAVOYRCRLDGLGYMSMNSP 628
Db 571 NYKLIYMEKGTDE-----QDVVSSHSTYTINGLKYTESEFRVAVNKKHGPV---STP 622
Qy 629 AVTVMDIVPMRGPEFWRIINQDTKKKKNVTLLMKPLMKNDSLCSVORVYVINH--TSC 687
Db 623 DVAVRFLSDVPSAAPONLSL---EVRNSKSIIMHQPPAPATONQITGYKIRYKASR 678
Qy 688 NQWSESDVGNHRTKFTL-----WTEQAHYVYLAINSIGASVANEHL--TESPMKSVNI 740
Db 679 KSDVETTLVSGTQLSQILGIDRGTEYNFRVAALTJNGTGPATDMLSAETPESDLETRV 738
Qy 741 VQ---SLASVPLNSSCVIYSWILSPSD-----YKLMYFI-----TEKMLNED 780
Db 739 PEVPSLHVRPLVTS-IVSW--TPPENQIVYRGALIGISPAQTIKVYK----- 790
Qy 781 GEIKWLRISSVAKKIYIHDHFIPIEKYQPSLPIFMEGCGKPKIINSFTODDIEKQSDA 840
Db 791 -----QRYTIENTLDPSSHVYTLKAFNNVGGIPLYESAVTRPHD--TSEV 836
Qy 841 GLYVI-----VPYIISSILLGLTLLISHORMKLFMEDVDPNPKNSMAOG 886
Db 837 DLFVINAPTVPDPPTPMMPVGVQASIL-----SHDTI-RITWADNSLPKH----- 882
Qy 887 LNFQRPETFEHLEFIKHTASVTCGPLLEPETISEDIVTSKKNKDEMPPTVVSILSTT 946
Db 883 ---QKITDSRYTVRW-----KTNPANTKRYKNNATLSTLYVGLKPN 923
Qy 947 DLEKSVCSIDQFNVSFNS-FAEGTEVTEDESQROPFKYATLLISNKSPEF----- 998
Db 924 TLYESVMTTKGRSSSTWSMTAHGT--TFELVPTSP--KDVTVSKESKPKTIIVNMOP 979
Qy 999 -GEOGLINSVTKCFSSKNSPLKDSFNSMSWEIE 1032
Db 980 PSEANGKITGYIIYYSTDVNAEIH-----WYIE 1008

RESULT 14

PCT-US02-09671-1150
Sequence 1150, Application PC/TUS0209671
GENERAL INFORMATION:
APPLICANT: Zycoos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370

Db 245 QTTIE-KVSCEMRYKATTTQOT-WNVKE-FDTNFTYQOSEFFYLEPNI--KYVFQVRQOE- 298
QY 617 DGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRILNGDTMKKEKNVTLMKPLMKNDLSY 676
Db 299 TGRRYQOPWSSPEFH-----KTPETVPQV-----TSKAFQHOT--W-----NSGLTV 338
QY 677 ORVYINHHTSCNGTWSDEDYGNHTKFTFLMTQOAHVTYVLAINSIGASVANPNLTF----- 731
Db 339 ASISTGHLTSDN---RGDIG-----LLIGMIVFAVMLSLSL--IGIFNRSFRGK 385
QY 732 -----SW-----PMKVNIVQSL---SAYPLNSCVIVSMI-----L 760
Db 386 RRILLIPKLYEDIPNMKNSVYKMLQENSELMNNSSQOVLVYDPMITEIKEIPPEH 445
QY 761 SPEDYK-----LMYFIEMKNLNDEGEIK 784
Db 446 KPDTYKKEKNTGPLETRDYQONSLFDNTVYIIPDLNTGYKPOISNPLPEGSHLSNNNEIT 505
QY 785 WLRISSVKRYIHDHPIPEKYQFSLYPIFMEGVGKPKI--INSFTODDIEKHQSDAGL 842
Db 506 SLTL-----KPPVDSLDGNNPRLQKHNPFA-- 531
QY 843 YVIVPYITISSILLGTLLISHQRMKKLFEDYVNPKNCSMAOGLNFOKPEFHEHFIKH 902
Db 532 FVSSVYNSLSNITFLGELSL-----ILNOGECSSPDIONSVEEET----- 571
QY 903 TASVTGPTLLEPETISEDISVDTSMKNKDEKMPYTVVSLSTTDLEKGSV-----CI 955
Db 572 -----TALLENDSPSETIPEOT-----LIPDEFVSCLGIYNEELPSINTYFPONIL 617
QY 956 SDOFNSVNESE 966
Db 618 ESHFNRLSILLE 628

Search completed: May 18, 2002, 07:00:08
Job time: 577 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 05:18:35 ; Search time 54.58 Seconds

(without alignments)
521.360 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254
Sequence: 1 MICQKRCVVLHMEPIYIVT.....QTCSGTQTHKIMENKMDLTV 1165Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/PCtus.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6254	100.0	1165	2 US-08-599-455B-4	Sequence 4, Appli
2	6254	100.0	1165	4 US-09-069-781B-4	Sequence 4, Appli
3	6246	99.9	1165	4 US-09-093-814-1	Sequence 1, Appli
4	6246	99.9	1165	4 US-08-618-957A-11	Sequence 11, Appli
5	6172	98.7	1165	4 US-08-640-389A-11	Sequence 11, Appli
6	4819.5	77.1	958	4 US-08-618-957A-8	Sequence 8, Appli
7	4819.5	77.1	960	1 US-08-355-888A-8	Sequence 8, Appli
8	4819.5	77.1	960	2 US-08-693-697-8	Sequence 8, Appli
9	4819.5	77.1	960	2 US-08-640-389A-3	Sequence 3, Appli
10	4819.5	77.1	960	2 US-08-693-697-8	Sequence 3, Appli
11	4816	77.0	908	2 US-08-693-697-33	Sequence 33, Appli
12	4814.5	77.0	960	2 US-08-588-190-3	Sequence 3, Appli
13	4814.5	77.0	960	4 US-08-618-957A-3	Sequence 3, Appli
14	4814	77.0	896	4 US-08-618-957A-10	Sequence 10, Appli
15	4814	77.0	898	2 US-08-693-697-36	Sequence 36, Appli
16	4814	77.0	906	4 US-08-618-957A-9	Sequence 9, Appli
17	4799	76.7	908	2 US-08-588-526-3	Sequence 3, Appli
18	4791.5	76.6	958	2 US-08-640-389A-8	Sequence 8, Appli
19	4788	76.6	906	2 US-08-640-389A-9	Sequence 9, Appli
20	4786	76.5	896	2 US-08-640-389A-10	Sequence 10, Appli
21	4784.5	76.5	1162	4 US-08-803-346-1	Sequence 1, Appli
22	4776.5	76.4	1162	4 US-08-827-962-15	Sequence 15, Appli
23	4770.5	76.3	1162	4 US-08-599-455B-43	Sequence 20, Appli
24	4770.5	76.3	1162	4 US-08-827-962-20	Sequence 43, Appli
25	4770.5	76.3	1162	4 US-09-069-781B-43	Sequence 43, Appli
26	3801	60.8	896	4 US-08-640-389A-12	Sequence 12, Appli
27	3792	60.6	894	4 US-08-618-957A-12	Sequence 12, Appli

28	3785	60.5	894	2 US-08-599-455B-2	Sequence 2, Appli
29	3785	60.5	894	4 US-09-069-781B-2	Sequence 2, Appli
30	3779	60.4	895	4 US-08-827-962-19	Sequence 19, Appli
31	3753	60.0	895	4 US-08-827-962-21	Sequence 21, Appli
32	3057	48.9	569	1 US-08-306-231-3	Sequence 3, Appli
33	421	6.7	77	4 US-08-803-346-64	Sequence 64, Appli
34	395	6.3	76	4 US-08-803-346-61	Sequence 61, Appli
35	377	6.0	77	4 US-08-803-346-62	Sequence 62, Appli
36	370	5.9	77	4 US-08-803-346-63	Sequence 63, Appli
37	345.5	5.5	918	2 US-08-825-558-6	Sequence 6, Appli
38	316	5.1	708	1 US-07-797-556-2	Sequence 2, Appli
39	316	5.1	708	1 US-08-308-881-2	Sequence 2, Appli
40	316	5.1	708	2 US-09-058-263-2	Sequence 2, Appli
41	316	5.1	708	2 US-09-059-099-2	Sequence 2, Appli
42	316	5.1	708	3 US-09-058-264-2	Sequence 2, Appli
43	316	5.1	708	5 PCT-US95-06530-2	Sequence 2, Appli
44	313	5.0	837	1 US-07-923-976-2	Sequence 2, Appli
45	309.5	4.9	75	4 US-08-803-346-60	Sequence 60, Appli

ALIGNMENTS

RESULT 1
US-08-599-455B-4
Sequence 4, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown


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SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-069-781b-4

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Query Match          100.0%; Score 6254; DB 4; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICOFCVLLHMEFIYITAFNLSTPTPMRFKLSGMPNSTYDYFLPAGLSKNTS 60
DB 1 MICOFCVLLHMEFIYITAFNLSTPTPMRFKLSGMPNSTYDYFLPAGLSKNTS 60
QY 61 NGHYETAVERPKNSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGTFVSNLSVF 120
DB 61 NGHYETAVERPKNSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGTFVSNLSVF 120
QY 121 QOIDANMNIOCMKGLDKLFCYVESLFRNRYNRYKVLHLYLPEVLEDSPLVPQKS 180
DB 121 QOIDANMNIOCMKGLDKLFCYVESLFRNRYNRYKVLHLYLPEVLEDSPLVPQKS 180
QY 181 FOMVHCNCSVHECCBGLVPPPTAKINDTLMLCKITSGGVIQSPIMVAPDPDP 240
DB 181 FOMVHCNCSVHECCBGLVPPPTAKINDTLMLCKITSGGVIQSPIMVAPDPDP 240
QY 241 LGLHMEITDDGNLTKISWSSPPLVPPLOQVYKSENSSTVIREADKIVATSILVDSILP 300
DB 241 LGLHMEITDDGNLTKISWSSPPLVPPLOQVYKSENSSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEVOVAGKRLDGPGLMSDMSPTPRVFTTODVIYFPFKILTVSGSNVSFHCYKKNKI 360
DB 301 GSSYEVOVAGKRLDGPGLMSDMSPTPRVFTTODVIYFPFKILTVSGSNVSFHCYKKNKI 360
QY 361 VPSKEIYVMNMLAEKIPQSQDYVSDHVSATVFENLNKPKGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMNMLAEKIPQSQDYVSDHVSATVFENLNKPKGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVDVNNINISCEGTGYLTAKMCHMSTSTIOSLAESTOLARHRSLSVCSOIPSH 480
DB 421 RYAEIYVDVNNINISCEGTGYLTAKMCHMSTSTIOSLAESTOLARHRSLSVCSOIPSH 480
QY 481 PISEPKDCVLOSDGFYECLFOPIFLLSGYTMIRINHSLSGLSDSPPTCYLPDSVAPLPP 540
DB 481 PISEPKDCVLOSDGFYECLFOPIFLLSGYTMIRINHSLSGLSDSPPTCYLPDSVAPLPP 540
QY 541 SSVKAEITINIGLTKISMEKPVFPENNLOFOIRYGLSGKEVOVMKATVEYDAKSVSLEPV 600
DB 541 SSVKAEITINIGLTKISMEKPVFPENNLOFOIRYGLSGKEVOVMKATVEYDAKSVSLEPV 600
QY 601 PGLCAVYAQVCKRLDGLGYWNSMNPAYVMDIKVYMRGPETRIINGSTMKKEKAV 660
DB 601 PGLCAVYAQVCKRLDGLGYWNSMNPAYVMDIKVYMRGPETRIINGSTMKKEKAV 660
QY 661 TLAMKPIKNDLSICSVORYVYINHHSTSCNGTSEEDVGNHKTFTLMEQAHVTVLAINSI 720
DB 661 TLAMKPIKNDLSICSVORYVYINHHSTSCNGTSEEDVGNHKTFTLMEQAHVTVLAINSI 720
QY 721 GASVANFNLTSPMPSKVNIVOSLSAYPLNSSCVIYSWILSPSDYKLMFIIEMKNLND 780
DB 721 GASVANFNLTSPMPSKVNIVOSLSAYPLNSSCVIYSWILSPSDYKLMFIIEMKNLND 780
QY 781 GEIKMLRISSSVKYYIHHTPIEKYQSLPIFMEGSGKRIINSFPDODIEKQSOA 840
DB 781 GEIKMLRISSSVKYYIHHTPIEKYQSLPIFMEGSGKRIINSFPDODIEKQSOA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQMKRLFEDVYPPNPKNSMAQGLNFOKQETFEHLFI 900
DB 841 GLYVIVPVISSSILLGLTLLISHQMKRLFEDVYPPNPKNSMAQGLNFOKQETFEHLFI 900

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QY 901 KHTASVTCGPLLLEPPTISEDISVDTSMKNKDEAMPITYVSLSTTDLEKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLLEPPTISEDISVDTSMKNKDEAMPITYVSLSTTDLEKSGVCSIDQFN 960
QY 961 SVNFEABGTEVYDESOROPFYKATLINSKSKSEGEEOGLNNSVTKCFSSKNSPL 1020
DB 961 SVNFEABGTEVYDESOROPFYKATLINSKSKSEGEEOGLNNSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPILTFSEGLDELKLEGNFPEENNKKSIYYL 1080
DB 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPILTFSEGLDELKLEGNFPEENNKKSIYYL 1080
QY 1081 GYTSIKKRESGYLLDCKSVSCPPAPCLFTDIRVLODSCSHFVENRNLGTSSKKTFS 1140
DB 1081 GYTSIKKRESGYLLDCKSVSCPPAPCLFTDIRVLODSCSHFVENRNLGTSSKKTFS 1140
QY 1141 YMPOTGCTGTHKIMENKMDLTV 1165
DB 1141 YMPOTGCTGTHKIMENKMDLTV 1165

```

```

RESULT 3
US-09-093-814-1
; Sequence 1, Application US/09093814
; Patent No. 6270981
; GENERAL INFORMATION:
; APPLICANT: Carpenter et al.
; TITLE OF INVENTION: ASSAY SYSTEMS FOR LEPTIN-ENHANCING AGENTS
; FILE REFERENCE: REG 580-A
; CURRENT APPLICATION NUMBER: US/09/093,814
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/049,108
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-093-814-1

```

```

Query Match          99.9%; Score 6246; DB 4; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MICOFCVLLHMEFIYITAFNLSTPTPMRFKLSGMPNSTYDYFLPAGLSKNTS 60
DB 1 MICOFCVLLHMEFIYITAFNLSTPTPMRFKLSGMPNSTYDYFLPAGLSKNTS 60
QY 61 NGHYETAVERPKNSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGTFVSNLSVF 120
DB 61 NGHYETAVERPKNSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGTFVSNLSVF 120
QY 121 QOIDANMNIOCMKGLDKLFCYVESLFRNRYNRYKVLHLYLPEVLEDSPLVPQKS 180
DB 121 QOIDANMNIOCMKGLDKLFCYVESLFRNRYNRYKVLHLYLPEVLEDSPLVPQKS 180
QY 181 FOMVHCNCSVHECCBGLVPPPTAKINDTLMLCKITSGGVIQSPIMVAPDPDP 240
DB 181 FOMVHCNCSVHECCBGLVPPPTAKINDTLMLCKITSGGVIQSPIMVAPDPDP 240
QY 241 LGLHMEITDDGNLTKISWSSPPLVPPLOQVYKSENSSTVIREADKIVATSILVDSILP 300
DB 241 LGLHMEITDDGNLTKISWSSPPLVPPLOQVYKSENSSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEVOVAGKRLDGPGLMSDMSPTPRVFTTODVIYFPFKILTVSGSNVSFHCYKKNKI 360
DB 301 GSSYEVOVAGKRLDGPGLMSDMSPTPRVFTTODVIYFPFKILTVSGSNVSFHCYKKNKI 360
QY 361 VPSKEIYVMNMLAEKIPQSQDYVSDHVSATVFENLNKPKGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMNMLAEKIPQSQDYVSDHVSATVFENLNKPKGKFTYDAVYCCNEHECHH 420

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OY 421 RYAEIYVIDVININISCEIDGYLTAKMTCRMSTSTIOSLAESTLOLRHRSLSYCDIPSIIH 480
DB 421 RYAEIYVIDVININISCEIDGYLTAKMTCRMSTSTIOSLAESTLOLRHRSLSYCDIPSIIH 480
OY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGSDSPPTCYLPDSVYKPLPP 540
DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGSDSPPTCYLPDSVYKPLPP 540
OY 541 SSVKAEITINILKLSMEKPVFPENNLOFOIRYGLSGEYOMKWEYVDASKSVSLPV 600
DB 541 SSVKAEITINILKLSMEKPVFPENNLOFOIRYGLSGEYOMKWEYVDASKSVSLPV 600
OY 601 PDLCAVYAVOVBCKRLDGLGYMSNNSPAYTVVMDIKYMRGPERFMRILNGDTMKENY 660
DB 601 PDLCAVYAVOVBCKRLDGLGYMSNNSPAYTVVMDIKYMRGPERFMRILNGDTMKENY 660
OY 661 TILMKPLKNDLSGVORYVIMHNTSCNGTSEDVGNHTKFTFLTECAHTVYVLAINSI 720
DB 661 TILMKPLKNDLSGVORYVIMHNTSCNGTSEDVGNHTKFTFLTECAHTVYVLAINSI 720
OY 721 GASVANFNLTFSPMSKVIVIOSLSAYPLNSCIVSWILSPSDYKLMVFIEMKNLND 780
DB 721 GASVANFNLTFSPMSKVIVIOSLSAYPLNSCIVSWILSPSDYKLMVFIEMKNLND 780
OY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGKPKIINSFTODDIEKHSDA 840
DB 781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGKPKIINSFTODDIEKHSDA 840
OY 841 GLIYVVPYIYSSIIILGLTLLISHQRMKLFMEDVNPKNCSMAOGLNFKQKETEHEHFI 900
DB 841 GLIYVVPYIYSSIIILGLTLLISHQRMKLFMEDVNPKNCSMAOGLNFKQKETEHEHFI 900
OY 901 KHTASVTCGPLLEPETISEDIVSTSMKNKDEMPPTVYSLSTLDEKSGVCSIDOPN 960
DB 901 KHTASVTCGPLLEPETISEDIVSTSMKNKDEMPPTVYSLSTLDEKSGVCSIDOPN 960
OY 961 SYNSEABEGTEVYEAESORQPFVYKATLISNKSPESTGEEOGLINSSVTKCFSSKNSPL 1020
DB 961 SYNSEABEGTEVYEAESORQPFVYKATLISNKSPESTGEEOGLINSSVTKCFSSKNSPL 1020
OY 1021 KQSFNSMSKEIQAOFILISDQHPNISPILTFESGLDELKLENEPENNDKSIYTL 1080
DB 1021 KQSFNSMSKEIQAOFILISDQHPNISPILTFESGLDELKLENEPENNDKSIYTL 1080
OY 1081 GVTSTIKRESGVLLTDKSRVSCPPAPCLFTDIRVLODSCSHFVENNINILGTSKRTFAS 1140
DB 1081 GVTSTIKRESGVLLTDKSRVSCPPAPCLFTDIRVLODSCSHFVENNINILGTSKRTFAS 1140
OY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

```

RESULT 4
US-08-618-957A-11
Sequence 11, Application US/08618957A
Patent No. 6355237

GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBSE
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA

```

? ZIP: 10036-2811
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/618,957A
? FILING DATE: 20-MAR-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Poissant, Brian M.
? REGISTRATION NUMBER: 28,462
? REFERENCE/DOCKET NUMBER: 008907-0033-999
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-493-4935
? TELEFAX: 650-493-5556
? TELEX: 66141 PENNIE
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1165 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-618-957A-11

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Query Match 99.9%; Score 6246; DB 4; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MLCQKFCVYLLHWEFTYITAFNLSTYPTPMRFKLSCHPNSTYVYFLLPALSKNTSNS 60
DB 1 MLCQKFCVYLLHWEFTYITAFNLSTYPTPMRFKLSCHPNSTYVYFLLPALSKNTSNS 60
OY 61 NGHYTAVEPKFNSSGTHESNLKTTFFHCCFRSEODRNCSLCADNIEGTFVYNSLVF 120
DB 61 NGHYTAVEPKFNSSGTHESNLKTTFFHCCFRSEODRNCSLCADNIEGTFVYNSLVF 120
OY 121 QOIDANMNIOCKDKDLKLFICYVESLEKRLFRNRYKYLHLYVPEVLEDSPLYPOKGS 180
DB 121 QOIDANMNIOCKDKDLKLFICYVESLEKRLFRNRYKYLHLYVPEVLEDSPLYPOKGS 180
OY 181 FQMVHNCNSVHECCGCLVVPYPAKLNDTLMLCKLITSGVIFQSPLSVQPINMKPDP 240
DB 181 FQMVHNCNSVHECCGCLVVPYPAKLNDTLMLCKLITSGVIFQSPLSVQPINMKPDP 240
OY 241 LGLHMEITDDGNLKIISWSSPPLVPELOYOVYSENSTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKIISWSSPPLVPELOYOVYSENSTVIREADKIVSATSLVDSILP 300
OY 301 GSSYEVQVRGKRLDGPGLMSDMSTPRVFTQDYIYFPKRLTSVGSNNSFHCYKKEKNI 360
DB 301 GSSYEVQVRGKRLDGPGLMSDMSTPRVFTQDYIYFPKRLTSVGSNNSFHCYKKEKNI 360
OY 361 VPSKEIVMMNLAEKIPOSQDYVDVSHVSKYFEMLNKPKRGKFTYDAVYCCNHECHH 420
DB 361 VPSKEIVMMNLAEKIPOSQDYVDVSHVSKYFEMLNKPKRGKFTYDAVYCCNHECHH 420
OY 421 RYAEIYVIDVININISCEIDGYLTAKMTCRMSTSTIOSLAESTLOLRHRSLSYCDIPSIIH 480
DB 421 RYAEIYVIDVININISCEIDGYLTAKMTCRMSTSTIOSLAESTLOLRHRSLSYCDIPSIIH 480
OY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGSDSPPTCYLPDSVYKPLPP 540
DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGSDSPPTCYLPDSVYKPLPP 540
OY 541 SSVKAEITINILKLSMEKPVFPENNLOFOIRYGLSGEYOMKWEYVDASKSVSLPV 600
DB 541 SSVKAEITINILKLSMEKPVFPENNLOFOIRYGLSGEYOMKWEYVDASKSVSLPV 600

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Db 541 SSVKAEITINIGLTKISMEKPFPPENNLOFOIRYGLSGKEVQWKAIEYVDASKSVSLPV 600
Qy 601 PDLCAVAVOVCKRLDGLGYWMSNPNAYTVYMDIKVPMRGPEFMRINIGDMKKEKNV 660
Db 601 PDLCAVAVOVCKRLDGLGYWMSNPNAYTVYMDIKVPMRGPEFMRINIGDMKKEKNV 660
Qy 661 TLIMKPLKNDLSCVQRYVINHTSCNGTWSGDVGNHTKFTFLTEQAHYTVLAINSI 720
Db 661 TLIMKPLKNDLSCVQRYVINHTSCNGTWSGDVGNHTKFTFLTEQAHYTVLAINSI 720
Qy 721 GASVANFNLFESPMKSVNIVOSLSAYPLNNSCVIYSWILSPSDYKLMFIEEMKRLNED 780
Db 721 GASVANFNLFESPMKSVNIVOSLSAYPLNNSCVIYSWILSPSDYKLMFIEEMKRLNED 780
Qy 781 GEIKMLRISSSVKKYIHDHFIPIEKYQFSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSSVKKYIHDHFIPIEKYQFSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Qy 841 GLYIVVPYIISILLGLILSHORMKLFMEDVDPNPKNCMAOGLNFOKRETFEHLFI 900
Db 841 GLYIVVPYIISILLGLILSHORMKLFMEDVDPNPKNCMAOGLNFOKRETFEHLFI 900
Qy 901 KRTASVTCGPLLEPTEISEDISVDTSMKNKDEMPPTVVSILSTDLKSGVCSISDOFN 960
Db 901 KRTASVTCGPLLEPTEISEDISVDTSMKNKDEMPPTVVSILSTDLKSGVCSISDOFN 960
Qy 961 SVNFSEAECEVTEYDESOQROPFVKYATLISNSKPESEGEQGLINSVYTKGFSSKNSPL 1020
Db 961 SVNFSEAECEVTEYDESOQROPFVKYATLISNSKPESEGEQGLINSVYTKGFSSKNSPL 1020
Qy 1021 KQSFENSSWEITAOAFILISDHPNITSPHLTFSEGLDELLEGNFPENNDRKITYYL 1080
Db 1021 KQSFENSSWEITAOAFILISDHPNITSPHLTFSEGLDELLEGNFPENNDRKITYYL 1080
Qy 1081 GVTJIKKRESGVLLDKSVSCPPFAPCLFTDIRVLDSCSHFVENNINLGTSSKRTFAS 1140
Db 1081 GVTJIKKRESGVLLDKSVSCPPFAPCLFTDIRVLDSCSHFVENNINLGTSSKRTFAS 1140
Qy 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

```

RESULT 5
US-08-640-389A-11
Sequence 11, Application US/08640389A
Patent No. 5912123

GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Clotfi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTION OF THE LEFTIN
TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-640-389A-11

Query Match 98.7% Score 6172: DB 2: length 1165;
Best Local Similarity 99.1% Pred. No. 0;
Matches 1155; Conservative 1; Mismatches 8; Indels 2; Gaps 2;

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Qy 1 MICQKPCVLLHMEFIYVITAFNLSTPIPMRFKISCMPPNSTYDYFLPAGISKNTSNS 60
Db 1 MICQKPCVLLHMEFIYVITAFNLSTPIPMRFKISCMPPNSTYDYFLPAGISKNTSNS 60
Qy 61 NGHYETAEPKFNSSGTHRSNLKTTFFHCCFNSQDRNCSLCADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAEPKFNSSGTHRSNLKTTFFHCCFNSQDRNCSLCADNIEGTFVSTVNSLVF 120
Qy 121 QQIDAMNNIQCMKLGDKLFCIVESLFRNLPFRNYKXHLIYVLEVEDSPVLVPOKGS 180
Db 121 QQIDAMNNIQCMKLGDKLFCIVESLFRNLPFRNYKXHLIYVLEVEDSPVLVPOKGS 180
Qy 181 FQWVHCNCSVHECCFLVYVPTAKLNDTLMLCKITSGGVIFQSPKSYQPIIMVVRDPP 240
Db 181 FQWVHCNCSVHECCFLVYVPTAKLNDTLMLCKITSGGVIFQSPKSYQPIIMVVRDPP 240
Qy 241 LGHMEITDGNLKISWSSPPLVPPLOQVOKYSENSTVIREADKIVSATSLVDSTLP 300
Db 241 LGHMEITDGNLKISWSSPPLVPPLOQVOKYSENSTVIREADKIVSATSLVDSTLP 300
Qy 301 GSSYEYQVGRKLDGCGISDMNSTPRVFTTQVYIYPPKILTVSGSVNSVHCYKKEKNI 360
Db 301 GSSYEYQVGRKLDGCGISDMNSTPRVFTTQVYIYPPKILTVSGSVNSVHCYKKEKNI 360
Qy 361 VPSKEIYMMNNIAEKIPQSOYDVVSDHVSQVTFPNLNETRPRKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYMMNNIAEKIPQSOYDVVSDHVSQVTFPNLNETRPRKFTYDAVYCCNEHECHH 420
Qy 421 RAELVYIDVNNISCEITDGYLTKMTCRMSTSTIOSLAESTILOLRYHRSLSYCSIDPSIH 480
Db 421 RAELVYIDVNNISCEITDGYLTKMTCRMSTSTIOSLAESTILOLRYHRSLSYCSIDPSIH 480
Qy 481 PISEPKDYLQSDGFYECIFQPIFLISGTYMIRIHSLGSLDSPICVLPDVSVPPLPP 540
Db 481 PISEPKDYLQSDGFYECIFQPIFLISGTYMIRIHSLGSLDSPICVLPDVSVPPLPP 540
Qy 541 SSVKAEITINIGLTKISMEKPFPPENNLOFOIRYGLSGKEVQWKAIEYVDASKSVSLPV 600
Db 541 SSVKAEITINIGLTKISMEKPFPPENNLOFOIRYGLSGKEVQWKAIEYVDASKSVSLPV 600
Qy 601 PDLCAVAVOVCKRLDGLGYWMSNPNAYTVYMDIKVPMRGPEFMRINIGDMKKEKNV 660
Db 601 PDLCAVAVOVCKRLDGLGYWMSNPNAYTVYMDIKVPMRGPEFMRINIGDMKKEKNV 660
Qy 661 TLIMKPLKNDLSCVQRYVINHTSCNGTWSGDVGNHTKFTFLTEQAHYTVLAINSI 720
Db 661 TLIMKPLKNDLSCVQRYVINHTSCNGTWSGDVGNHTKFTFLTEQAHYTVLAINSI 720
Qy 721 GASVANFNLFESPMKSVNIVOSLSAYPLNNSCVIYSWILSPSDYKLMFIEEMKRLNED 780
Db 721 GASVANFNLFESPMKSVNIVOSLSAYPLNNSCVIYSWILSPSDYKLMFIEEMKRLNED 780

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RESULT 7
: Sequence 8, Application US/08355888A
: Patent No. 5763211
: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. R.
: APPLICANT: Cioffi, Joseph
: APPLICANT: Zupancic, Thomas J.
: APPLICANT: Shafer, Alan W.
: TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
: TITLE OF INVENTION: RECEPTOR
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/355.888A
: FILING DATE: 14-DEC-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 7225-078
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 869-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 960 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-355-888A-8

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Query Match      77.1%; Score 4819.5; DB 1; Length 960;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

```

```

QY 1 MLCQFCVLLHMERFYVTAFTNLSYPIPMRFKLSGMPNSTYDYFLLPAGLSKNTS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3 MLCQFCVLLHMERFYVTAFTNLSYPIPMRFKLSGMPNSTYDYFLLPAGLSKNTS 62
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 NGHYTAAVEPKFNSSGTFHESNLSTKTFHCCFSEDRNCSLCADNTEGTFVSTNSLVE 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 63 NGHYTAAVEPKFNSSGTFHESNLSTKTFHCCFSEDRNCSLCADNTEGTFVSTNSLVE 122
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 QOIDANMNIOCKLKGDKLFTCYVESLFRNNYKVALLYLPEVLEDSPLVPQKGS 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 123 QOIDANMNIOCKLKGDKLFTCYVESLFRNNYKVALLYLPEVLEDSPLVPQKGS 182
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 FQMVHNCNSVHCCBCECLVVPPTAKLNDTLMLCKLITSGVIFQSPILMSVQPINMVRPDP 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 183 FQMVHNCNSVHCCBCECLVVPPTAKLNDTLMLCKLITSGVIFQSPILMSVQPINMVRPDP 242
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 LGLHMEITDDGKLKISWSSPPLVPPLOQVYKSENSTTVIRADKIVATSILVDSILP 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 243 LGLHMEITDDGKLKISWSSPPLVPPLOQVYKSENSTTVIRADKIVATSILVDSILP 302
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 GSSYEVOVGKRLDGPGLMSDSTPRVFTTODVYIFPPKILTVSGNSVNFHCYKKEKNTI 360
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DB 303 GSSYEVOVGKRLDGPGLMSDSTPRVFTTODVYIFPPKILTVSGNSVNFHCYKKEKNTI 362
QY 361 VPSKEIYMMNLAEKIPQSDYDVSDHVSQVTFEFLNLTETKPRGKFTYDAVYCCNEHECH 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 363 VPSKEIYMMNLAEKIPQSDYDVSDHVSQVTFEFLNLTETKPRGKFTYDAVYCCNEHECH 422
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 RYAEIYIDVNNINISCEYDGYLTKMTCRWSTSTQSLASTLQLRHRSLSYCSIDPSIH 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 423 RYAEIYIDVNNINISCEYDGYLTKMTCRWSTSTQSLASTLQLRHRSLSYCSIDPSIH 482
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 PISEPRDCLQSDGFEECFOPILFLISGYTMMIRINHSIGSLDSPTCVLPSPYKPLPP 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 483 PISEPRDCLQSDGFEECFOPILFLISGYTMMIRINHSIGSLDSPTCVLPSPYKPLPP 542
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 SSVKAEITINIGLILKISWEKPVPEPENNLOFQIRYGLSGKEVOYKMEYVDASKSVSLPV 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 543 SSVKAEITINIGLILKISWEKPVPEPENNLOFQIRYGLSGKEVOYKMEYVDASKSVSLPV 602
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 601 PDLCAVYAVQVRCRKLDSIGYWSNMSNPAYTVYMDIKVPMRGPEFWRITNGDTMKKEKRV 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 603 PDLCAVYAVQVRCRKLDSIGYWSNMSNPAYTVYMDIKVPMRGPEFWRITNGDTMKKEKRV 662
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 661 TLLMKPLKNDLSQVORVYINHHNHSNCTGSEDOGNHRTKFTFLMTEQAHYTVLAINSI 720
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 663 TLLMKPLKNDLSQVORVYINHHNHSNCTGSEDOGNHRTKFTFLMTEQAHYTVLAINSI 722
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 721 GASVANFNTFSPMPSKVNIVOSLSAYPLNSSCVIYSWILSPDYKLMWFIEMKLNLD 780
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 723 GASVANFNTFSPMPSKVNIVOSLSAYPLNSSCVIYSWILSPDYKLMWFIEMKLNLD 782
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 781 GEIKWLRISSVYKYYIHDFIPIEKYQSLVPIEMEGYKPKIINSFTODIEKHQSDA 840
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 783 GEIKWLRISSVYKYYIHDFIPIEKYQSLVPIEMEGYKPKIINSFTODIEKHQSDA 842
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 841 GLVYIVPVIISSIIILGTLISHSORMKLFMEDVNPNCNSAAGLNOK-----DE 893
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 843 GLVYIVPVIISSIIILGTLISHSORMKLFMEDVNPNCNSAAGLNOK-----DE 902
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 894 TFEHLFIKHT-ASYTCGP-----LLEPETISEDLSYDTSKKNDE 933
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 903 SHHHSLSSTQGHKRGGRQGPLHRTKRLDCLSLVYLLTLPPLISTYPAKSPVRRNQE 960
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```

```

RESULT 8
: Sequence 8, Application US/08693697
: Patent No. 5869610
: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. R.
: APPLICANT: Cioffi, Joseph
: APPLICANT: Zupancic, Thomas J.
: APPLICANT: Shafer, Alan W.
: TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
: TITLE OF INVENTION: RECEPTOR
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/693.697
: FILING DATE: 05-AUG-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.

```

REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 8907-0037-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TELETYPE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 960 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-693-697-8

Query Match 77.1%; Score 4819.5; DB 2; Length 960;
 Best Local Similarity 94.1%; Pred. No. 0;
 Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICOFCVLLHMERIYITAFNLSTPTPMRFKLSCLMPNSTYDFLLPAGLSKNTNS 60
 DB 3 MICOFCVLLHMERIYITAFNLSTPTPMRFKLSCLMPNSTYDFLLPAGLSKNTNS 62
 QY 61 NGHYETAEPKNSGTHFSNLSTKTHPCFRSEODRNCISLCAONIIEKTEFVSTNSLVF 120
 DB 63 NGHYETAEPKNSGTHFSNLSTKTHPCFRSEODRNCISLCAONIIEKTEFVSTNSLVF 122
 QY 121 QOIDANMNIOQWLKGLDLFLICYVESLEFKNLFRNRYKVHLLYVLEVEDSPLYPOKGS 180
 DB 123 QOIDANMNIOQWLKGLDLFLICYVESLEFKNLFRNRYKVHLLYVLEVEDSPLYPOKGS 182
 QY 181 FQWVHCNSVHECCCECLPVVPYAKLNDLILMLKITSGVITQSPKMSVOPINMKPPDP 240
 DB 183 FQWVHCNSVHECCCECLPVVPYAKLNDLILMLKITSGVITQSPKMSVOPINMKPPDP 242
 QY 241 LGLHMEITDDGWLKISWSSPPLVPPLOYVYSENSTTVIREAKIYASLSLVDSTLP 300
 DB 243 LGLHMEITDDGWLKISWSSPPLVPPLOYVYSENSTTVIREAKIYASLSLVDSTLP 302
 QY 301 GSSYEVQVGRKRLDGLGIMSDMSTPRVFTYDVIYFPKILNSVGSNVSFCIYKREKNT 360
 DB 303 GSSYEVQVGRKRLDGLGIMSDMSTPRVFTYDVIYFPKILNSVGSNVSFCIYKREKNT 362
 QY 361 VPSKRIYMMNIAEKIPQSDYVSDHYSKVTFENLNEKPRGKTTDYAVYCNHECHH 420
 DB 363 VPSKRIYMMNIAEKIPQSDYVSDHYSKVTFENLNEKPRGKTTDYAVYCNHECHH 422
 QY 421 RYAEIYVIDVNIINISCEITDGYLTMTGCRNSTTQSLAESTQLRYHRSLSYCSIPSIH 480
 DB 423 RYAEIYVIDVNIINISCEITDGYLTMTGCRNSTTQSLAESTQLRYHRSLSYCSIPSIH 482
 QY 481 PISEPKDCYLGSDGFYECIFQPIFLLSGYTWIRINHSIGSLDSPPTCVLPDYSVKPLPP 540
 DB 483 PISEPKDCYLGSDGFYECIFQPIFLLSGYTWIRINHSIGSLDSPPTCVLPDYSVKPLPP 542
 QY 541 SSVKAEITINIGLKIYSMEKRPVPENNLQFOIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
 DB 543 SSVKAEITINIGLKIYSMEKRPVPENNLQFOIRYGLSGKEVQWKMYEYDAKSKSVSLPV 602
 QY 601 PDLCAVYVAVQVCKRLDGLGIMSNMSPAYVYMDIKVPMRQPERWRIINGDTMKKEKNV 660
 DB 603 PDLCAVYVAVQVCKRLDGLGIMSNMSPAYVYMDIKVPMRQPERWRIINGDTMKKEKNV 662
 QY 661 TLLMKPLKNDLSICVQRYVINHTSCNGTWSGSEVDGNHTKFFLTDEDAHPTVLAISNI 720
 DB 663 TLLMKPLKNDLSICVQRYVINHTSCNGTWSGSEVDGNHTKFFLTDEDAHPTVLAISNI 722
 QY 721 GASVANFULTSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIIEWKNLMD 780
 DB 723 GASVANFULTSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIIEWKNLMD 782
 QY 781 GEIKRLRISSSVKKYIYIHDFIPIEKYQSLYPIFMEGVGKPKILNSTODDIEKHQSDA 840

DB 783 GEIKRLRISSSVKKYIYIHDFIPIEKYQSLYPIFMEGVGKPKILNSTODDIEKHQSDA 842
 QY 841 GLYIVPIYIISSSILLGTLLISHQRMKLEFEDVYPNKNCMAQNLFOK-----PE 893
 DB 843 GLYIVPIYIISSSILLGTLLISHQRMKLEFEDVYPNKNCMAQNLFOKLEBSMFKV 902
 QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISDIDSVTSWKKDE 933
 DB 903 SHHNSLISSTQGHKGRPOGLHRRTRDLSLVLLPLLSYDPAKSPSVRTOE 960

RESULT 9
 US-08-640-389A-3
 Sequence 3, Application US/08640389A
 Patent No. 5912123

GENERAL INFORMATION:
 APPLICANT: Snodgrass, H. R.
 APPLICANT: Cioffi, Joseph
 APPLICANT: Zupancic, Thomas J.
 APPLICANT: Shater, Alan W.
 TITLE OF INVENTION: DETECTION OF THE LEPTIN
 TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
 TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/640,389A
 FILING DATE: 29-Apr-1996

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Poissant, Brian M.
 REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 8907-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELETYPE: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 960 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-640-389A-3

Query Match 77.1%; Score 4819.5; DB 2; Length 960;
 Best Local Similarity 94.1%; Pred. No. 0;
 Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICOFCVLLHMERIYITAFNLSTPTPMRFKLSCLMPNSTYDFLLPAGLSKNTNS 60
 DB 3 MICOFCVLLHMERIYITAFNLSTPTPMRFKLSCLMPNSTYDFLLPAGLSKNTNS 62
 QY 61 NGHYETAEPKNSGTHFSNLSTKTHPCFRSEODRNCISLCAONIIEKTEFVSTNSLVF 120
 DB 63 NGHYETAEPKNSGTHFSNLSTKTHPCFRSEODRNCISLCAONIIEKTEFVSTNSLVF 122
 QY 121 QOIDANMNIOQWLKGLDLFLICYVESLEFKNLFRNRYKVHLLYVLEVEDSPLYPOKGS 180
 DB 123 QOIDANMNIOQWLKGLDLFLICYVESLEFKNLFRNRYKVHLLYVLEVEDSPLYPOKGS 182

QY 181 FQMHNCNSVHECCCECLVPTAKLNDTLMLCLITSGVIFQSPMLNSVOYINMKPPDP 240
Db 183 FQMHNCNSVHECCCECLVPTAKLNDTLMLCLITSGVIFRSLMSVOYINMKPPDP 242
QY 241 LGLHMETIDDDGNLKISSMSPPLVPPLOQYKYSNSSTTVIREADKIVSATSILVDSILP 300
Db 243 LGLHMETIDDDGNLKISSMSPPLVPPLOQYKYSNSSTTVIREADKIVSATSILVDSILP 302
QY 301 GSSYEVOYRGKRLDGPGLMSDMSPTPRVFTQDVLYFPFKILTSGVSNVSPHCITYKKENKI 360
Db 303 GSSYEVOYRGKRLDGPGLMSDMSPTPRVFTQDVLYFPFKILTSGVSNVSPHCITYKKENKI 362
QY 361 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSKEYTFENLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSKEYTFENLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVDVNNINISCEFDGYLTMTCKRMSSTIOSLAESTLOLRYHSSLYCSDIPSIH 480
Db 423 RYAEIYVDVNNINISCEFDGYLTMTCKRMSSTIOSLAESTLOLRYHSSLYCSDIPSIH 482
QY 481 PISEPKDCYLOSDFEYECIFQPIFILSGYTMIRINHSLSGLSDSPPTCVLPDSVYKPLPP 540
Db 483 PISEPKDCYLOSDFEYECIFQPIFILSGYTMIRINHSLSGLSDSPPTCVLPDSVYKPLPP 542
QY 541 SSVKAEITINIGLKIISWEKVPFENNLOFOIRYGLSGKEVQMKMYEYVDAKSKVSLPV 600
Db 543 SSVKAEITINIGLKIISWEKVPFENNLOFOIRYGLSGKEVQMKMYEYVDAKSKVSLPV 602
QY 601 PDLCAVYAVOYRCKRLDGLGYMSNNSNPATYVMDIKYPMGCPREWRRIINDGTMKKEKNV 660
Db 603 PDLCAVYAVOYRCKRLDGLGYMSNNSNPATYVMDIKYPMGCPREWRRIINDGTMKKEKNV 662
QY 661 TLLMKPLKNDLSGVQRYVINHTSCNGTSESDVGNHTKFTFLMTBOAHFTVLAINSI 720
Db 663 TLLMKPLKNDLSGVQRYVINHTSCNGTSESDVGNHTKFTFLMTBOAHFTVLAINSI 722
QY 721 GASVANFULTSPWPKSKNIYQSLATYPLNNSCVATSWILSPDKMLFIITEMKNLMD 780
Db 723 GASVANFULTSPWPKSKNIYQSLATYPLNNSCVATSWILSPDKMLFIITEMKNLMD 782
QY 781 GEIKMLRISSSVKYYIHDFPIPIEKYOFSLYPIFMEGVGPKIINSTODDIEKHOSDA 840
Db 783 GEIKMLRISSSVKYYIHDFPIPIEKYOFSLYPIFMEGVGPKIINSTODDIEKHOSDA 842
QY 841 GLYVIVPYIISSTILGLTLLISHQRMKKLFMEDVYPNFKNSMAOGLNFQK-----PE 893
Db 843 GLYVIVPYIISSTILGLTLLISHQRMKKLFMEDVYPNFKNSMAOGLNFQKLEGSMEYK 902
QY 894 TPEHLEFTRHT-ASYTCGP-----LLEPETISDISVDISWKKKDE 933
Db 903 SHHSLISTQGHKHCGRPOGPLRHKTRDLCSLVYLTLPLLSYDPAKSPSVRTQOE 960

RESULT 10
US-08-693-696-8
Sequence 8, Application US/08693696
Patent No. 6005080
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: HQ-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,888
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-693-696-8

Query Match 77.1%; Score 4819.5; DB 3; Length 960;
Best Local Similarity 94.1%; Pred. NO. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVALLHMERFIYVITAFNLISYPTIPWRFKLSGMPNNTYDYFLPAGLSKNTSNS 60
Db 3 MICQKFCVALLHMERFIYVITAFNLISYPTIPWRFKLSGMPNNTYDYFLPAGLSKNTSNS 62
QY 61 NGHYTAVEPKPNSGTHPSNLSKTTFHCCFSEEDRNCSLCADNIEGTFYVSNLSVF 120
Db 63 NGHYTAVEPKPNSGTHPSNLSKATFHCCFSEEDRNCSLCADNIEGTFYVSNLSVF 122
QY 121 QOIIDANNINOCGLKEDLKFICVYESLFRNNRYVHLVYLYPEVLEDSPLVPQKS 180
Db 123 QOIIDANNINOCGLKEDLKFICVYESLFRNNRYVHLVYLYPEVLEDSPLVPQKS 182
QY 181 FQMHNCNSVHECCCECLVPTAKLNDTLMLCLITSGVIFQSPMLNSVOYINMKPPDP 240
Db 183 FQMHNCNSVHECCCECLVPTAKLNDTLMLCLITSGVIFRSLMSVOYINMKPPDP 242
QY 241 LGLHMETIDDDGNLKISSMSPPLVPPLOQYKYSNSSTTVIREADKIVSATSILVDSILP 300
Db 243 LGLHMETIDDDGNLKISSMSPPLVPPLOQYKYSNSSTTVIREADKIVSATSILVDSILP 302
QY 301 GSSYEVOYRGKRLDGPGLMSDMSPTPRVFTQDVLYFPFKILTSGVSNVSPHCITYKKENKI 360
Db 303 GSSYEVOYRGKRLDGPGLMSDMSPTPRVFTQDVLYFPFKILTSGVSNVSPHCITYKKENKI 362
QY 361 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSKEYTFENLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSKEYTFENLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVDVNNINISCEFDGYLTMTCKRMSSTIOSLAESTLOLRYHSSLYCSDIPSIH 480
Db 423 RYAEIYVDVNNINISCEFDGYLTMTCKRMSSTIOSLAESTLOLRYHSSLYCSDIPSIH 482
QY 481 PISEPKDCYLOSDFEYECIFQPIFILSGYTMIRINHSLSGLSDSPPTCVLPDSVYKPLPP 540
Db 483 PISEPKDCYLOSDFEYECIFQPIFILSGYTMIRINHSLSGLSDSPPTCVLPDSVYKPLPP 542
QY 541 SSVKAEITINIGLKIISWEKVPFENNLOFOIRYGLSGKEVQMKMYEYVDAKSKVSLPV 600
Db 543 SSVKAEITINIGLKIISWEKVPFENNLOFOIRYGLSGKEVQMKMYEYVDAKSKVSLPV 602
QY 601 PDLCAVYAVOYRCKRLDGLGYMSNNSNPATYVMDIKYPMGCPREWRRIINDGTMKKEKNV 660

Db 603 PDLCAVAVAVQVCKRDLGIGVWSNMSNPAYTYVMDIKVPMRGPETWRIINGDTMKREKNV 662
Qy 661 TLLMKPLKNDLSICVQRYVINHTSCNGTMSSEVGNHTKFTFLMTQAHVTVLAINSI 720
Db 663 TLLMKPLKNDLSICVQRYVINHTSCNGTMSSEVGNHTKFTFLMTQAHVTVLAINSI 722
Qy 721 GASVANFNLTFSPMSKVNIVQSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLND 780
Db 723 GASVANFNLTFSPMSKVNIVQSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLND 782
Qy 781 GEIKMLRISSSVKYKYYIHDFPIEKYQSLYPIFMEGVGRKLIINSFODDIEKHQSDA 840
Db 783 GEIKMLRISSSVKYKYYIHDFPIEKYQSLYPIFMEGVGRKLIINSFODDIEKHQSDA 842
Qy 841 GLYIVAVPIISSILLGLTLISHQRMKLFMEDVYPNPKNCMAOGLNFOK-----PE 893
Db 843 GLYIVAVPIISSILLGLTLISHQRMKLFMEDVYPNPKNCMAOGLNFOKLESMFYK 902
Qy 894 TFEHLPIKHT-ASVTCGP-----LLEPETISDIDSVISWKNKDE 933
Db 903 SHHNSLISTQGHKCHGPRQGLHRRKTRDLSLVYLLPLLSYDPAKSPSVRNTQOE 960

RESULT 11

US-08-693-697-33
; Sequence 33, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: HU-BI.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-5556
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-693-697-33

Query Match 77.0% Score 4816; DB 2: Length 908;
Best Local Similarity 99.1% Pred. No. 0;

Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
Qy 1 MICQKFCVLLHMEFTIYTAENLSYPIPMRFKLSCHPNSYDYFLPPLAGLSKNTSNS 60
Db 3 MICQKFCVLLHMEFTIYTAENLSYPIPMRFKLSCHPNSYDYFLPPLAGLSKNTSNS 62
Qy 61 NGHETAVEPKNSSGTHFSNLSKTTFHCCFSEDDRCNSLACADINECKTFSTVNSLVF 120
Db 63 NGHETAVEPKNSSGTHFSNLSKATFHCCFSEDDRCNSLACADINECKTFSTVNSLVF 122
Qy 121 QOIDANMNIOCKLKGDKLFICYVESLFKNLFRNNYKHLVYLPVEVLEDSPLVPOKGS 180
Db 123 QOIDANMNIOCKLKGDKLFICYVESLFKNLFRNNYKHLVYLPVEVLEDSPLVPOKGS 182
Qy 181 FQMVHNCNSVHECCCLVPPVPAKLDLTLMLCKITTSQGVIFQSPDMSVOPINWKPDPDP 240
Db 183 FQMVHNCNSVHECCCLVPPVPAKLDLTLMLCKITTSQGVIFQSPDMSVOPINWKPDPDP 242
Qy 241 LGLHMEITDDGNLKISMSSPPLVPPLOYQVYKSENSSTVIREAKIYVSATSLVDSTLP 300
Db 243 LGLHMEITDDGNLKISMSSPPLVPPLOYQVYKSENSSTVIREADKIVSATSLLVDSTLP 302
Qy 301 GSSYEVQYRGKRLDGPGLMSDMSTPRVFTTODVIFYEPFKILTSVGSNSVFCIYKKNKI 360
Db 303 GSSYEVQYRGKRLDGPGLMSDMSTPRVFTTODVIFYEPFKILTSVGSNSVFCIYKKNKI 362
Qy 361 VPSKEIYVMNMLAEKIPQSOYDVSDHYSKYTFENLNETKPRGKFTYDAVYCCNHECHH 420
Db 363 VPSKEIYVMNMLAEKIPQSOYDVSDHYSKYTFENLNETKPRGKFTYDAVYCCNHECHH 422
Qy 421 RYAEIYVIDVNNINISCEFDGYITKMTCKMSTSTIOSLAESTLOLRHHSSLYCSIPSLH 480
Db 423 RYAEIYVIDVNNINISCEFDGYITKMTCKMSTSTIOSLAESTLOLRHHSSLYCSIPSLH 482
Qy 481 PISEPKDYLQSDGFECEIFOPIFLLSGYTMWIRLNHSGSLDSPICVLPDSVYKPLPP 540
Db 483 PISEPKDYLQSDGFECEIFOPIFLLSGYTMWIRLNHSGSLDSPICVLPDSVYKPLPP 542
Qy 541 SSVKAETINIGLKTISMEKPYFPENNLOFQIRYGLSGKEVOMKRYEYVDAKSQSVSLPV 600
Db 543 SSVKAETINIGLKTISMEKPYFPENNLOFQIRYGLSGKEVOMKRYEYVDAKSQSVSLPV 602
Qy 601 PDLCAVAVAVQVCKRDLGIGVWSNMSNPAYTYVMDIKVPMRGPETWRIINGDTMKREKNV 660
Db 603 PDLCAVAVAVQVCKRDLGIGVWSNMSNPAYTYVMDIKVPMRGPETWRIINGDTMKREKNV 662
Qy 661 TLLMKPLKNDLSICVQRYVINHTSCNGTMSSEVGNHTKFTFLMTQAHVTVLAINSI 720
Db 663 TLLMKPLKNDLSICVQRYVINHTSCNGTMSSEVGNHTKFTFLMTQAHVTVLAINSI 722
Qy 721 GASVANFNLTFSPMSKVNIVQSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLND 780
Db 723 GASVANFNLTFSPMSKVNIVQSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLND 782
Qy 781 GEIKMLRISSSVKYKYYIHDFPIEKYQSLYPIFMEGVGRKLIINSFODDIEKHQSDA 840
Db 783 GEIKMLRISSSVKYKYYIHDFPIEKYQSLYPIFMEGVGRKLIINSFODDIEKHQSDA 842
Qy 841 GLYIVAVPIISSILLGLTLISHQRMKLFMEDVYPNPKNCMAOGLNFOK--PETPHL 898
Db 843 GLYIVAVPIISSILLGLTLISHQRMKLFMEDVYPNPKNCMAOGLNFOKPKMGETKELL 902

RESULT 12

US-08-588-190-3
; Sequence 3, Application US/08588190
; Patent No. 5856098
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: DETECTION OF A LEFTIN RECEPTOR

```

: TITLE OF INVENTION: VARIANT AND METHODS FOR REGULATING OBESITY
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of The Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036-2811
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/588,190
: FILING DATE: 18-JAN-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 008907-0029-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-493-4935
: TELEFAX: 650-493-5556
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 960 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-588-190-3

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Query Match          77.0%; Score 4814.5; DB 2; Length 960;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 900; Conservative 7; Mismatches 26; Indels 25; Gaps 3;

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QY 1 MICGFCVLLHMEIYITAFNLSTPTPMPFKLSKMPNSTYDFLLPAGLSKNTS 60
DB 3 MICGFCVLLHMEIYITAFNLSTPTPMPFKLSKMPNSTYDFLLPAGLSKNTS 62
QY 61 NGHETAEKPEKNSGTHFSKTHHCCFRSEDRNCSICADNIEKTFSTYNSLVE 120
DB 63 NGHETAEKPEKNSGTHFSKTHHCCFRSEDRNCSICADNIEKTFSTYNSLVE 122
QY 121 QOIDANMNIQCMKGLDKLFLCYVESLFKNLFRNRYNYKHLLYLPEVLEDSPLVPKGS 180
DB 123 QOIDANMNIQCMKGLDKLFLCYVESLFKNLFRNRYNYKHLLYLPEVLEDSPLVPKGS 182
QY 181 FQWVHCNCSVHECCCELVVPFAKINDTLMLCKLITSGGVLFQSPPLMSVQPINWKPDP 240
DB 183 FQWVHCNCSVHECCCELVVPFAKINDTLMLCKLITSGGVLFQSPPLMSVQPINWKPDP 242
QY 241 LGLHMETDDCNLKSMSSPPLVPPLOYOYKYSNSTTVIREAKIYSATSLVDSILP 300
DB 243 LGLHMETDDCNLKSMSSPPLVPPLOYOYKYSNSTTVIREAKIYSATSLVDSILP 302
QY 301 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTDDVIPEPKILTSVGSNVSEHCITKKENKI 360
DB 303 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTDDVIPEPKILTSVGSNVSEHCITKKENKI 362
QY 361 VPSKEIVMMNLAEKIPQSOYDVVSDHYSKYTFENLNETKPRGKFTYAVVYCCNEHECHH 420
DB 363 VPSKEIVMMNLAEKIPQSOYDVVSDHYSKYTFENLNETKPRGKFTYAVVYCCNEHECHH 422
QY 421 RYAEIYVDVNNINISCEFDGKITKTKCWSTSTIOSLAESTIQLKRYHSSLYCSIDPSIH 480

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DB 423 RYAEIYVDVNNINISCEFDGKITKTKCWSTSTIOSLAESTIQLKRYHSSLYCSIDPSIH 482
QY 481 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMWIRINHSIGSDSPFCVLPDSYVKKPLP 540
DB 483 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMWIRINHSIGSDSPFCVLPDSYVKKPLP 542
QY 541 SSYKAEITINIGLKTIWEKPEPENNLOFOIRYGLSGREYQWKYEVYDAKSKSVSLPV 600
DB 543 SSYKAEITINIGLKTIWEKPEPENNLOFOIRYGLSGREYQWKYEVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCRKLDELGLGYSNMSNPAITYVMDIKYPMGPEWRIINDTKKKNV 660
DB 603 PDLCAVYAVQVRCRKLDELGLGYSNMSNPAITYVMDIKYPMGPEWRIINDTKKKNV 662
QY 661 TLMKPLKKNNSLCVQRYVINHHTSCNGTSEDEGNGHTKFFLWTEDAHYTVLAISI 720
DB 663 TLMKPLKKNNSLCVQRYVINHHTSCNGTSEDEGNGHTKFFLWTEDAHYTVLAISI 722
QY 721 GASVANFNLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPDYKLMVFIIEMKNLMD 780
DB 723 GASVANFNLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPDYKLMVFIIEMKNLMD 782
QY 781 GEIKMLRISSSVKKYIINDHPIPIEKYQPSLYPTMEGVGKRIINSTODDIEKHQSDA 840
DB 783 GEIKMLRISSSVKKYIINDHPIPIEKYQPSLYPTMEGVGKRIINSTODDIEKHQSDA 842
QY 841 GLYVIVPVISSSILLGTLISHQMKKLFEDVPPNPKNCMAOGLNFOK-----PE 893
DB 843 GLYVIVPVISSSILLGTLISHQMKKLFEDVPPNPKNCMAOGLNFOK-----PE 902
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISDISVDSWKMKDE 933
DB 903 SHHSLISSGQHKHKGHPQGLHRRKTRDLSLVYLLTLPILLSYDPAKSPSVRNTQE 960

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RESULT 13
US-08-618-957A-3
: Sequence 3, Application US/08618957A
: Patent No. 6355237
: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. Ralph
: APPLICANT: Cioffi, Joseph
: APPLICANT: Zupancic, Thomas Joel
: APPLICANT: Shafer, Alan Wayne
: TITLE OF INVENTION: METHODS FOR USING THE OBSE
: TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
: TITLE OF INVENTION: DEVELOPMENT
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of The Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036-2811
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/618,957A
: FILING DATE: 20-MAR-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 008907-0033-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-493-4935

```

TELEFAX: 650-493-5556
 TELE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 960 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-618-957A-3

Query Match 77.0%; Score 4814.5; DB 4; Length 960;
 Best Local Similarity 93.9%; Pred. No. 0;
 Matches 900; Conservative 7; Mismatches 26; Indels 25; Gaps 3;

1 MICQRCVLLHMEFYITAFNLSPITPMRFKLSCMPNSTYDFLLPAGLSKNTS 60
 3 MICQRCVLLHMEFYITAFNLSPITPMRFKLSCMPNSTYDFLLPAGLSKNTS 62
 61 NGHYTAEVPEKNSGTHSNLSKTTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
 63 NGHYTAEVPEKNSGTHSNLSKATFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 122
 121 QOIDANMNIOCLKDKLKFICYVESLFKNLFRNRYKYHLLYVLPVLEDSPLVPQKS 180
 123 QOIDANMNIOCLKDKLKFICYVESLFKNLFRNRYKYHLLYVLPVLEDSPLVPQKS 182
 181 FQMHVNCNSVHECCCLVLPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMKPDPP 240
 183 FQMHVNCNSVHECCCLVLPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMKPDPP 242
 241 LGLHMEITDDGNLKTISWSSPLVPPLOYQVYKSENSTVIREADKIYATSILVDSILP 300
 243 LGLHMEITDDGNLKTISWSSPLVPPLOYQVYKSENSTVIREADKIYATSILVDSILP 302
 301 GSSYEVQVGRKLDGPGTMSDSTPRVFTODVITYFPFKILTSVGSNVSFHCITYKKENKI 360
 303 GSSYEVQVGRKLDGPGTMSDSTPRVFTODVITYFPFKILTSVGSNVSFHCITYKKENKI 362
 361 VPSKEIVMMNLAEKIPQSOYDVSDVHSKYTFEFLNETKPRGKFTYADVCCNEHECHH 420
 363 VPSKEIVMMNLAEKIPQSOYDVSDVHSKYTFEFLNETKPRGKFTYADVCCNEHECHH 422
 421 RRAELIYDVNINISCEFDGILTAKTCRWSTSTIOSLAESTLQLRHNSLYCSDIPSIH 480
 423 RRAELIYDVNINISCEFDGILTAKTCRWSTSTIOSLAESTLQLRHNSLYCSDIPSIH 482
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 483 PISEPKDCYLOSDFEYECIFOPIFILSGTWMIRINHSLSGLDSPPTCVLPDSVVKPLPP 542
 541 SSVKAETINIGLKTISMEKPVFPENNLOFOIRYGLSGREYOMKYEYVDASKSVSLPV 600
 543 SSVKAETINIGLKTISMEKPVFPENNLOFOIRYGLSGREYOMKYEYVDASKSVSLPV 602
 601 PDLCAVYAVQVCKRLDGLGYSNNSNPATYVMDIKYPMRGPPEFRRIINGDTMKKEKV 660
 603 PDLCAVYAVQVCKRLDGLGYSNNSNPATYVMDIKYPMRGPPEFRRIINGDTMKKEKV 662
 661 TLLMKPLKNDSLGVORVYINHTSCNGTMSDYGNNHKTFLMTEDQAHYTVLAINSI 720
 663 TLLMKPLKNDSLGVORVYINHTSCNGTMSDYGNNHKTFLMTEDQAHYTVLAINSI 722
 721 GASVANFNLTSWPMKSVNIYOSLSAYPLNSCIVSWILSPSDYKLMFYIEMNLNED 780
 723 GASVANFNLTSWPMKSVNIYOSLSAYPLNSCIVSWILSPSDYKLMFYIEMNLNED 782
 781 GEIKLRLISSYKYYIHDFPIPIEKYQSLPIFMEGVGKPKIINSTODDIEKHQSDA 840
 783 GEIKLRLISSYKYYIHDFPIPIEKYQSLPIFMEGVGKPKIINSTODDIEKHQSDA 842
 841 GLYIVPVISSILLGLTLLISHQRMKKLFWEVDVNPFRKNCMAGLNFQK-----PE 893

DB 843 GLYIVPVISSILLGLTLLISHQRMKKLFWEVDVNPFRKNCMAGLNFQKLEGSMPVK 902
 QY 894 TFEHFIKHT-ASVTCG-----LLEPEISDYSVDTGKNKDE 933
 DB 903 SHHSLISTGCKHCKGRCGPGPLHRTKTRDLCILVILLTLPPLSIDPAPSPVRYTQE 960

RESULT 14
 US-08-618-957A-10
 ; Sequence 10, Application US/08618957A
 ; Patent No. 6355237
 ; GENERAL INFORMATION:
 ; APPLICANT: Snodgrass, H. Ralph
 ; APPLICANT: Cioffi, Joseph
 ; APPLICANT: Zupancic, Thomas Joel
 ; APPLICANT: Shaffer, Alan Wayne
 ; TITLE OF INVENTION: METHODS FOR USING THE OBSE
 ; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of The Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/618, 957A
 ; FILING DATE: 20-MAR-1996
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; PRIORITY APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Polissant, Brian M.
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 008907-0033-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; SEQUENCE CHARACTERISTICS:
 ; INFORMATION FOR SEQ ID NO: 10:
 ; LENGTH: 896 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-618-957A-10

Query Match 77.0%; Score 4814; DB 4; Length 896;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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 1 MICQRCVLLHMEFYITAFNLSPITPMRFKLSCMPNSTYDFLLPAGLSKNTS 60
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 61 NGHYTAEVPEKNSGTHSNLSKATFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
 121 QOIDANMNIOCLKDKLKFICYVESLFKNLFRNRYKYHLLYVLPVLEDSPLVPQKS 180
 121 QOIDANMNIOCLKDKLKFICYVESLFKNLFRNRYKYHLLYVLPVLEDSPLVPQKS 180


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QY 181 FQMHGNCNVHECCCLVPPVPAKNDTLMLCKITSGGVIFQSPILMSVQPINMKVDPDP 240
DB 181 FQMHGNCNVHECCCLVPPVPAKNDTLMLCKITSGGVIFRSPILMSVQPINMKVDPDP 240
QY 241 LGLHEITDDGNLKTSMSSPPLVPPLOQYQVYKSNSTTVIREAKIYVATSILVDSILP 300
DB 241 LGLHEITDDGNLKTSMSSPPLVPPLOQYQVYKSNSTTVIREAKIYVATSILVDSILP 300
QY 301 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTTODVIFPPKILTVSGSNVSFHCITYKKEKNI 360
DB 301 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTTODVIFPPKILTVSGSNVSFHCITYKKEKNI 360
QY 361 VPSKEITVMMNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEITVMMNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIVIDVNNINISCEIDGYLTIKMTCRMSTSTIOSLAESTOLRYHRSLSLCSIDPSIH 480
DB 421 RYAEIVIDVNNINISCEIDGYLTIKMTCRMSTSTIOSLAESTOLRYHRSLSLCSIDPSIH 480
QY 481 PISEKDCYLOSDFGEYECIFQPIFLISGYTMMIRINHSIGSLDSEPTCYLPDSVYKPLPP 540
DB 481 PISEKDCYLOSDFGEYECIFQPIFLISGYTMMIRINHSIGSLDSEPTCYLPDSVYKPLPP 540
QY 541 SSYKAEITINIGLKTISWEKVPFPENNLOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
DB 541 SSYKAEITINIGLKTISWEKVPFPENNLOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVOVCKRDLGIGYWSNMSNPAYTYVMDIKVPMRGPEFRILNGDTMKKEKAV 660
DB 601 PDLCAVYAVOVCKRDLGIGYWSNMSNPAYTYVMDIKVPMRGPEFRILNGDTMKKEKAV 660
QY 661 TLAKPLMKNDLSICVQRYVINHHTSCNGTWSGDNHRTFTLMEQAHYTVLAINSI 720
DB 661 TLAKPLMKNDLSICVQRYVINHHTSCNGTWSGDNHRTFTLMEQAHYTVLAINSI 720
QY 721 GASVANFNLTSPMSKYNIVOSLSAYPLNSSCVIYWSILSPSDYKLMFTIEKMLNED 780
DB 721 GASVANFNLTSPMSKYNIVOSLSAYPLNSSCVIYWSILSPSDYKLMFTIEKMLNED 780
QY 781 GRIMKLRISSSVKYYIHDFPIEKYOFLPIFMEGKGRKTIINSFQODDIEKHQSDA 840
DB 781 GRIMKLRISSSVKYYIHDFPIEKYOFLPIFMEGKGRKTIINSFQODDIEKHQSDA 840
QY 841 GLYIVIVPILSSILLGLTLLISHQRMKLFWEDEVNPNKNCMAQGLNFOK 891
DB 841 GLYIVIVPILSSILLGLTLLISHQRMKLFWEDEVNPNKNCMAQGLNFOK 891

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RESULT 15
US-08-693-697-36
Sequence 36, Application US/08693697
Patent No. 5869610

GENERAL INFORMATION:
APPLICANT: Smogdass, H. R.
APPLICANT: Clotoff, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-693-697-36

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Query Match 77.0%; Score 4814; DB 2; Length 898;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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DB 3 MICOKRCVLLHMEFYVTAFNLSPITPMRFKLSGMPNPNYDVELLPAGISKRTNS 62
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DB 63 NGHYETAVEPKENSSGTHRSNLKATFHCCFRSEODRNCSLCADNIEGTFTVSTNSLVF 122
QY 121 QQIDANNNIQQCMKGLKLPICYVESLFKNLFRNNYKXKHLILVLPVLEDESPVYQKKS 180
DB 123 QQIDANNNIQQCMKGLKLPICYVESLFKNLFRNNYKXKHLILVLPVLEDESPVYQKKS 182
QY 181 FQMHGNCNVHECCCLVPPVPAKNDTLMLCKITSGGVIFQSPILMSVQPINMKVDPDP 240
DB 183 FQMHGNCNVHECCCLVPPVPAKNDTLMLCKITSGGVIFRSPILMSVQPINMKVDPDP 242
QY 241 LGLHEITDDGNLKTSMSSPPLVPPLOQYQVYKSNSTTVIREAKIYVATSILVDSILP 300
DB 243 LGLHEITDDGNLKTSMSSPPLVPPLOQYQVYKSNSTTVIREAKIYVATSILVDSILP 302
QY 301 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTTODVIFPPKILTVSGSNVSFHCITYKKEKNI 360
DB 303 GSSYEVQVGRKRLDGPGLMSDMSPTPRVFTTODVIFPPKILTVSGSNVSFHCITYKKEKNI 362
QY 361 VPSKEITVMMNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
DB 363 VPSKEITVMMNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIVIDVNNINISCEIDGYLTIKMTCRMSTSTIOSLAESTOLRYHRSLSLCSIDPSIH 480
DB 423 RYAEIVIDVNNINISCEIDGYLTIKMTCRMSTSTIOSLAESTOLRYHRSLSLCSIDPSIH 482
QY 481 PISEKDCYLOSDFGEYECIFQPIFLISGYTMMIRINHSIGSLDSEPTCYLPDSVYKPLPP 540
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QY 601 PDLCAVYAVOVCKRDLGIGYWSNMSNPAYTYVMDIKVPMRGPEFRILNGDTMKKEKAV 660
DB 603 PDLCAVYAVOVCKRDLGIGYWSNMSNPAYTYVMDIKVPMRGPEFRILNGDTMKKEKAV 662
QY 661 TLAKPLMKNDLSICVQRYVINHHTSCNGTWSGDNHRTFTLMEQAHYTVLAINSI 720

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Db 663 TLLMKPLMKNDLSCVQRYVINHHHTSCNCTWSEEDYGNHTKFTFLMTQEAHTVTYLAINSI 722
Qy 721 GASVANFNLTFSWPMKSKVNIYOSLSAYPLNNSCVIYSATLSPSDYKLMFTLEKKNLND 780
Db 723 GASVANFNLTFSWPMKSKVNIYOSLSAYPLNNSCVIYSATLSPSDYKLMFTLEKKNLND 782
Qy 781 GEIKMLRISSSVKYYIHDHFIPIEKYOPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKMLRISSSVKYYIHDHFIPIEKYOPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
Qy 841 GLYIVPVITISSILLGTLLISHQRMKLFWEEDVVPNPNKNCMAOGLNFQK 891
Db 843 GLYIVPVITISSILLGTLLISHQRMKLFWEEDVVPNPNKNCMAOGLNFQK 893
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Search completed: May 18, 2002, 06:53:57
Job time: 5722 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 07:00:11 ; Search time 24.69 Seconds

(without alignments)
4533.984 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 1165

Sequence: 1 MICOQFCVVLHMEFIYIT.....QFCSTQTHKIMENKMDLTV 1165

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database: PIR_71.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	3.6	805	2	S68441
2	42	3.6	892	2	S68439
3	42	3.6	900	2	S68437
4	42	3.6	904	2	S68440
5	42	3.6	1162	2	S68438
6	42	3.6	1162	2	PC4184
7	41	3.5	895	2	S74225
8	8	0.7	124	2	T38142
9	8	0.7	222	2	B97118
10	8	0.7	236	2	S75373
11	8	0.7	425	2	S83990
12	8	0.7	459	2	F83602
13	8	0.7	498	2	J02353
14	8	0.7	608	2	S09790
15	8	0.7	864	2	T48474
16	8	0.7	937	2	G87640
17	8	0.7	1270	2	T21269
18	8	0.7	1291	2	T21267
19	8	0.7	1318	2	T21266
20	8	0.7	1327	2	T21268
21	7	0.6	64	2	H82849
22	7	0.6	72	2	S34404
23	7	0.6	87	2	T44104
24	7	0.6	94	2	AD1704
25	7	0.6	94	2	AE1333
26	7	0.6	101	4	S59321
27	7	0.6	104	2	AC1159
28	7	0.6	104	2	AC1518
29	7	0.6	123	2	AC2259

30	7	0.6	127	2	AE1445	hypothetical prote
31	7	0.6	127	2	AE1362	hypothetical prote
32	7	0.6	134	2	D70518	probable membrane
33	7	0.6	141	2	C82889	hypothetical prote
34	7	0.6	144	2	C70937	hypothetical prote
35	7	0.6	146	1	R5BR5	ribosomal protein
36	7	0.6	152	2	AE1193	hypothetical prote
37	7	0.6	154	2	E87029	hypothetical prote
38	7	0.6	181	2	C84592	hypothetical prote
39	7	0.6	185	1	YOECPP	fibrillar protein p
40	7	0.6	187	1	YOECXS	KS71a fibrillar pro
41	7	0.6	187	1	C43597	plin type F7-1 pr
42	7	0.6	188	1	YOECR2	F7-2 fibrillar prot
43	7	0.6	190	2	AE1863	cysteine synthase
44	7	0.6	191	2	AA3597	plin type F9 prec
45	7	0.6	197	1	C71022	hypothetical prote
46	7	0.6	211	2	C90031	hypothetical prote
47	7	0.6	219	2	S75541	hypothetical prote
48	7	0.6	220	1	A35996	metalloproteinase
49	7	0.6	231	1	C69798	probable membrane
50	7	0.6	231	2	H72234	uridylylate kinase -
51	7	0.6	233	2	T01205	sulfate transport
52	7	0.6	235	2	S48924	hypothetical prote
53	7	0.6	237	2	S63388	hypothetical prote
54	7	0.6	240	2	C83428	probable amidotran
55	7	0.6	243	2	G81736	conserved hypotet
56	7	0.6	245	2	F71474	probable muramidase
57	7	0.6	252	2	F70711	probable membranep
58	7	0.6	253	2	B89130	protein F52el.2 li
59	7	0.6	254	2	T51562	hypothetical prote
60	7	0.6	257	2	B69012	probable membrane
61	7	0.6	258	2	T32939	hypothetical prote
62	7	0.6	259	2	C75410	methionine aminope
63	7	0.6	264	2	P00478	plisl extensin-11
64	7	0.6	275	2	A65552	unknown protein. 9
65	7	0.6	277	2	B72226	hypothetical prote
66	7	0.6	282	2	T24693	hypothetical prote
67	7	0.6	283	2	S65961	main protein - Par
68	7	0.6	291	1	NCBPT5	phosphodiesterase
69	7	0.6	293	2	G64050	N-acetylneuraminat
70	7	0.6	293	2	E90186	conserved hypotet
71	7	0.6	295	2	H86320	3-phosphoserine ph
72	7	0.6	295	2	T51362	phosphoserine phos
73	7	0.6	295	2	T20629	hypothetical prote
74	7	0.6	305	2	T06763	hypothetical prote
75	7	0.6	309	2	E97175	cysteine synthase/

ALIGNMENTS

RESULT 1
S68441
leptin receptor, splice form Ob-Re - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68441
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68441
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-605 <LEP>
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AC52424.1; PID:g1195493
A:Experimental source: splice form Re; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
A:Gene: Ob-Re
C:Keywords: alternative splicing; appetite.

Query Match 3.6%; Score 42; DB 2; Length 805;
 Best Local Similarity 100.0%; Pred. No. 2.6e-35;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINSHSLGSLDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 498 FQPIFLSGYTMWIRINSHSLGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 2

leptin receptor, splice form Ob-Rc - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
 C:Accession: S68439; S68441
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Davishzadeh, J.G.; Lee, J.I.; F.
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68439
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 664-892 <LEE2>
 A:Cross-references: EMBL:U49108; NID:g1195488; PIDN:AC52422.1; PID:g1195489
 A:Experimental source: splice form Rc; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Accession: S68441
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-796, 'GMCTVLFMD' <LEE2>
 A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AC52424.1; PID:g1195493
 A:Experimental source: splice form Re; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Note: this sequence from splice form Re is included to produce a complete sequence
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439, PIR:S68439
 C:Genetics:
 A:Gene: Ob-Rc
 C:Keywords: alternative splicing; appetite

Query Match 3.6%; Score 42; DB 2; Length 892;
 Best Local Similarity 100.0%; Pred. No. 2.9e-35;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINSHSLGSLDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 498 FQPIFLSGYTMWIRINSHSLGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 3

leptin receptor, splice form Ob-Ra - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
 C:Accession: S68437
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Davishzadeh, J.G.; Lee, J.I.; F.
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68437
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-894 <LEE2>
 A:Cross-references: EMBL:U49106; NID:g1195484; PIDN:AC52420.1; PID:g1195485
 A:Experimental source: splice form Ra; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439, PIR:S68439
 C:Genetics:
 A:Gene: Ob-Ra
 C:Keywords: alternative splicing; appetite

Query Match 3.6%; Score 42; DB 2; Length 894;
 Best Local Similarity 100.0%; Pred. No. 2.9e-35;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINSHSLGSLDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 498 FQPIFLSGYTMWIRINSHSLGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 4

leptin receptor, splice form Ob-Rd - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2000
 C:Accession: S68440
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Davishzadeh, J.G.; Lee, J.I.; F.
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68440
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-900 <LEE2>
 A:Cross-references: EMBL:U49109; NID:g1195490; PIDN:AC52423.1; PID:g1195491
 A:Experimental source: tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439, PIR:S68439
 C:Genetics:
 A:Gene: Ob-Rd
 C:Keywords: alternative splicing; appetite; transmembrane protein
 F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 3.6%; Score 42; DB 2; Length 900;
 Best Local Similarity 100.0%; Pred. No. 2.9e-35;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINSHSLGSLDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 498 FQPIFLSGYTMWIRINSHSLGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 5

leptin receptor, splice form Ob-Rb - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1998 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
 C:Accession: S68438; S68441
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Davishzadeh, J.G.; Lee, J.I.; F.
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68438
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 664-1162 <LEE2>
 A:Cross-references: EMBL:U49107; NID:g1195486; PIDN:AC52421.1; PID:g1195487
 A:Experimental source: splice form Rb; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Note: only a part of the translation is shown
 A:Accession: S68441
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-796, 'GMCTVLFMD' <LEE2>
 A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AC52424.1; PID:g1195493
 A:Experimental source: splice form Re; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439, PIR:S68439
 C:Genetics:
 A:Gene: Ob-Rb
 C:Keywords: alternative splicing; appetite

Query Match 3.6%; Score 42; DB 2; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 3.6e-35;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FOPFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 498 FOPFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 6

leptin receptor, Ob-Rb - rat
 PC4184
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 01-Dec-2000
 C:Accession: J04895; J04896; J04897; PC4184; J04797
 R:Takaya, K., Ogawa, Y., Ise, N., Okazaki, T., Sach, N., Masuzaki, H., Mori, K., Tamu
 Biochem. Biophys. Res. Commun. 225, 75-83, 1996
 A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identificat
 A:Reference number: J04895; MUID:96332408
 A:Accession: J04895
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1162 <TAK>
 A:Cross-references: DDBJ:D85558; NID:91526441; PIDN:BA012831.1; PID:d1013515; PID:g15264
 A:Accession: J04896
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-889, 'RADTL', <TA2>
 A:Cross-references: DDBJ:D85557
 A:Accession: J04897
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-796, 'G', 1157-1158, 'TWLLN' <TA3>
 A:Cross-references: DDBJ:D85559
 R:Iida, M., Murakami, T., Ishida, K., Mizuno, A., Kuwajima, M., Shima, K.
 Biochem. Biophys. Res. Commun. 224, 597-604, 1996
 A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R) cDN
 A:Reference number: PC4184; MUID:96295531
 A:Accession: PC4184
 A:Molecule type: mRNA
 A:Residues: 840-1162 <IID>
 A:Cross-references: DDBJ:D84550
 R:Iida, M., Murakami, T., Ishida, K., Mizuno, A., Kuwajima, M., Shima, K.
 Biochem. Biophys. Res. Commun. 222, 19-26, 1996
 A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker fat
 A:Reference number: J04797; MUID:96212906
 A:Accession: J04797
 A:Molecule type: mRNA
 A:Residues: 1-889, 'RADTL', <IT2>
 A:Cross-references: DDBJ:D84125; NID:91374707; PIDN:BA012230.1; PID:g1374708
 A:Experimental source: adipose cell
 C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa) r
 C:Genetics:
 A:Gene: fa
 C:Keywords: appetite; transmembrane protein
 F:840-860/Domain: transmembrane #status predicted <TMM>
 F:861-1162/Domain: intracellular #status predicted <INT>

Query Match 3.6%; Score 42; DB 2; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 3.6e-35;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FOPFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 498 FOPFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 7

leptin receptor, isoform Ob-Rf - rat
 S74225
 C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999
 C:Accession: S74225
 R:Mang, M.Y., Zhou, Y.T., Newgard, C.B., Unger, R.H.
 FEBS Lett. 392, 87-90, 1996
 A:Title: A novel leptin receptor isoform in rat.
 A:Reference number: S74225; MUID:96368027
 A:Accession: S74225
 A:Molecule type: mRNA
 A:Residues: 1-895 <MAN>
 A:Cross-references: EMBL:U53144; NID:91395212; PIDN:AA03088.1; PID:g1395213
 A:Experimental source: strain Sprague-Dawley; tissue type brain
 C:Genetics:
 A:Gene: rob-R
 C:Keywords: appetite; transmembrane protein
 F:840-860/Domain: transmembrane #status predicted <TMM>

Query Match 3.5%; Score 41; DB 2; Length 895;
 Best Local Similarity 100.0%; Pred. No. 3.3e-34;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 501 OPTFLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 499 OPTFLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 8

hypothetical protein SPAC22A12.02c - fission yeast (Schizosaccharomyces pombe)
 T38142
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
 C:Accession: T38142
 R:Pearson, D., Churcher, C.M., Barrell, B.G., Rajandream, M.A., Wood, V.
 submitted to the EMBL Data Library, September 1997
 A:Reference number: Z21774
 A:Accession: T38142
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-124 <PEA>
 A:Cross-references: EMBL:Z99295; PIDN:CA016572.1; GSPDB:GN00066; SPDB:SPAC22A12.02c
 A:Experimental source: strain 972h-; cosmid c22A12
 C:Genetics:
 A:Gene: SPDB:SPAC22A12.02c
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC22A12.02c

Query Match 0.7%; Score 8; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 AGLSKNTS 58
 ||||||||
 Db 45 AGLSKNTS 52

RESULT 9

hypothetical protein CAC1767 [imported] - Clostridium acetobutylicum
 B97118
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 R:Noelling, J., Breton, G., Omelchenko, M.V., Markarova, K.S., Zeng, Q., Gibson, R., L
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: B97118
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-222 <KUP>
 A:Cross-references: GB:AF001437; PIDN:AAK79733.1; PID:g15024737; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:
A:Gene: CAC1767

Query Match 0.7%: Score 8; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 KNLFRNYYN 156
|||||
DB 4 KNLFRNYYN 11

RESULT 10
S75373
probable DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - *Sulfolobus solfataricus*
N:Alternate names: endonuclease III; protein C04006
C:Species: *Sulfolobus solfataricus*
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
C:Accession: S75373
R:Sense: C.W.; Klenk, H.P.; Singh, R.R.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A:Title: Organizational characteristics and information content of an archaeal genome: 1
A:Reference number: S73076; MUID:97055432
A:Accession: S75373
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <SEN>
A:Cross-references: EMBL:X08257; NID:g1707772; PID:g1707778
A:Experimental source: strain P2
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C:Superfamily: apurinic/apyrimidinic endonuclease III
C:Keywords: 4fe-4s; carbon-oxygen lyase; metalloprotein
F:204,211,214,219/Binding site: 4fe-4s cluster (Cys) (covalent) #status predicted

Query Match 0.7%: Score 8; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1058 DELLKLEG 1065
|||||
DB 122 DELLKLEG 129

RESULT 11
F83990
lactose transport system (lactose-binding protein) BH2726 [imported] - *Bacillus halodurans*
C:Species: *Bacillus halodurans*
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: F83990
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F83990
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-425 <STO>
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA06445.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2726

Query Match 0.7%: Score 8; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 854 ILLGTLL 861
|||||
DB 8 ILLGTLL 15

RESULT 12
F83602
hypothetical protein PA0344 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83602
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardly, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: F83602
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <STO>
A:Cross-references: GB:AE004472; GB:AE004091; NID:g9946188; PIDN:AAG03733.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0344
C:Superfamily: *Neisseria meningitidis* hypothetical protein NMB1644

Query Match 0.7%: Score 8; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 838 SDAGLYVI 845
|||||
DB 116 SDAGLYVI 123

RESULT 13
J02353
glycoprotein E precursor - turkey herpesvirus
N:Alternate names: ORF 8 protein
C:Species: turkey herpesvirus
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C:Accession: J02353
R:Zelnik, V.; Bartell, R.; Andonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ro
J. Gen. Virol. 74, 2151-2162, 1993
A:Title: The complete sequence and gene organization of the short unique region of he
A:Reference number: J02346; MUID:94014999
A:Accession: J02353
A:Molecule type: DNA
A:Residues: 1-498 <ZEL>
C:Keywords: glycoprotein; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-498/Product: glycoprotein E #status predicted <MAT>
F:396-412/Domain: transmembrane #status predicted <TM>
F:44,60,133,148,370/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 0.7%: Score 8; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 DAGLYVIV 846
|||||
DB 318 DAGLYVIV 325

RESULT 14
S09790
hypothetical protein UL27 - human cytomegalovirus (strain AD169)
C:Species: human cytomegalovirus, human herpesvirus 5
A>Note: host Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C:Accession: S09790
R:Chen, M.S.; Bankier, A.T.; Beck, S.; Bohm, R.; Brown, C.M.; Cerny, R.; Horsnell, T
M.; Bartell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A>Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
 A:Reference number: S09749; MUID:90269039
 A:Accession: S09790
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-608 <CHE>
 A:Cross-references: EMBL:X17403; NID:959591; PIDN:CAA35426.1; PID:959632
 A>Note: this sequence was submitted to the EMBL Data Library, December 1989

Query Match 0.7%; Score 8; DB 2; Length 608;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 DYFLPAG 52
 |||||||
 Db 369 DYFLPAG 376

RESULT 15
 T48474
 hypothetical protein T1E3.140 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T48474
 R:Byan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De
 ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 224491
 A:Accession: T48474
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-864 <BEV>
 A:Cross-references: EMBL:AL162972
 A:Experimental source: cultivar Columbia; BAC clone T1E3
 C:Genetics:
 A:Map position: 5
 A:introns: 612/2; 626/3; 677/1; 696/3; 770/3
 A>Note: T1E3.140

Query Match 0.7%; Score 8; DB 2; Length 864;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 RSLYCS 475
 |||||||
 Db 640 RSLYCS 647

RESULT 16
 G87640
 TonB-dependent receptor [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: G87640
 R:Nietman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolon
 n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: G87640
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-937 <STO>
 A:Cross-references: GB:AE005673; NID:913424831; PIDN:AAK25123.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC3161

Query Match 0.7%; Score 8; DB 2; Length 937;
 Best Local Similarity 100.0%; Pred. No. 32;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 626 SNPATYV 633
 |||||||
 Db 724 SNPATYV 731

RESULT 17
 T21269
 hypothetical protein F22E10.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T21269
 R:Gardner, A.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19398
 A:Accession: T21269
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1270 <WIL>
 A:Cross-references: EMBL:Z67882; PIDN:CAA91802.1; GSPDB:GN00028; CESP:F22E10.4
 A:Experimental source: clone F22E10
 C:Genetics:
 A:Gene: CESP:F22E10.4
 A:Map position: X
 A:introns: 69/2; 120/2; 162/3; 207/2; 264/3; 680/2; 828/3; 923/3; 972/2; 1131/3; 1204
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 0.7%; Score 8; DB 2; Length 1270;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 IREADKIV 288
 |||||||
 Db 623 IREADKIV 630

RESULT 18
 T21267
 hypothetical protein F22E10.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T21267
 R:Gardner, A.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19398
 A:Accession: T21267
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1291 <WIL>
 A:Cross-references: EMBL:Z67882; PIDN:CAA91800.1; GSPDB:GN00028; CESP:F22E10.2
 A:Experimental source: clone F22E10
 C:Genetics:
 A:Gene: CESP:F22E10.2
 A:Map position: X
 A:introns: 19/3; 63/2; 81/3; 114/2; 156/3; 201/2; 258/3; 354/1; 642/2; 724/1; 791/3;
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 0.7%; Score 8; DB 2; Length 1291;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 IREADKIV 288
 |||||||
 Db 584 IREADKIV 591

RESULT 19
 T21266
 hypothetical protein F22E10.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T21266
 R:Gardner, A.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19398
 A:Accession: T21266
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1318 <M1>
 A:Cross-references: EMBL:Z67882; PIDN:CAA91799.1; GSPDB:GN00028; CESP:F22E10.1
 A:Experimental source: clone F22E10
 C:Genetics:
 A:Gene: CESP:F22E10.1
 A:Map position: X
 A:introns: 26/3; 81/3; 114/2; 156/3; 201/2; 258/3; 300/2; 396/3; 676/2; 818/3; 939/3; 10
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 0.7%; Score 8; DB 2; Length 1318;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 281 IREADKIV 288
 |||||
 DB 617 IREADKIV 624

RESULT 20
 T21266
 hypothetical protein F22E10.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T21268
 R:Gardner, A.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19398
 A:Accession: T21268
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1327 <M1>
 A:Cross-references: EMBL:Z67882; PIDN:CAA91801.1; GSPDB:GN00028; CESP:F22E10.3
 A:Experimental source: clone F22E10
 C:Genetics:
 A:Gene: CESP:F22E10.3
 A:Map position: X
 A:introns: 23/3; 92/3; 213/2; 270/3; 686/2; 827/3; 1261/3
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 0.7%; Score 8; DB 2; Length 1327;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 281 IREADKIV 288
 |||||
 DB 629 IREADKIV 636

RESULT 21
 H82849
 hypothetical protein XF0098 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: H82849
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A62515; MUID:20365717
 A>Note: for a complete list of authors see reference number A59328 below
 A:Accession: H82849
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-64 <S1M>

A:Cross-references: GB:AE003863; GB:AE003849; MID:99104853; PIDN:AAE82911.1; GSPDB:GN
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Relinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
 as Neto, E.; Docena, C.; El-Porri, H.; Facinani, A.P.; Ferreira, A.J.S.
 submitted to Genbank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kitzger, J.E.; Kuramae, E.E.; La
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins
 A:Authors: Martins, E.M.F.; Matukuna, A.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeiri,
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.C.; Sancelli, R.V.; Sawa
 M.; Tsuboko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF0098

Query Match 0.6%; Score 7; DB 2; Length 64;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 LAEKIPQ 378
 |||||
 DB 29 LAEKIPQ 35

RESULT 22
 S34404
 ribosomal protein L15 - Bacillus licheniformis (fragment)
 C:Species: Bacillus licheniformis
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
 C:Accession: S34404
 R:Rschander, S.; Driessen, A.J.M.; Freudl, R.
 Mol. Gen. Genet. 235, 147-152, 1992
 A:Title: Cloning and molecular characterization of the secY genes from Bacillus liche
 A:Reference number: S30115; MUID:93062802
 A:Accession: S34404
 A:Molecule type: DNA
 A:Residues: 1-72 <TSC>
 A:Cross-references: EMBL:X70087
 C:Genetics:
 A:Gene: rpl15
 C:Superfamily: Escherichia coli ribosomal protein L15
 C:Keywords: protein biosynthesis; ribosome

Query Match 0.6%; Score 7; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 967 AEGTEVT 973
 |||||
 DB 12 AEGTEVT 18

RESULT 23
 T44104
 hypothetical protein [imported] - Staphylococcus aureus (fragment)
 C:Species: Staphylococcus aureus
 C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 11-May-2000
 C:Accession: T44104
 R:Rito, T.; Katayama, Y.; Hiratsuyu, K.
 Antimicrob. Agents Chemother. 43, 1449-1458, 1999
 A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-m
 A:Reference number: Z22733; MUID:99278010
 A:Accession: T44104
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-67 <TSC>
 A:Cross-references: EMBL:D86934; PIDN:BAAB2206.1

A:Experimental source: strain N315

Query Match 0.6%; Score 7; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1109 LFTDIRV 1115
|||||
DB 8 LFTDIRV 14

RESULT 24

AD1704
class I heat-shock protein (chaperonin) GroES [imported] - Listeria innocua (strain Clif
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD1704
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlan, K.D.; Fslh, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1704
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-94 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97404.1; PID:g16414686; GSPDB:GN00178
A:Experimental source: strain Clif11262
C:Genetics:
A:Gene: groES

Query Match 0.6%; Score 7; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 GTEVTE 975
|||||
DB 71 GTEVTE 77

RESULT 25

AE1333
class I heat-shock protein (chaperonin) GroES [imported] - Listeria monocytogenes (strai
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1333
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlan, K.D.; Fslh, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1333
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-94 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD00147.1; PID:g16411539; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: groES

Query Match 0.6%; Score 7; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 GTEVTE 975
|||||
DB 71 GTEVTE 77

RESULT 26

S59321
hypothetical protein IJ125 (IJ123 internal orf) - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 29-Nov-1995 #sequence_revision 05-Sep-1996 #text_change 20-Oct-2000
C:Accession: S59321
R:Delius, H.
submitted to the EMBL Data Library, June 1995
A:Description: 36.8 kb of S.cerevisiae chromosome XII including ACE2, CK11, PDC5, SLS
A:Reference number: S59313
A:Accession: S59321
A:Status: conceptual translation of pseudogene
A:Molecule type: DNA
A:Residues: 1-101
A:Cross-references: EMBL:X91258; NID:g995666; PIDN:CAA62344.1; PID:g995695
A:Experimental source: strain S288C
C:Comment: There is no evidence that this sequence is expressed.
C:Genetics:
A:Map position: 12R
C:Keywords: pseudogene

Query Match 0.6%; Score 7; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 KGDCLKF 140
|||||
DB 53 KGDCLKF 59

RESULT 27

AC1159
hypothetical protein lmo0675 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1159
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlan, K.D.; Fslh,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1159
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC98753.1; PID:g1641064; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0675

Query Match 0.6%; Score 7; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 TLLISHQ 865
|||||
DB 47 TLLISHQ 53

RESULT 28

AC1518
hypothetical protein lmo683 [imported] - Listeria innocua (strain Clif11262)
C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AC1518
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; Me Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AC1518
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-104 <GLA>
 A:Cross-References: GB:AL592022; PIDN:CAC95915.1; PID:g16413135; GSPDB:GN00178
 A:Experimental source: strain Cl1p11262
 C:Genetics:
 A:Gene: l1n0683

Query Match 0.6%; Score 7; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 859 TLLISHQ 865
 |||||
 DB 47 TLLISHQ 53

RESULT 29
 AC2259
 hypothetical protein all3626 [imported] - *Anabaena* sp. (strain PCC 7120)
 C:Species: *Anabaena* sp.
 A:Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
 C:Accession: AC2259
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi, Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AC2259
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-123 <KUR>
 A:Cross-References: GB:BA000019; PIDN:BA075325.1; PID:g17132759; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all3626

Query Match 0.6%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1014 SSKNSPL 1020
 |||||
 DB 16 SSKNSPL 22

RESULT 30
 AE1445
 hypothetical protein l1n0100 [imported] - *Listeria innocua* (strain Cl1p11262)
 C:Species: *Listeria innocua*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AE1445
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; Me Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AE1445
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-127 <GLA>
 A:Cross-References: GB:AL592022; PIDN:CAC95333.1; PID:g16412520; GSPDB:GN00178
 A:Experimental source: strain Cl1p11262
 C:Genetics:
 A:Gene: l1n0100

Query Match 0.6%; Score 7; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1057 LDLELKL 1063
 |||||
 DB 27 LDLELKL 33

RESULT 31
 A11362
 hypothetical protein lmo2305 [imported] - *Listeria monocytogenes* (strain EGD-e)
 C:Species: *Listeria monocytogenes*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: A11362
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; Me Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: A11362
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-127 <GLA>
 A:Cross-References: GB:NC_003210; PIDN:CAD00383.1; PID:g16411775; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo2305

Query Match 0.6%; Score 7; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1057 LDLELKL 1063
 |||||
 DB 27 LDLELKL 33

RESULT 32
 D70518
 probable membrane protein - *Mycobacterium tuberculosis* (strain H37RV)
 C:Species: *Mycobacterium tuberculosis*
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
 C:Accession: D70518
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: D70518
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-134 <COD>
 A:Cross-References: GB:297193; GB:AL123456; NID:g3261816; PIDN:CAB10033.1; PID:e32486
 A:Experimental source: strain H37RV
 C:Genetics:

A:Gene: RV1903
C:Superfamily: hypothetical protein yvld

Query Match 0.6%; Score 7; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 755 IYSWILS 761
DB 115 IYSWILS 121

RESULT 33

C82889
hypothetical protein U0445 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: C82889
R:Glass, J.L.; Letkowitz, E.J.; Glass, J.S.; Helner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mr
A:Reference number: A82870
A:Accession: C82889
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <GLA>
A:Cross-references: GB:AE002141; GB:AF222894; NID:g6899434; PIDN:AAF30857.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: U0445
A:Genetic code: SGC3

Query Match 0.6%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 801 FIPIERY 807
DB 49 FIPIERY 55

RESULT 34

C70937
hypothetical protein RV2185c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: C70937
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70300; MUID:98293587
A:Accession: C70937
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <COI>
A:Cross-references: GB:AL021957; GB:AL123456; NID:g342293; PIDN:CAA17489.1; PID:g291110
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV2185c
C:Superfamily: streptomyces coelicolor hypothetical protein scgC10.02c

Query Match 0.6%; Score 7; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 969 GTEVTE 975
DB 11111111

DB 103 GTEVTE 109

RESULT 35

R5BSLS

ribosomal protein L15 - Bacillus subtilis

C:Species: Bacillus subtilis
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000
C:Accession: S12682; JS0491; S08628; A69696
R:Yoshikawa, H.; Dol, R.H.
Nucleic Acids Res. 18, 1647, 1990
A:Title: Sequence of the Bacillus subtilis spectinomycin resistance gene region.
A:Reference number: S12680; MUID:90221911
A:Accession: S12682
A:Molecule type: DNA
A:Residues: 1-146 <YOS>

A:Cross-references: EMBL:M31102; NID:g1184272; PIDN:AA959117.1; PID:g143577
R:Nakamura, K.; Nakamura, A.; Takamatsu, H.; Yoshikawa, H.; Yamane, K.
J. Biochem. 107, 603-607, 1990

A:Title: Cloning and characterization of a Bacillus subtilis gene homologous to E. co
A:Reference number: JS0490; MUID:90292990
A:Accession: JS0491

A:Molecule type: DNA

A:Residues: 1-146 <NAK>
A:Cross-references: DDBJ:D00619; NID:g216336; PIDN:BA00494.1; PID:g216338
R:Sub, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.
Mol. Microbiol. 4, 305-314, 1990

A:Title: Isolation of a secY homologue from Bacillus subtilis: evidence for a common
A:Reference number: S08628; MUID:90251170

A:Accession: S08628

A:Molecule type: DNA

A:Residues: 94-146 <SUH>
A:Cross-references: EMBL:X51329; NID:g40132; PIDN:CA93711.1; PID:g40133

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.: Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erlingsson, J.; Fabre, C.; Ferrari,
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fultz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holseppel, S.; Hosono, S.; Hullo, M
koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogihara, A.; Ono, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portete
Krieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scani
A:Authors: Schleich, S.; Schroeter, R.; Sciofione, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, Y.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033
A:Accession: A69580
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-146 <KUN>

A:Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CA811911.1; PID:g26324
A:Experimental source: strain 168
C:Genetics:
A:Gene: rplO
C:Superfamily: Escherichia coli ribosomal protein L15

A:Keywords: protein biosynthesis; ribosome

Query Match 0.6%; Score 7; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 967 ABCTEVT 973
DB 86 ABCTEVT 92

RESULT 36

hypothetical protein lmo0952 [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: *Listeria monocytogenes*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AH1193
 R:Glaeser, P.; Frangouli, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussange, O.; Entlian, K.D.; Fshhi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; Meok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1193
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-152 <GLA>
 A:Cross-References: GB:NC_003210; PIDN:CAC99030.1; PID:916410354; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo0952

Query Match 0.6%; Score 7; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 939 VWSLST 945
 DB 116 VWSLST 122

RESULT 37
 E87029
 hypothetical protein [imported] - *Mycobacterium leprae*
 C:Species: *Mycobacterium leprae*
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: E87029
 R:Coile, S.T.; Englester, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hoam, M.A.; Rutherford, K.M.; Davies, R.M.; Devlin, K.; Dutfoy, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; SQ
 A:Title: Massive gene decay in the leprosy bacillus.
 A:Reference number: A86909; MUID:21128732; PMID:11234002
 A:Accession: E87029
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <STO>
 A:Cross-References: GB:AL450380; NID:q13093011; PIDN:CAC31344.1; GSPDB:GN00147
 C:Genetics:
 A:Gene: ML0963

Query Match 0.6%; Score 7; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 943 LSTTDL 949
 DB 39 LSTTDL 45

RESULT 38
 C84592
 hypothetical protein At2g20700 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: G84592
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Neus, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-766, 1999
 A:Title: Sequence analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: AB4420; MUID:20083487

A:Accession: C84592
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-181 <STO>
 A:Cross-References: GB:AE002093; NID:g4454478; PIDN:AA020925.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g20700
 A:Map position: 2
 C:Superfamily: *Arabidopsis thaliana* probable GPI-anchored protein F26K10.160

Query Match 0.6%; Score 7; DB 2; Length 181;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 502 PIFLLSG 508
 DB 13 PIFLLSG 19

RESULT 39
 YOBCP
 fimbrial protein papA precursor - *Escherichia coli*
 M:Alternate names: pap pili
 C:Species: *Escherichia coli*
 C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
 C:Accession: A23221; S25216; A05229; S16395
 R:Bag, M.; Normark, S.; Hardy, J.; O'Hanley, P.; Lark, D.; Olsson, O.; Schoolnik, G. J. Bacteriol. 157, 330-333, 1984
 A:Title: Nucleotide sequence of the papA gene encoding the pap pilus subunit of human
 A:Reference number: A91794; MUID:84087728
 A:Accession: A23221
 A:Molecule type: DNA
 A:Residues: 1-185 <BAG>
 A:Cross-References: GB:X03391; GB:X03392; NID:q42309; PIDN:CAA27126.1; PID R.Martlund, B.I.; Tennent, J.M.; Garcia, E.; Hamers, A.; Bag, M.; Lindberg, F.; Gaas Mol. Microbiol. 6, 2225-2242, 1992
 A:Title: Horizontal gene transfer of the *Escherichia coli* pap and prs pili operons as
 A:Reference number: S25205; MUID:93023852
 A:Accession: S25216
 A:Molecule type: DNA
 A:Residues: 1-185 <MA2>
 A:Cross-References: EMBL:X61239; NID:q42290; PIDN:CAA43562.1; PID:q42293
 A:Experimental source: strain J96
 C:Genetics:
 A:Gene: papA
 C:Superfamily: F7-2 fimbrial protein
 C:Keywords: fimbria
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-185/Product: fimbrial protein papA #status predicted <MAT>

Query Match 0.6%; Score 7; DB 1; Length 185;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 VANFNLT 730
 DB 177 VANFNLT 183

RESULT 40
 YOBCS
 KS71A fimbrial protein precursor - *Escherichia coli*
 M:Alternate names: KS71A pilin
 C:Species: *Escherichia coli*
 C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
 C:Accession: A23117
 R:Rhen, M.; van Die, I.; Rhen, V.; Bergmans, H. Eur. J. Biochem. 151, 573-577, 1985
 A:Title: Comparison of the nucleotide sequences of the genes encoding the KS71A and F
 A:Reference number: A23117; MUID:85285072
 A:Accession: A23117

A:Molecule type: DNA
A:Residues: 1-187 <RHE>
A:Cross-references: GB:X02921; NID:g41880; PIDN:CAA26678.1; PID:g41881
C:Superfamily: F7-2 fimbrial protein
C:Keywords: fimbria
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-187/Product: KS71a fimbrial protein #status predicted <MAT>

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 187;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 VANFNLT 730
|||||
DB 179 VANFNLT 185

RESULT 41

pilin type F7-1 precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 26-Aug-1999
C:Accession: C43597
R:Denich, K.; Blyn, L.B.; Craiu, A.; Braaten, B.A.; Hardy, J.; Low, D.A.; O'Hanley, P.D.
A:Title: DNA sequences of three pAPA genes from uropathogenic Escherichia coli strains:
A:Reference number: A43597; MUID:92040048
A:Accession: C43597
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <DEN>
A:Cross-references: GB:M68061; NID:g147072; PIDN:AAA24279.1; PID:g147073
C:Superfamily: F7-2 fimbrial protein

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 187;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 VANFNLT 730
|||||
DB 179 VANFNLT 185

RESULT 42

YOECP2
F7-2 fimbrial protein precursor - Escherichia coli
N:Alternate names: F7-2 pilin
C:Species: Escherichia coli
C:Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 16-Jul-1999
C:Accession: A03496; B43597
R:Van Die, I.; Bergmans, H.
Gene 32: 83-90, 1984
A:Title: Nucleotide sequence of the gene encoding the F7-2 fimbrial subunit of a uropath
A:Reference number: A03496; MUID:8515489
A:Accession: A03496
A:Molecule type: DNA
A:Residues: 1-188 <VAN>
A:Cross-references: GB:M12861; NID:g145963; PIDN:AAA23778.1; PID:g145964
R:Denich, K.; Blyn, L.B.; Craiu, A.; Braaten, B.A.; Hardy, J.; Low, D.A.; O'Hanley, P.D.
A:Title: DNA sequences of three pAPA genes from uropathogenic Escherichia coli strains:
A:Reference number: A43597; MUID:92040048
A:Accession: B43597
A:Molecule type: DNA
A:Residues: 1-188 <DEN>
A:Cross-references: GB:M68060; NID:g147070; PIDN:AAA24278.1; PID:g147071
C:Genetics:
A:Gene: pAPA
C:Function:
A:Description: one of the fimbrial proteins involved in mannose-resistant hemagglutinat

ubunits into fimbriae, or regulation of phase variation

C:Superfamily: F7-2 fimbrial protein
C:Keywords: fimbria; mannose-resistant hemagglutination
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-188/Product: F7-2 fimbrial protein #status predicted <MAT>

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 188;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 VANFNLT 730
|||||
DB 180 VANFNLT 186

RESULT 43

A41863
cysteine synthase (EC 4.2.99.8) cysM [similarity] - Pseudomonas syringae (fragment)
N:Alternate names: O-acetylserine (thiol)-lyase B
C:Species: Pseudomonas syringae
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-May-2000
C:Accession: A41863
R:Hrabak, E.M.; Willis, D.K.
J. Bacteriol. 174: 3011-3020, 1992
A:Title: The jemA gene required for pathogenicity of Pseudomonas syringae pv. syringae
A:Reference number: A41863; MUID:92234961
A:Accession: A41863
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <HR>
A:Cross-references: GB:M60477; NID:g151327; PIDN:AAA25876.1; PID:g151328
A:Experimental source: pv. syringae
A:Note: sequence extracted from NCBI backbone (NCBIN:97411, NCBI:97414)
C:Genetics:
A:Gene: cysM
C:Superfamily: threonine dehydratase
C:Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate
F:66/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 190;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1060 LKLEGN 1066
|||||
DB 53 LKLEGN 59

RESULT 44

A43597
pilin type F9 precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 26-Aug-1999
C:Accession: A43597
R:Denich, K.; Blyn, L.B.; Craiu, A.; Braaten, B.A.; Hardy, J.; Low, D.A.; O'Hanley, P.
A:Title: DNA sequences of three pAPA genes from uropathogenic Escherichia coli strain
A:Reference number: A43597; MUID:92040048
A:Accession: A43597
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <DEN>
A:Cross-references: GB:M68059; NID:g147068; PIDN:AAA24277.1; PID:g147069
C:Superfamily: F7-2 fimbrial protein

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 191;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 VANFNLT 730
|||||

Db 183 VANFNTL 189

RESULT 45
C71022

hypothetical protein PH1472 - *Pyrococcus horikoshii*

C:Species: *Pyrococcus horikoshii*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: C71022

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A:Reference number: A71000; MUID:98344137

A:Accession: C71022

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1197 <KAM>

A:Cross-references: GB:AP000006; NID:g3236133; PIDN:BA030579.1; PID:g3257896

A:Experimental source: strain 073

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1472

C:Superfamily: Archaeoglobus probable DNA-polymerase

Query Match 0.6%; Score 7; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1057 LDELKL 1063
|||||
Db 70 LDELKL 76

RESULT 46

hypothetical protein SA2111 [imported] - *Staphylococcus aureus* (strain N315)

C:Species: *Staphylococcus aureus*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: C90031

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.

Lancet 357, 1235-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C90031

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-211 <KUR>

A:Cross-references: GB:BA000018; PID:g13702120; PIDN:BA043412.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA2111

Query Match 0.6%; Score 7; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 541 SSVKAEI 547
|||||
Db 104 SSVKAEI 110

RESULT 47

hypothetical protein s11218 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C:Accession: S75541

R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*

S.

A:Reference number: S74322; MUID:97061201

A:Accession: S75541

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-219 <KAM>

A:Cross-references: EMBL:D90911; GB:AB001339; NID:g1653033; PIDN:BA18102.1; PID:g165

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: yci39

C:Superfamily: hypothetical protein YMR090W

Query Match 0.6%; Score 7; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 912 LLEPFI 918
|||||
Db 52 LLEPFI 58

RESULT 48
A35996

metalloproteinase inhibitor 2 precursor - bovine

N:Alternate names: collagenase inhibitor; tissue inhibitor of metalloproteinases (TIM)

C:Species: *Bos primigenius* (taurus) (cattle)

C:Date: 16-Nov-1990 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999

C:Accession: A35996; A34468; A25322; S28151

R:Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.

Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804, 1990

A:Title: cDNA cloning and expression of a metalloproteinase inhibitor related to tiss

A:Reference number: A35996; MUID:90207285

A:Accession: A35996

A:Molecule type: mRNA

A:Residues: 1-220 <BOO>

A:Cross-references: GB:M32303; NID:g163341; PIDN:AA03036.1; PID:g163342

A:Experimental source: aortic endothelial cDNA library

R:De Clerck, Y.A.; Yeau, T.D.; Natzkin, B.J.; Lu, H.S.; Langley, K.E.

J. Biol. Chem. 264, 17445-17453, 1989

A:Title: Purification and characterization of two related but distinct metalloprotein

A:Reference number: A34468; MUID:90008914

A:Accession: A34468

A:Molecule type: protein

A:Residues: 27-71 <DEC>

A:Experimental source: culture medium of aortic endothelial cells

R:Murray, J.B.; Allison, K.; Sudhalter, J.; Langer, R.

J. Biol. Chem. 261, 4154-4159, 1986

A:Title: Purification and partial amino acid sequence of a bovine cartilage-derived c

A:Reference number: A25322; MUID:86140235

A:Accession: A25322

A:Molecule type: protein

A:Residues: 27-41, 'C', '43-55', 'EX', '58-59', 'X', '61-66', 'XS', '69-71' <MUR>

A:Experimental source: cartilage

R:Decker, Y.A.; Yeau, T.D.; Lee, Y.; Tomlich, J.M.; Langley, K.E.

Biochem. J. 289, 65-69, 1993

A:Title: Characterization of the functional domain of tissue inhibitor of metalloprot

A:Reference number: S28151; MUID:93143691

A:Contents: annotation: functional domain

A:Description: regulation of extracellular matrix remodeling by inhibition of matrix

possibly controlling their activation: TIMP-1 and TIMP-2 possess erythroid potentiati

C:Superfamily: metalloproteinase inhibitor

C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitoge

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>

F:27-98, 29-127, 39-152, 154-201, 159-164, 172-193/Dissulfide bonds: #status predicted

Query Match 0.6%; Score 7; DB 1; Length 220;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 855 LILGTL 861
 DB 15 LILGTL 21

RESULT 49

C69798

probable membrane protein yetF - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: C69798

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berton
 C.; Bron, S.; Brouillet, S.; Krogli, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gallier
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koeter, P.; Koningstein, G.; Krogli, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,
 A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y. M.; Ogawa, K.; Ogilware, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelid
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A.; Authors: Schleich, S.; Schroeter, R.; Scifone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 aeneuhl, M.; Tamakoshi, A.; Tanaka, T.; Tognoni, A.; Tostato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumelein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033

A:Accession: C69798

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-231 <KUN>

A:Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12533.1; PID:g2633027

A:Experimental source: strain 168

C:Genetics:

A:Gene: yetF

C:Superfamily: probable membrane protein ycap

Query Match 0.6%; Score 7; DB 1; Length 231;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 593 SKVSILP 599

DB 164 SKVSILP 170

RESULT 50

H72234

uridylylate kinase - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: H72234

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316

A:Accession: H72234

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-231 <ARN>

A:Cross-references: GB:AE001804; GB:AE000512; NID:g4982160; PIDN:AAD36671.1; PID:g498217

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1604

C:Superfamily: uridine 5'-monophosphate kinase

Query Match 0.6%; Score 7; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1049 PHLTFSE 1055
 DB 174 PHLTFSE 180

Search completed: May 18, 2002, 07:04:33
 Job time: 262 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 07:04:17 ; Search time 15.27 Seconds

(without alignments)
2954.046 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 1165
Sequence: 1 MICQKRCVVLHMEFTVIT.....QTCSTQTHKMKMODLIV 1165

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 segs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1064	91.3	1165	1	LEPR_HUMAN
2	42	3.6	1162	1	LEPR_MOUSE
3	42	3.6	1162	1	LEPR_RAT
4	8	0.7	608	1	U27_HCMVA
5	8	0.7	4036	1	RRL_DUGBY
6	7	0.6	72	1	RL15_BACLI
7	7	0.6	146	1	RL15_BACSU
8	7	0.6	169	1	CYSM_PSESY
9	7	0.6	185	1	PAPA_ECOLI
10	7	0.6	187	1	FMK1_ECOLI
11	7	0.6	188	1	FMK2_ECOLI
12	7	0.6	220	1	TIME_BOVIN
13	7	0.6	231	1	PYRH_THEMA
14	7	0.6	235	1	VHRA_YEAST
15	7	0.6	237	1	BIOD_YEAST
16	7	0.6	232	1	YF91_MYCTU
17	7	0.6	290	1	MAUN_PARDE
18	7	0.6	283	1	EXOS_BP75
19	7	0.6	293	1	NPL_HAEIN
20	7	0.6	310	1	YGYJ_ECOLI
21	7	0.6	311	1	PP11_YEAST
22	7	0.6	329	1	Y654_ARCFU
23	7	0.6	335	1	KCC1_SCHPO
24	7	0.6	336	1	LEU3_MYCHO
25	7	0.6	336	1	LEU3_MYCTU
26	7	0.6	342	1	GGH_SOYBN
27	7	0.6	349	1	SOHB_ECOLI
28	7	0.6	353	1	SOHB_HAEIN
29	7	0.6	363	1	CHSB_PHANI
30	7	0.6	373	1	RC1L_HUMAN
31	7	0.6	373	1	RC1L_MOUSE
32	7	0.6	379	1	Y801_METYA
33	7	0.6	384	1	PURT_BACSU

34	7	0.6	386	1	RPA2_METYA	P14247 methanococ
35	7	0.6	396	1	CHSB_IPOPU	P48398 ipomoea pur
36	7	0.6	420	1	YMS7_YEAST	O03694 saccharomyc
37	7	0.6	426	1	EXLP_TOBAC	Q03211 nicotiana t
38	7	0.6	454	1	TBB2_PHYPO	P12458 physarum po
39	7	0.6	455	1	TBB_DICDI	P33256 dictyosteli
40	7	0.6	503	1	ZNT1_MOUSE	O60738 mus musculu
41	7	0.6	507	1	GGPD_CHIMU	O9PKX8 chlamydia m
42	7	0.6	507	1	ZNT1_RAT	O67720 rattus norv
43	7	0.6	508	1	SPA2_STAUV	P38507 staphylococ
44	7	0.6	524	1	SPAL_STAUV	P02976 staphylococ
45	7	0.6	539	1	IL2B_MOUSE	P16297 mus musculu
46	7	0.6	555	1	C166_CARAE	O90304 carassius a
47	7	0.6	564	1	C166_BRARE	O90460 brachydantio
48	7	0.6	569	1	ILIR_HUMAN	P14778 homo sapien
49	7	0.6	574	1	ERGL_HUMAN	Q14534 homo sapien
50	7	0.6	583	1	GTBI_MOUSE	O08582 mus musculu
51	7	0.6	584	1	GTBI_HUMAN	O00178 homo sapien
52	7	0.6	609	1	COPA_PSESM	P13374 pseudomonas
53	7	0.6	609	1	CP11_YEAST	P53306 saccharomyc
54	7	0.6	616	1	YAMG_SCHPO	Q10190 schizosach
55	7	0.6	622	1	PRCC_CHICK	P05153 gallus gall
56	7	0.6	632	1	PTMA_BUCAT	P57635 buchnera ap
57	7	0.6	644	1	YGM4_YEAST	P53129 saccharomyc
58	7	0.6	652	1	ILV3_BRANA	P17597 arabidopsis
59	7	0.6	655	1	ILV1_BRANA	P27818 brassica na
60	7	0.6	662	1	SOT2_STYHA	P33392 stylosanth
61	7	0.6	665	1	YJBO_HUMAN	O9BY84 homo sapien
62	7	0.6	666	1	YJBO_YEAST	P47077 saccharomyc
63	7	0.6	667	1	SVT1_STYHA	P53391 stylosanth
64	7	0.6	670	1	ILV3_ARATH	P17597 arabidopsis
65	7	0.6	678	1	FLHA_MOUSE	O67265 aquifex ae
66	7	0.6	760	1	CO2_MOUSE	P21180 mus musculu
67	7	0.6	769	1	PIGR_RAT	P18083 rattus norv
68	7	0.6	776	1	CHS1_CANAL	P23316 candida alb
69	7	0.6	788	1	CADA_HUMAN	O9Y6N8 homo sapien
70	7	0.6	789	1	CADA_CHICK	P73995 gallus gall
71	7	0.6	831	1	PRIA_SYNY3	P74397 synecocyst
72	7	0.6	848	1	ENV_HV1JR	P20871 human immun
73	7	0.6	881	1	YEPT_HAEIN	P44288 haemophilus
74	7	0.6	950	1	CDAS_HUMAN	O9Y5H8 homo sapien
75	7	0.6	960	1	VP41_LYCSES	P93231 lycopersico

ALIGNMENTS

RESULT 1	LEPR_HUMAN	STANDARD:	PRT: 1165 AA.
ID	LEPR_HUMAN		
AC	P48357:		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	01-FEB-1996 (Rel. 41, Last annotation update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).		
GN	LEPR OR ORF.		
OS	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteria; Primates; Carnivora; Homidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=96128129; PubMed=8548812;		
RA	Tarragila L.A., Dembski M., Weng X., Deng N., Culpepper J.,		
RA	Devois R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,		
RA	Muller C., Sanker S., Mortuary A., Moore K.J., Smutko J.S.,		
RA	Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;		
RT	"Identification and expression cloning of a leptin receptor, OB-R."		
RL	Cell 83:1263-1271(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Thompson D.B., Ossowski V., Sutherland J., Apel W.,		

RA Bleserfeldt J.; to the EMBL/Genbank/DBJ databases.
RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP VARIANT ARG-223.
RX MEDLINE-96270489; PubMed-8666155;
RA Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;
RT "The hypothalamic leptin receptor in humans: identification of
RT incidental sequence polymorphisms and absence of the db/db mouse and
RT fa/fa rat mutations.";
RL Diabetes 45:992-994(1996).
RN [4]
RP VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE-97289527; PubMed-9144432;
RA Echalald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,
RA Andersen T., Chung W.K., Leibel R.L., Pedersen O.;
RT "Amino acid variants in the human leptin receptor: lack of association
RT to juvenile onset obesity.";
RL Biochem. Biophys. Res. Commun. 233:248-252(1997).
RN [5]
RP VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE-97431549; PubMed-9287054;
RA Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,
RA Southern M., Udall J.N., Kahle B., Leibel R.L.;
RT "Exonic and intronic sequence variation in the human leptin receptor
RT gene (LEPR).";
RL Diabetes 46:1509-1511(1997).
RN [6]
RP VARIANTS ARG-109 AND ARG-223.
RX MEDLINE-97301763; PubMed-9158141;
RA Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;
RT "Structure and sequence variation at the human leptin receptor gene in
RT lean and obese Pima Indians.";
RL Hum. Mol. Genet. 6:675-679(1997).
RN [7]
RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
RX MEDLINE-99075638; PubMed-9860295;
RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,
RA Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
RT "Transmission disequilibrium and sequence variants at the leptin
RT receptor gene in extremely obese German children and adolescents.";
RL Hum. Genet. 103:540-546(1998).
RN [8]
RP VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE-97318795; PubMed-9175732;
RA Strosberg A.D., McKeligue P.M., Scott J., Altman T.J.;
RT "Leptin receptor gene variation and obesity: lack of association in a
RT white British male population.";
RL Hum. Mol. Genet. 6:869-876(1997).
CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC
DR EMBL: U43168; AAB93015.1; -;
DR EMBL: U59263; AAB09673.1; -;
DR EMBL: U59248; AAB09673.1; JOINED.
DR EMBL: U59249; AAB09673.1; JOINED.
DR EMBL: U59250; AAB09673.1; JOINED.
DR EMBL: U59252; AAB09673.1; JOINED.
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DR EMBL: U59254; AAB09673.1; JOINED.
DR EMBL: U59255; AAB09673.1; JOINED.
DR EMBL: U59256; AAB09673.1; JOINED.
DR EMBL: U59257; AAB09673.1; JOINED.

DR EMBL: U59258; AAB09673.1; JOINED.
DR EMBL: U59259; AAB09673.1; JOINED.
DR EMBL: U59260; AAB09673.1; JOINED.
DR EMBL: U59261; AAB09673.1; JOINED.
DR EMBL: U59262; AAB09673.1; JOINED.
DR HSSP: P40189; IBOU.
DR MIM: 601007; -;
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3_2.
DR SMART: SM00060; FN3_1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 1165
FT DOMAIN 22 841
FT TRANSMEM 842 862
FT DOMAIN 863 1165
FT DOMAIN 237 320
FT DOMAIN 537 623
FT DOMAIN 738 823
FT CARBOHD 23 23
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FT VARIANT 109 109
FT VARIANT 204 204
FT VARIANT 223 223
FT VARIANT 656 656
FT VARIANT 675 675
FT SEQUENCE 1165 AA; 132449 MW; 8F21D9AF5125808 CRC64;
SQ
Query Match 91.3%; Score 1064; DB 1; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MTCQRCVYLLHMERIYYITANLSYPTTPMRFKSKMPNSTYVYFLPALSKNTNS 60
QY 61 NCHYETAPEPKNSSGTHPSNLSKTFPHCCFSEDDRNCSLCADNIEGTFVSTNSLVF 120
DB 61 NCHYETAPEPKNSSGTHPSNLSKTFPHCCFSEDDRNCSLCADNIEGTFVSTNSLVF 120
QY 121 QSIDANMNIIQCKLKGDLKFLICYVESLFKNLFRNRYKVVLLYVLEVLDSPLVPQGS 180
DB 121 QSIDANMNIIQCKLKGDLKFLICYVESLFKNLFRNRYKVVLLYVLEVLDSPLVPQGS 180
QY 181 FQMHGNCSEVHECCCLVVPVPTAKLNDILLMCLKITSGGVITPSPLMASYQPINMKPDP 240
DB 181 FQMHGNCSEVHECCCLVVPVPTAKLNDILLMCLKITSGGVITPSPLMASYQPINMKPDP 240

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Db 181 FQWNCSCSVHECCGLVPPATKLNDFLTMCKITSGGIVFOSPLMSVPIINNVKDPDP 240
QY 241 LGLHMETDGNKIKISWSPPLVPFLOQVKSSENSTYIRADKIVASTSLVDSILP 300
Db 241 LGLHMETDGNKIKISWSPPLVPFLOQVKSSENSTYIRADKIVASTSLVDSILP 300
QY 301 GSSYEVOVRKRLDGPGLMSDMSTPRVFTTQDIYEPFKILTSVGSNVSPHCYKKNKI 360
Db 301 GSSYEVOVRKRLDGPGLMSDMSTPRVFTTQDIYEPFKILTSVGSNVSPHCYKKNKI 360
QY 361 VPSKEIYVMMNLAEKIPQSYDVVSDHVKVTFPNNMETPRGKFITYDAYCCNEHCCH 420
Db 361 VPSKEIYVMMNLAEKIPQSYDVVSDHVKVTFPNNMETPRGKFITYDAYCCNEHCCH 420
QY 421 RYAEIYVIVNINISCTEDYLFKMTCRMSTSTIOSLAESTLRLRHRSLSYCSIDPSIH 480
Db 421 RYAEIYVIVNINISCTEDYLFKMTCRMSTSTIOSLAESTLRLRHRSLSYCSIDPSIH 480
QY 481 PISEPKCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLP 540
Db 481 PISEPKCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLP 540
QY 541 SSYKAETTTIGLKTSMERPVPENNLOFOIRYGLSGKEVOKMYVYAKSKSVSLPV 600
Db 541 SSYKAETTTIGLKTSMERPVPENNLOFOIRYGLSGKEVOKMYVYAKSKSVSLPV 600
QY 601 PDLCAVAVOVRCKRLDGLGYMSNMSNPATYVMDIVKPRGPEFMRINDGDMKKRKNV 660
Db 601 PDLCAVAVOVRCKRLDGLGYMSNMSNPATYVMDIVKPRGPEFMRINDGDMKKRKNV 660
QY 661 TLIMKPLMKNDLSCSVQRYVYNHHTSCNGTWSBDVGNHTKFTFLMTBOAHTVYLAINSI 720
Db 661 TLIMKPLMKNDLSCSVQRYVYNHHTSCNGTWSBDVGNHTKFTFLMTBOAHTVYLAINSI 720
QY 721 GASVAPNLTFFSMPMSVNVVQSLAAPLMSCVIYVMIISPSYKLMYTIEMKNLNED 780
Db 721 GASVAPNLTFFSMPMSVNVVQSLAAPLMSCVIYVMIISPSYKLMYTIEMKNLNED 780
QY 781 GEIKMLRISSSVKRYIHDHFIPIEKYQSLYPIFMEGVCKPKIINSFTODDIEKHOSDA 840
Db 781 GEIKMLRISSSVKRYIHDHFIPIEKYQSLYPIFMEGVCKPKIINSFTODDIEKHOSDA 840
QY 841 GLYIVPVIISSSILLLGTLISHQRMKLFMEDVNPKNCSMAQGLNFQKPEFHEHFT 900
Db 841 GLYIVPVIISSSILLLGTLISHQRMKLFMEDVNPKNCSMAQGLNFQKPEFHEHFT 900
QY 901 KHTASVTCGFLLEPRTISDIDVTSKKNKDEMPITYVLSLSTDLKSGVCSISQFN 960
Db 901 KHTASVTCGFLLEPRTISDIDVTSKKNKDEMPITYVLSLSTDLKSGVCSISQFN 960
QY 961 SVNFSAEGETEYVEDESQOPFEKYATILSNKRPSTGEQGLINSYVRCFSSKRSPL 1020
Db 961 SVNFSAEGETEYVEDESQOPFEKYATILSNKRPSTGEQGLINSYVRCFSSKRSPL 1020
QY 1021 KDSFNSNSWEIEAQAFITLSDQHPNIIISPHLJFSEGLDELKLGPNPEENNKKSIYLL 1080
Db 1021 KDSFNSNSWEIEAQAFITLSDQHPNIIISPHLJFSEGLDELKLGPNPEENNKKSIYLL 1080
QY 1081 GVSISIKKREGVLLTDKSRVSCPPAPCLFTDRVLODSCSHPEENNINIGTSSKKNFAS 1140
Db 1081 GVSISIKKREGVLLTDKSRVSCPPAPCLFTDRVLODSCSHPEENNINIGTSSKKNFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

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DT 01-FEB-1996 (Rel. 33, last sequence update)
DE 01-MAR-2002 (Rel. 41, last annotation update)
DT Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219
DE receptor).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT A).
RC TISSUE=Choroid plexus;
RX MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
RA Mui C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;
RT "Identification and expression cloning of a leptin receptor, OB-R.";
RL Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT B).
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=96190816; PubMed=8608603;
RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
RA Ellis S.J., Lacey N.D., Culpepper J., Moore K.J., Breibart R.E.,
RA Duyk G.M., Tepper R.I., Morgenstern J.P.;
RT "Evidence that the diabetes gene encodes the leptin receptor:
RT identification of a mutation in the leptin receptor gene in db/db
RL mice.";
RL Cell 84:491-495(1996).
RN [3]
RP SEQUENCE FROM N.A. (VARIANTS A TO E).
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=96231997; PubMed=8628397;
RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
RA Lee J.I., Friedman J.M.;
RT "Abnormal splicing of the leptin receptor in diabetic mice.";
RL Nature 379:632-635(1996).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT C).
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=96206286; PubMed=8616721;
RA Croft J.A., Saffer A.W., Zupancic T.J., Smith-Gbur J.,
RA Mikhail A., Platika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
RN [5]
RP SEQUENCE FROM N.A. (VARIANT B).
RC STRAIN=NEW ZEALAND OB/SE / NKO; TISSUE=Hypothalamus;
RX MEDLINE=97462708; PubMed=9322935;
RA Igel M., Becker W., Herberg L., Joost H.G.;
RT "Hypoleptinemia, leptin resistance, and polymorphic leptin receptor
RT in the New Zealand obese mouse.";
RL Endocrinology 138:4234-4239(1997).
RN [6]
RP SEQUENCE FROM N.A. (VARIANTS A AND B).
RC STRAIN=FVB/N; TISSUE=Spleen;
RX MEDLINE=96270520; PubMed=8692797;
RA Gillard N., Ziegler S., Wiestner A., Stoffel R., Helm M.H.,
RA Skoda R.C.;
RT "Defective STAT signaling by the leptin receptor in diabetic mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
RN [7]
RP SEQUENCE FROM N.A. (VARIANT E).
RC STRAIN=129/T;
RX MEDLINE=98008913; PubMed=9344648;
RA Chua S.C., Koutiras I.K., Han L., Liu S.M., Kay J., Young S.J.,
RA Chung W.K., Leibel R.L.;
RT "Fine structure of the murine leptin receptor gene: splice site
RT suppression is required to form two alternatively spliced
RL transcripts.";
RL Genomics 45:264-270(1997).

```

FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 686 686 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 695 695 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 726 726 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 890 894 PERFE -> RTDL (IN ISOFORM A).
 FT VASPLIC 895 1162 MISSING (IN ISOFORM A).
 FT VASPLIC 890 892 PET -> VTV (IN ISOFORM C).
 FT VASPLIC 893 1162 MISSING (IN ISOFORM C).
 FT VASPLIC 890 900 PETHEFLTKH -> DISFHVFLTR (IN ISOFORM D).
 FT VASPLIC 901 1162 MISSING (IN THE ISOFORM D).
 FT VASPLIC 797 805 DNFEPIEYK -> GMCVLEFMD (IN ISOFORM E).
 FT VASPLIC 806 1162 MISSING (IN ISOFORM E).
 FT VARIANT 541 541 V -> I (IN STRAIN NO2).
 FT VARIANT 651 651 V -> I (IN STRAIN NO2).
 FT VARIANT 1044 1044 T -> I (IN STRAIN NO2).
 FT CONFLICT 140 140 F -> I (IN REF. 6).
 FT CONFLICT 720 720 A -> T (IN REF. 5).
 SQ SEQUENCE 1162 AA; 130788 MW; 0E1E75B076BA60A2 CRC64;

Query Match 3.6%; Score 42; DB 1; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 3.1e-35;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 500 FQPIFLSGTWMTRINHSGLSDSPPCVLPDSVYKRLPS 541
 Db 498 FQPIFLSGTWMTRINHSGLSDSPPCVLPDSVYKRLPS 539
 ||||||||||||||||||||||||||||||||||||||||

RESULT 3
 LEPR_RAT ID LEPR_RAT STANDARD PRT: 1162 AA.
 AC Q62955; Q63007; P70493; P70494; P70495; Q63385; Q63386; O54805;
 AC P97589; Q35772;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Leptin receptor precursor (Lepr-R) (OB-receptor) (OB-R).
 GN LEPR OR OBPR OR FA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
 RC STRAIN-ZUCKER; TISSUE-Hypothalamus;
 RX MEDLINE-96241565; PubMed-8673096;
 RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,
 RA Hess J.F.;
 RT "Leptin receptor missense mutation in the fatty Zucker rat.";
 RL Nat. genet. 13:18-19(1996).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
 RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE-Brain;
 RX MEDLINE-96295531; PubMed-8702432;
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwayama M., Shima K.;
 RT "Substitution at codon 269 (glutamine --> proline) of the leptin
 RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
 RT (fa/fa) rat.";
 RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANTS A; B AND E).
 RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
 RX MEDLINE-96332408; PubMed-8765097;
 RA Takaya K., Ogawa Y., Ise N., Okazaki T., Satoh N., Masuzaki H.,

Query Match	Best Local Similarity	3.6%	Score 42	DB 1	Length 1162
Matches 42	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY 500	FOPIFLSLGYTWMIRINHSLSGLSDSPPTCVLPDSVVKPLPSS 541				
DB 498	FOPIFLSLGYTWMIRINHSLSGLSDSPPTCVLPDSVVKPLPSS 549				
RESULT 4	UL27_HCMVA STANDARD: PRT: 608 AA.				
ID UL27_HCMVA	AC P16763:				
DT 01-AUG-1990	(Rel. 15, Created)				
DT 01-AUG-1990	(Rel. 15, Last sequence update)				
DT 01-OCT-1996	(Rel. 34, Last annotation update)				
DE Hypothetical protein UL27.					
EN Human cytomegalovirus (strain AD169):					
DR EMBL: D85559	: BAA12832.1	:			
DR EMBL: U60151	: AAB06616.1	:			
DR EMBL: D84125	: BAA12230.1	:			
DR EMBL: D84126	: BAA12231.1	:			
DR EMBL: AB011006	: BAA24899.1	:			
DR EMBL: U67207	: AAB40654.1	:			
DR EMBL: AF007818	: AAB63201.1	:			
DR InterPro: IPR002966	: CRA.	:			
DR InterPro: IPR003961	: FN_III	:			
DR InterPro: IPR003529	: Hematopo_receptor_L_F2	:			
DR Pfam: PF00041	: fn3.2	:			
DR PROSITE: PS01353	: HEMATOPO_REC_L_F2; 1.	:			
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;					
KW Polymorphism; Alternative splicing					
FT CHAIN	1 21				POTENTIAL.
FT DOMAIN	22 1162				LEPTIN RECEPTOR.
FT TRANSMEM	22 839				EXTRACELLULAR (POTENTIAL).
FT DOMAIN	840 860				POTENTIAL.
FT DOMAIN	861 1162				CYTOPLASMIC (POTENTIAL).
FT DOMAIN	236 318				FIBRONECTIN TYPE-III 1.
FT DOMAIN	535 621				FIBRONECTIN TYPE-III 2.
FT DOMAIN	736 821				FIBRONECTIN TYPE-III 3.
FT CARBOHD	55 55				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	56 56				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	73 73				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	98 98				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	187 187				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	275 275				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	345 345				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	356 356				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	431 431				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	514 514				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	622 622				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	657 657				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	668 668				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	686 686				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	695 695				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	698 698				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	726 726				N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC	890 894				PETPE -> RADTL (IN ISOFORM A).
FT VARSPLIC	895 1162				MISSING (IN ISOFORM A).
FT VARSPLIC	890 892				PET -> VTV (IN ISOFORM C).
FT VARSPLIC	893 1162				MISSING (IN ISOFORM C).
FT VARSPLIC	797 805				DNEPIRELY -> SMCYLLIN (IN ISOFORM E).
FT VARSPLIC	806 1162				MISSING (IN ISOFORM E).
FT VARIANT	269 269				Q -> P (IN FA).
FT CONFLICT	2 2				T -> M (IN REF. 4).
FT CONFLICT	12 12				H -> P (IN REF. 6).
FT CONFLICT	34 34				K -> R (IN REF. 6).
FT CONFLICT	751 752				CV -> SL (IN REF. 7).
FT CONFLICT	846 846				I -> V (IN REF. 8).
SO SEQUENCE	1162 AA; 130832 MW; 130832 MW; BAA12CA2D2DE52AF CRC64;				

```

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohm R., Brown C.M., Cerny R.,
RA Hornell T., Hutchinson C.A. III, Kozarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrett B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND
CC HSV-7 04, HSV-6 AND HSV-7 05 AND HCMV UL27.
CC -----
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CC -----
CC EMBL: X17403; CA35426.1;
CC PIR: S09790; S09790.
CC Hypothetical protein.
DR SEQUENCE 608 AA; 69220 MW; 81225A5D0E2980E CRC64;
SQ
Query Match 0.7%; Score 8; DB 1; Length 608;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 45 DYFLPAG 52
DB 369 DYFLPAG 376
|||||
RESULT 5
ID RRPL_DUGBV STANDARD; PRT; 4036 AA.
AC 066431;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (L protein).
GN L.
OS Dugbe virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Nairovirus.
OX NCBI_TaxID=11595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE ARD 44313;
RX MEDLINE=96332515; PubMed=8760425;
RA Marriott A.C., Nuttall P.A.;
RT "Large RNA segment of Dugbe nairovirus encodes the putative RNA
RT polymerase."
RL J. Gen. Virol. 77:1775-1780(1996).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC {RNA}(N).
CC -----
CC -1- SIMILARITY: CONTAINS 1 OTU DOMAIN.
CC -----
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CC -----
CC EMBL: U15018; AAB18834.1;
CC PIR: S09790; S09790.
CC InterPro: IPR003323; OTU.
DR InterPro; IPR000822; Znf-C2H2.

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DR Pfam; PF02338; OTU; 1.
DR PROSITE; PS50802; OTU; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
RW Transferase; Nucleotidyltransferase; RNA-directed RNA polymerase.
FT DOMAIN 29 158
FT SEQUENCE 4036 AA; 459382 MW; E2EDF0B4358E31BD CRC64;
SQ
Query Match 0.7%; Score 8; DB 1; Length 4036;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1003 GLINSSVT 1010
DB 2685 GLINSSVT 2692
|||||
RESULT 6
ID RL15_BACLI STANDARD; PRT; 72 AA.
AC P35138;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE 50S ribosomal protein L15 (fragment).
GN RPLD.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93062802; PubMed=1435726;
RA Tschander S., Driessen A.J.M., Frendl R.;
RT "Cloning and molecular characterization of the secY genes from
RT Bacillus licheniformis and Staphylococcus carnosus: comparative
RT analysis of nine members of the secY family."
RL Mol. Gen. Genet. 235:147-152(1992).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL: X70087; -; NOT_ANNOTATED_CDS.
DR PIR: S34404; S34404.
DR InterPro; IPR001196; Ribosomal_L15.
DR Pfam; PF00256; L15; 1.
DR PROSITE; PS00475; RIBOSOMAL_L15; 1.
RW Ribosomal protein; rRNA-binding.
FT NON_TER 1
FT SEQUENCE 72 AA; 7441 MW; 6DC3BA681492E6C9 CRC64;
SQ
Query Match 0.6%; Score 7; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 967 AEGTEVT 973
DB 12 AEGTEVT 18
|||||
RESULT 7
ID RL15_BACSU STANDARD; PRT; 146 AA.
AC P19946;
DT 01-FEB-1991 (Rel. 17, Created)

```

DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L15.
 GN RPL0.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 NX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-90292990; PubMed-2113521;
 RX Nakamura K., Nakamura A., Takamatsu H., Yoshikawa H., Yamane K.,
 RT "Cloning and characterization of a Bacillus subtilis gene homologous
 to E. coli secY";
 RL J. Biochem. 107:603-607(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90221911; PubMed-2139212;
 RA Yoshikawa H., Doi R.H.,
 RT "Sequence of the Bacillus subtilis spectinomycin resistance gene
 region";
 RL Nucleic Acids Res. 18:1647-1647(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / MAREBURG;
 RX MEDLINE-96186897; PubMed-8635744;
 RA Suh J.W., Boylan S.A., Oh S.H., Price C.W.,
 RT "Genetic and transcriptional organization of the Bacillus subtilis
 spe-alpha region";
 RL Gene 169:17-23(1996).
 RN [4]
 RP SEQUENCE OF 94-146 FROM N.A.
 RC STRAIN-168;
 RX MEDLINE-90251170; PubMed-2110998;
 RA Suh J.W., Boylan S.A., Thomas S.M., Dolan K.M., Oliver D.B.,
 RT Price C.W.,
 RL "Isolation of a secY homologue from Bacillus subtilis: evidence for a
 common protein export pathway in eubacteria";
 RL Mol. Microbiol. 4:305-314(1990).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -1- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS:

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 CC
 CC EMBL; D00619; BAA00494.1; -
 DR EMBL; X51329; CAA35711.1; -
 DR EMBL; L47971; AAB06818.1; -
 DR EMBL; M31102; AAB59117.1; -
 DR EMBL; 299104; CAB19111.1; -
 DR PIR; S12682; R5BSL5.
 DR Subtilist; BG10444; rplO.
 DR InterPro: IPR001196; Ribosomal_L15.
 DR Pfam: PF00256; L15; 1.
 DR Pfam: PF01305; Ribosomal_L15; 1.
 DR PROSITE: PS00475; RIBOSOMAL_L15; 1.
 DR Ribosomal protein; rRNA-binding; Complete proteome.
 KW RIBOSOMAL L15 AA; 15383 MW; 5DB07A902B266C11 CRC64;
 SQ SEQUENCE

Query Match 0.6%; Score 7; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 967 AECEVT 973
 DB 86 AECEVT 92

RESULT 8
 ID CYSM_PSESX
 AC P48028;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cysteine synthase B (EC 4.2.99.8) (O-acetylserine sulphydrylase B)
 DE (O-acetylserine (thiol)-lyase B) (CSASE B) (Fragment).
 GN CYSM.
 OS Pseudomonas syringae (pv. syringae).
 OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 NX NCBI_TaxID=321;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92234961; PubMed-1314807;
 RA Hrabak E.M., Willis D.K.,
 RT "The lemA gene required for pathogenicity of Pseudomonas syringae pv.
 syringae on bean is a member of a family of two-component
 regulators";
 RL J. Bacteriol. 174:3011-3020(1992).
 CC -1- CATALYTIC ACTIVITY: O3-acetyl-L-serine + H(2)S = L-cysteine +
 acetate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-
 SYNTHASE FAMILY.

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 CC
 CC EMBL; M80477; AA25876.1; -
 DR HSSP; P12674; IOAS.
 DR InterPro: IPR001216; Cys-synthase.
 DR InterPro: IPR001926; PALP.
 DR Pfam: PF00291; PALP; 1.
 DR PROSITE: PS00901; CYS-SYNTHASE; 1.
 DR Kyras; Cysteine biosynthesis; Pyridoxal phosphate.
 FT BINDING 45 45
 FT NON_TER 169 169
 SO SEQUENCE 169 AA; 18023 MW; E12781E90CA7F87 CRC54;

Query Match 0.6%; Score 7; DB 1; Length 169;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1060 LKLEGN 1066
 DB 32 LKLEGN 38

RESULT 9
 ID PARA_ECOLI
 AC P04127;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PAP fimbrial major pilin protein precursor (PAP pilin).
 GN PARA.
 OS Escherichia coli.
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 NX NCBI_TaxID=562;
 RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN-96;
RX MEDLINE-84087728; PubMed-6140260;
RA Baga M., Normark S., Hardy J., O'Hanley P., Lark D., Olsson O.,
RT Schoolnik G., Falkow S.;
RT Nucleotide sequence of the ppa gene encoding the Pap pilus subunit
RT of human uropathogenic Escherichia coli.
RL J. Bacteriol. 157:330-333(1984).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-96;
RX MEDLINE-93023852; PubMed-1357526;
RA Marklund B., Tennent J.M., Garcia E., Hamers A., Baga M.,
RT Lindberg F., Gaastera W., Normark S.;
RT Horizontal gene transfer of the Escherichia coli pap and pps pilI
RT operons as a mechanism for the development of tissue-specific
RT adhesive properties.
RL Mol. Microbiol. 6:2223-2242(1992).
CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- DISEASE: STRAINS OF E. COLI THAT CAUSE INFECTION OF THE HUMAN
CC URINARY TRACT PRODUCE PAP-PILI WHICH ARE HAIR-LIKE APPENDAGES
CC CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE
CC PROTEIN PAPA. THESE PILI MEDIATE BINDING TO DIGLYCOSIDE-
CC CONTAINING GLYCOLIPIDS PRESENT ON THE EPITHELIAL CELLS WHICH
CC LINE THE URINARY TRACT.
CC -1- SIMILARITY: BELONGS TO THE FIMB/PAPA FAMILY OF FIMBRIA PROTEINS.
CC -----
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CC -----
DR EMBL: X0391; CAA27126.1; -
DR EMBL: X61239; CAA43562.1; -
DR PIR: A23221; YOECP.
DR InterPro: IPR000259; Fimbril.
DR Pfam: PF00419; Fimbril; 1.
DR Fimbril; Signal.
FT SIGNAL 1 22
FT CHAIN 23 185 PAPA FIMBRIAL MAJOR PILIN PROTEIN,
FT DISUFID 44 83 PROBABLE
FT SEQUENCE 185 AA; 18686 MW; 93DB4FDDA211C671 CRC64;
SQ

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Query Match          0.6%; Score 7; DB 1; Length 185;
Best local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 724 VANFNLT 730
DB 177 VANFNLT 183

```

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RESULT 10
FIMB_ECOLI STANDARD; PRT; 187 AA.
AC P04740;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE KS71A fimbriilin precursor (P-fimbrial antigen).
GN KS71A.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;

```

```

RN
RP SEQUENCE FROM N.A.
RX MEDLINE-85285072; PubMed-2992970;
RA Rhen M., van Die I., Rhen V., Bergmans H.;
RT "Comparison of the nucleotide sequences of the genes encoding the
RT KS71A and F7(1) fimbrial antigens of uropathogenic Escherichia
RT coli."
RL Eur. J. Biochem. 151:573-577(1985).
RN
RP SEQUENCE FROM N.A.
RC MEDLINE-92040048; PubMed-1682251;
RA Denich K., Blyn L.B., Craiu A., Braaten B.A., Hardy J., Low D.A.,
RT O'Hanley P.D.;
RT "DNA sequences of three ppa genes from uropathogenic Escherichia
RT coli strains: evidence of structural and serological conservation."
RL Infect. Immun. 59:3849-3858(1991).
CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -1- SIMILARITY: BELONGS TO THE FIMB/PAPA FAMILY OF FIMBRIA PROTEINS.
CC -----
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CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: X02921; CAA26678.1; -
DR PIR: A23117; YOECS.
DR InterPro: IPR000259; Fimbril.
DR Pfam: PF00419; Fimbril; 1.
DR Fimbril; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 187 POTENTIAL.
FT DISUFID 43 82 KS71A FIMBRIILIN.
FT SEQUENCE 187 AA; 19310 MW; 799E438264C638DC CRC64;
SQ

```

```

Query Match          0.6%; Score 7; DB 1; Length 187;
Best local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 724 VANFNLT 730
DB 179 VANFNLT 185

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RESULT 11
FIMB2_ECOLI STANDARD; PRT; 188 AA.
AC P02972;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE F7-2 fimbrial protein precursor (F7-2.pilin).
GN F7-2 OR PAPA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-85155489; PubMed-6152241;
RA van Die I., Bergmans H.;
RT "Nucleotide sequence of the gene encoding the F72 fimbrial subunit of
RT a uropathogenic Escherichia coli strain."
RL Gene 32:83-90(1984).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-92040048; PubMed-1682251;
RA Denich K., Blyn L.B., Craiu A., Braaten B.A., Hardy J., Low D.A.,
RT O'Hanley P.D.;
RT "DNA sequences of three ppa genes from uropathogenic Escherichia
RT coli strains: evidence of structural and serological conservation."
RL Infect. Immun. 59:3849-3858(1991).
CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -1- SIMILARITY: BELONGS TO THE FIMB/PAPA FAMILY OF FIMBRIA PROTEINS.
CC -----
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CC -----
DR EMBL: X02921; CAA26678.1; -
DR PIR: A23117; YOECS.
DR InterPro: IPR000259; Fimbril.
DR Pfam: PF00419; Fimbril; 1.
DR Fimbril; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 187 POTENTIAL.
FT DISUFID 43 82 KS71A FIMBRIILIN.
FT SEQUENCE 187 AA; 19310 MW; 799E438264C638DC CRC64;
SQ

```


COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
 -1- DISEASE: THIS IS ONE OF THE FIBRILAL PROTEINS INVOLVED IN
 CC MANNOS-RESISTANT HEMAGGLUTINATION OF HUMAN ERYTHROCYTES.
 CC -1- SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL: M1261; AAA23778.1; -
 CC EMBL: M68060; AAA24278.1; -
 CC PIR: A03496; YOECP2.
 CC PIR: B43597; B43597.
 CC InterPro: IPR000259; Fimbrlal.
 CC Pfam: PF00419; Fimbrlal; 1.
 CC Fimbrlal; Signal.
 CC FIMBRIAL; Signal.
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 188 FT-2 FIMBRIAL PROTEIN.
 CC FT DISULFID 43 82 PROBABLE.
 CC SO SEQUENCE 188 AA; 19184 MW; 0EEF750CFD843157 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 VANFNIT 730
 DB 180 VANFNLT 186

RESULT 12
 TIM2_BOVIN STANDARD; PRT; 220 AA.
 AC P16368; Q9TVB1;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (tissue inhibitor of
 DE metalloproteinase-2) (collagenase inhibitor).
 GN TIMP2.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90207285; PubMed=2157214;
 RA Boone T.C., Johnson M.J., de Clerck Y.A., Langley K.E.;
 RT "CDNA cloning and expression of a metalloproteinase inhibitor related
 RT to tissue inhibitor of metalloproteinases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2800-2804(1990).
 RN [2]
 RP SEQUENCE OF 22-218 FROM N.A.
 RC TISSUE-Skeletal muscle;
 RA Balcerzak D., Quenengesser L., Dixon W.T., Baracos V.E.;
 RT "Involvement of fibroblasts and muscle cells in the expression of an
 RT extracellular proteolytic cascade in bovine skeletal muscle.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 27-71.
 RC TISSUE-Cartilage;
 RA MEDLINE=86140235; PubMed=3005321;
 RA Murray J.B., Allison K., Sudhalter J., Langer R.;
 RT "Purification and partial amino acid sequence of a bovine cartilage-
 RT derived collagenase inhibitor.";
 RL J. Biol. Chem. 261:4154-4159(1986).
 RN [4]

RP SEQUENCE OF 27-71.
 RX MEDLINE=90008914; PubMed=2551903;
 RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;
 RT "Purification and characterization of two related but distinct
 RT metalloproteinase inhibitors secreted by bovine aortic endothelial
 RT cells.";
 RL J. Biol. Chem. 264:17445-17453(1989).
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATES THEM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
 CC -----
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 CC -----
 CC EMBL: M32303; AAA30636.1; -
 CC EMBL: AF144764; AAD30304.1; -
 CC PIR: A25322; A25322.
 CC PIR: A35996; A35996.
 CC PIR: A34468; A34468.
 CC HSSP: P16035; 1BR9.
 CC InterPro: IPR001820; TIMP.
 CC Pfam: PF00965; TIMP; 1.
 CC SMART: SM00206; TIMP; 1.
 CC DR PROSITE: PS00288; TIMP; 1.
 CC KW Metalloproteinase inhibitor; Signal.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.
 CC FT DISULFID 27 98 BY SIMILARITY.
 CC FT DISULFID 29 127 BY SIMILARITY.
 CC FT DISULFID 39 152 BY SIMILARITY.
 CC FT DISULFID 154 201 BY SIMILARITY.
 CC FT DISULFID 159 164 BY SIMILARITY.
 CC FT DISULFID 172 193 BY SIMILARITY.
 CC FT CONFLICT 42 42 D -> C (IN REF. 3).
 CC FT CONFLICT 56 56 D -> E (IN REF. 3).
 CC FT CONFLICT 68 68 R -> S (IN REF. 3).
 CC SO SEQUENCE 220 AA; 24355 MW; 9A5438737110E7B7 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 220;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 LLLGTL 861
 DB 15 LLLGTL 21

RESULT 13
 PYRH_THEME STANDARD; PRT; 221 AA.
 AC Q9X100;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase)
 DE (UMP kinase).
 GN PYRH OR TML604.
 OS Thermotoga maritima.
 CC Bacteria; Thermotogales; Thermotoga.
 CC NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.D., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
 RT Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of *Thermotoga maritima*.
 RL Nature 399:323-329(1999).
 CC -1- FUNCTION: URIDINE MONOPHOSPHATE KINASE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + UMP -> ADP + UDP.
 CC -1- SIMILARITY: TO OTHER UMP KINASE; SOME, TO ASPARTOKINASES AND TO
 CC GLUTAMATE KINASES.
 CC -----
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 CC -----
 DR EMBL: AE001804; AAD36671.1; -
 DR TIGR: TM1604; -
 DR InterPro: IPR001048; Aakkinase.
 DR Pfam: PF006696; aakkinase; 1.
 KW Transferase; Kinase; Pyrimidine biosynthesis; Complete proteome.
 SQ SEQUENCE 231 AA; 25235 MW; 4563E9E15FA0C5ED CRC64;

Query Match 0.6%; Score 7; DB 1; Length 231;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1049 PHLTFSF 1055
 |||||
 Db 174 PHLTFSF 180

RESULT 14
 YHE4_YEAST
 ID YHE4_YEAST STANDARD; PRT: 235 AA.
 AC P38737;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 27.0 kDa protein in CBP2 5' region.
 GN YH1044W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / AB972;
 RC MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 RA Kueba T., Hillier L., Jier M., Johnston L., Langston Y.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
 RA Nhan M., Rifkin L., Riles L., St Peter H., Trevisan E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome
 VII.";
 RL Science 265:2077-2082(1994).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE DUP/COS FAMILY.
 CC -----
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 CC -----
 DR EMBL: U11583; AAB65056.1; -
 DR PIR: S48924; S48924.
 DR SGD: S0001036; YH1044W.
 DR InterPro: IPR001142; DUP.
 DR Pfam: PF00674; DUP; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 45 65
 FT TRANSNEM 73 93 POTENTIAL.
 SQ SEQUENCE 235 AA; 26972 MW; 2A789B6020870928 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 989 LISNSKP 995
 |||||
 Db 6 LISNSKP 12

RESULT 15
 BIOD_YEAST
 ID BIOD_YEAST STANDARD; PRT: 237 AA.
 AC P53630;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dethiobiotin synthetase (EC 6.3.3.3) (Dethiobiotin synthase) (DTB
 DE synthetase) (DTBS).
 GN B104 OR YNR057C OR N3506.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FL100;
 RA Phalip V., Jeltsch J.M., Lemoine Y.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Duesterhoeft A., Floeth M., Fritze C., Heuss-Neitzel D., Hilbert H.,
 RA Moestl D.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + 7,8-diaminononanoate + CO(2) -> ADP +
 CC phosphate + dethiobiotin.
 CC -1- COFACTOR: MAGNESIUM.
 CC -1- PATHWAY: BIOCONVERSION OF PIMELATE INTO DETHIOBIOTIN.
 CC -1- SIMILARITY: BELONGS TO THE DETHIOBIOTIN SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U53467; AAB63971.1; -
 DR EMBL: Z71672; CAA96339.1; -
 DR SGD: S0005340; B104.
 KW Biotin biosynthesis; Ligase; Magnesium; ATP-binding.
 FT NP_BIND 18 26
 SQ SEQUENCE 237 AA; 26257 MW; F1147B18DA40735 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 237;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GKTEVST 114
 DB 24 GKTEVST 30

RESULT 16

YE91_MYCTU STANDARD: PRT: 252 AA.
 ID YE91_MYCTU
 AC P71772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 26.6 kDa protein RV1491c.
 GN RV1491C OR MT1538 OR MTCY277.13C.
 OS Mycobacterium tuberculosis.
 OC Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 NCBI_TaxID=1773;
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE-98295987; PubMed-9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
 Hornsby T., Jagels K., Krogan A., McLean J., Moule S., Murphy L.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 [2]

SEQUENCE FROM N.A.

RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 Kolonay J.F., Nelson W.C., Umayan L.A., Ermolaeva M.D., Salzberg S.L.,
 Delcher A.L., Utterback T., Weidman J., Khouri H., Gail J., Mikula A.,
 Bishop W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE UPF0043 FAMILY.
 CC -----
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 CC -----
 CC
 DR EMBL: Z79701; CAB02041.1;
 DR EMBL: AE007022; AAK45805.1;
 DR TIGR: MT1538;
 DR TubercuList: RV1491c;
 DR KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 32 52 POTENTIAL.
 FT TRANSMEM 64 84 POTENTIAL.
 FT TRANSMEM 88 108 POTENTIAL.
 FT TRANSMEM 149 169 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 209 229 POTENTIAL.
 SQ SEQUENCE 252 AA: 26575 MW: 3E63BE13217B8201 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 252;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 LVPVPTA 203
 DB 48 LVPVPTA 54

RESULT 17

MAUN_PARDE STANDARD: PRT: 283 AA.
 ID MAUN_PARDE
 AC O51660;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Methylamine utilization ferredoxin-type protein maun.
 GN MAUN.
 OS Paracoccus denitrificans.
 OC Bacteria: Proteobacteria; alpha subdivision; Rhodospirillum group;
 OC Paracoccus.
 NCBI_TaxID=266;
 OX NCBI_TaxID=266;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PD 1222;
 RX MEDLINE-95324575; PubMed-7601147;
 RA van der Palen C.J., Slotboom D.J., Jongejans L., Reijnders W.N.,
 Harms N., Duine J.A., van Spanning R.J.;
 RT "Mutational analysis of mau genes involved in methylamine metabolism
 RT in Paracoccus denitrificans."
 RL Eur. J. Biochem. 230:860-871(1995).
 CC -1- FUNCTION: INVOLVED IN ELECTRON TRANSFER (POTENTIAL).
 CC -1- PATHWAY: METHYLAMINE UTILIZATION.
 CC -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
 CC 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
 CC -----

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC
 DR EMBL: U15028; AAB6469.1;
 DR HSSP: P00195; 1CLF.
 DR InterPro: IPR001450; 4Fe4S_ferredoxin.
 DR Pfam: PF00037; fer4; 2.
 DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; 2.
 KW Electron transport; Iron-sulfur; 4Fe-4S.

FT METAL 227 227 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
 FT METAL 230 230 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
 FT METAL 233 233 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
 FT METAL 237 237 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 FT METAL 260 260 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 FT METAL 263 263 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 FT METAL 266 266 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 FT METAL 270 270 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 283 AA: 31035 MW: FB2C87C9B8917BDE CRC64;

Query Match 0.6%; Score 7; DB 1; Length 283;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 LLLGTLT 861
 DB 142 LLLGTLT 148

RESULT 18

EXOS_BPT5 STANDARD: PRT: 290 AA.
 ID EXOS_BPT5
 AC P06229;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Exodeoxyribonuclease (EC 3.1.11.3) (5' exonuclease).
 GN D15.
 OS Bacteriophage T5.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=10726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86108899; PubMed=3002857;
 RA Kallman A.V., Krutillina A.I., Kryukov V.M., Bayev A.A.;
 RT "Cloning and DNA sequence of the 5'-exonuclease gene of bacteriophage T5."
 RL FEBS Lett. 195;61-64(1986).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RA MEDLINE=96273035; PubMed=8657312;
 RA Ceska T.A., Sayers J.R., Stier G., Suck D.;
 RT "A helical arch allowing single-stranded DNA to thread through T5 5'-exonuclease."
 RL Nature 382;90-93(1996).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS), AND MUTAGENESIS.
 RA MEDLINE=99093486; PubMed=9874768;
 RA Garforth S.J., Ceska T.A., Suck D., Sayers J.R.;
 RT "Mutagenesis of conserved lysine residues in bacteriophage T5 5'-3' exonuclease suggests separate mechanisms of endo- and exonucleolytic cleavage."
 RL Proc. Natl. Acad. Sci. U.S.A. 96;38-43(1999).
 CC -1- CATALYTIC ACTIVITY: DEGRADATION OF DOUBLE-STRANDED AND SINGLE-STRANDED DNA. IT ACTS PROGRESSIVELY IN A 5' TO 3' DIRECTION, RELEASING 5'-PHOSPHONONUCLEOTIDES.
 CC -1- CORRECTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 5'-3' EXONUCLEASE DOMAIN.
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 CC -----
 DR EMBL: X03402; CAA27136.1; -
 DR EMBL: A0001191; CAA04588.1; -
 DR PIR: A23610; NCBP75.
 DR PDB: 1XN1; 07-JUL-97.
 DR PDB: 1X01; 12-APR-99.
 DR InterPro: IPR002421; 5_3_exonuclease.
 DR InterPro: IPR000513; EXO_N.T.
 DR InterPro: IPR003584; HHH_2.
 DR Pfam: PF01367; 5_3_exonuclease; 1.
 DR SMART: SM00475; 53EXOC; 1.
 DR SMART: SM00279; HHH2; 1.
 KM Hydrolyase; Nuclease; Exonuclease; 3D-structure.
 FT INIT_MER 0
 SQ SEQUENCE 290 AA; 33316 MW; 0947BCA05BC3BBF CRC64;

Query Match 0.6%; Score 7; DB 1; Length 290;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 452 STIOSLA 458
 ID |||||
 DB 48 STIOSLA 54

RESULT 19
 NPL_HAEIN STANDARD; PRT; 293 AA.
 AC P44539;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable N-acetylneuraminatase lyase subunit (EC 4.1.3.3) (N-acetylneuraminic acid aldolase) (N-acetylneuraminatase pyruvate lyase)
 GN (Nalase).
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=RD / KW20 / ATCC 51907;
 RA MEDLINE=95350630; PubMed=7342800;
 RA Felschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty R.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley G., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Uterback T.R., Hanna M.C., Nguyen D.T., Saudex D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small R.V., Fraser C.M., Smith H.O., Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."
 RL Science 269;496-512(1995).
 CC -1- CATALYTIC ACTIVITY: N-acetylneuraminatase - N-acetyl-D-mannosamine + pyruvate.
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE DHPS FAMILY.
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 CC -----
 DR EMBL: U32700; AAC21814.1; -
 DR HSSP: P06995; INML.
 DR TIGR: H10142; -
 DR InterPro: IPR002220; DHPS.
 DR Pfam: PF00701; DHPS; 1.
 DR PRINTS: PR00146; DHPICNTNASE.
 DR PRODOM: PD001859; DHPS; 1.
 DR PROSITE: PS00665; DHPS_1; 1.
 DR PROSITE: PS00666; DHPS_2; 1.
 KM Lyase; Complete proteome.
 FT ACT_SITE 164
 SQ SEQUENCE 293 AA; 32564 MW; ACA755D0A5D93D33 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 293;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1059 ELIKLEG 1065
 ID |||||
 DB 256 ELIKLEG 262

RESULT 20
 YCYJ_ECOLI STANDARD; PRT; 310 AA.
 AC P76049; P77483; P76844;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein ycjY.
 GN YCYJ OR B1327.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.

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OX NCB1_TaxID=562;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blatner F.R., Plunkett G., Ilti, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97251357; PubMed-9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasa H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
RA Oshima T., Saito N., Sempel G., Seki Y., Sivasubraman S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horuchi T.;
RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map."
RL DNA Res. 3:363-377(1996).
CC -1- SIMILARITY: TO P.AERUGINOSA HYPOTHETICAL 40.7 kDa PROTEIN IN OPDE
CC 3'REGION (AC Q01609).
CC
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CC -----
CC DR EMBL: AE000230; AAC74409.1; -
CC DR EMBL: D90770; BAA14809.1; -
CC DR EMBL: D90771; BAA14920.1; -
CC DR EMBL: D90772; BAA14930.1; -
CC DR Ecogene: EG13922; ycyJ.
CC DR InterPro: IPR000379; Est_lip_thioest_actsite.
CC KW Hypothetical protein: Complete proteome.
CC CONFLICT 259 259 S -> R (IN REF. 2).
CC FT SEQUENCE 310 AA; 34117 MW; 20291A71BD367B70 CRC64;
SQ

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Query Match          0.6%: Score 7; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 333 VYFPPK 339
    |||||
DB 25 VYFPPK 31

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RESULT 21
PPI1_YEAST STANDARD: PRT; 311 AA.
AC P20604;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Serine/threonine protein phosphatase PPI-1 (EC 3.1.3.16).
GN PPI1 OR SIT4 OR YDL047W OR D2693.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCB1_TaxID=4932;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-89136000; PubMed-2537149;
RA Arndt K.T., Styles C.A., Fink G.R.;

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RT "A suppressor of a HIS4 transcriptional defect encodes a protein with
RT homology to the catalytic subunit of protein phosphatases."
RL Cell 56:527-537(1989).
RN
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-S288C;
RA Paulin L., Saren A.M., Laanen P.;
RA Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
RL [3]
RN CHARACTERIZATION.
RX MEDLINE-91172202; PubMed-1848673;
RA Sutton A., Immanuel D., Arndt K.T.;
RT "The SIT4 protein phosphatase functions in late G1 for progression
RT into S phase."
RL Mol. Cell. Biol. 11:2133-2148(1991).
CC -1- FUNCTION: INVOLVED IN THE DEPHOSPHORYLATION OF THE LARGE SUBUNIT
CC OF RNA POLYMERASE II. IS REQUIRED IN LATE G1 FOR NORMAL G1 CYCLIN
CC EXPRESSION, BUD INITIATION AND EXPRESSION OF CERTAIN GENES THAT
CC ARE PERIODICALLY EXPRESSED DURING LATE G1. ASSOCIATES WITH THE
CC SAP PROTEINS IN A CELL CYCLE-DEPENDENT MANNER.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DEVELOPMENTAL STAGE: FUNCTIONS IN THE LATE CELL CYCLE G1 PHASE FOR
CC PROGRESSION INTO THE S PHASE, POSSIBLY ASSOCIATED IN TWO SEPARATE
CC COMPLEXES WITH THE PHOSPHORYLATED FORMS OF P155 AND P190, TWO HIGH
CC MW PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-V
CC SUBFAMILY.
CC -----
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CC -----
CC DR EMBL: M24395; AA556864.1; -
CC DR EMBL: 271781; CAA96442.1; -
CC DR EMBL: 274095; CAA98609.1; -
CC DR PIR: A31874; PABY1.
CC DR HSP: P08129; IFTM.
CC DR SGD: S0002205; SIT4.
CC DR InterPro: IPR000934; Ser_thr_phosphatase.
CC DR Pfam: PF00149; STPhosphatase; 1.
CC DR PRINTS: PR00114; STPHPTASE.
CC DR SMART: SM00156; PP2AC; 1.
CC DR PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.
CC KW Hydrolyase; Iron; Manganese; Cell cycle; Mitosis; Multigene family.
CC FT METAL 53 53 IRON (BY SIMILARITY).
CC FT METAL 55 55 IRON (BY SIMILARITY).
CC FT METAL 82 82 IRON AND MANGANESE (BY SIMILARITY).
CC FT METAL 114 114 MANGANESE (BY SIMILARITY).
CC FT ACT SITE 115 115 GENERAL ACID (BY SIMILARITY).
CC FT METAL 164 164 MANGANESE (BY SIMILARITY).
CC FT METAL 238 238 MANGANESE (BY SIMILARITY).
CC FT SEQUENCE 311 AA; 35537 MW; AF52BC65E4E715EC CRC64;
SQ

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Query Match          0.6%: Score 7; DB 1; Length 311;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 208 TLIMCKL 214
    |||||
DB 95 TLIMCKL 101

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RESULT 22
YG54_ARCFU STANDARD: PRT; 329 AA.
ID YG54_ARCFU
AC O28619;

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DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hypothetical protein AF1654.
GN AF1654.
OS Archaeoglobus fulgidus.
OC Archaeae; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
ON NCBI_TaxID=2234;
RX STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RA MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Claydon R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kariya A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann D.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirsnes E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodex A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Colton M.D., Spriggs T., Arlrich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RT Nature 390:364-370(1997).
CC -----
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CC -----
DR EMBL: AE000989; AAB89615.1; -
DR TIGR: AF1654; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 13 35
FT TRANSMEM 229 248
FT SEQUENCE 329 AA; 37776 MW; E307CAAI61193DE CRC64;
SQ

```

Query Match 0.6%; Score 7; DB 1; Length 329;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 893 ETEFHF 899
DB 301 ETEFHF 307

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RESULT 23
 KCCL_SCHPO STANDARD; PRT; 335 AA.
 ID KCCL_SCHPO STANDARD; PRT; 335 AA.
 AC 099712; 074235;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
 DE (CaMK-I).
 DE CMKI OR SPAC25D11.02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 ON NCBI_TaxID=4896;
 RX STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RA MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Claydon R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kariya A.R., Graham D.E., Kyriades N.C.,
 RA Fleischmann D.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirsnes E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodex A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Colton M.D., Spriggs T., Arlrich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus."
 RT Nature 390:364-370(1997).
 CC -----
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 CC -----
 DR EMBL: AE000989; AAB89615.1; -
 DR TIGR: AF1654; -
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 13 35
 FT TRANSMEM 229 248
 FT SEQUENCE 329 AA; 37776 MW; E307CAAI61193DE CRC64;
 SQ

```

RT pombe.;
RL J. Biol. Chem. 275:685-690(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
RL Submitted (Feb-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: IMPORTANT IN CELL CYCLE REGULATION.
CC -1- CATALYTIC ACTIVITY: ATP + protein -> ADP + O-phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC -----
DR EMBL: AF073893; AAC26005.1; -
DR EMBL: AL157993; CAB76233.1; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase;
KW Calmodulin-binding; Phosphorylation.
FT DOMAIN 31 291
FT NP_BIND 37 45
FT DOMAIN 310 334
FT ACT_SITE 154 154
FT MOD_RES 192 192
FT MUTAGEN 192 192 T->D: 15-FOLD INCREASE IN ACTIVITY.
FT CONFLICT 115 115 E->A (IN REF. 1).
FT CONFLICT 294 295 KR->NG (IN REF. 1).
FT SEQUENCE 335 AA; 38163 MW; 8761BRCF6882B02 CRC64;
SQ

```

Query Match 0.6%; Score 7; DB 1; Length 335;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 504 FLLSGY 510
DB 225 FLLSGY 231

```

RESULT 24
 LEU3_MYCBO STANDARD; PRT; 336 AA.
 ID LEU3_MYCBO STANDARD; PRT; 336 AA.
 AC P94929;
 DT 15-DEC-1998 (rel. 37, Created)
 DT 15-DEC-1998 (rel. 37, Last sequence update)
 DT 15-DEC-1998 (rel. 37, Last annotation update)
 DE 3-Isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)
 DE (IMDH) (3-IPM-DH).
 DE LEUB.
 OS Mycobacterium bovis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 ON NCBI_TaxID=1765;
 RX STRAIN-BGC;
 RA MEDLINE=97266124; PubMed=9111927;
 RA Han M.Y., Son M.Y., Lee S.H., Kim J.K., Huh J.S., Kim J.H., Choe I.S.,
 RA Chung T.W., Choe Y.K.;
 RT "Molecular cloning of the leub genes from Mycobacterium bovis BCG and

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RT Mycobacterium tuberculosis";
CC Blochem. Mol. Biol. Int. 41:657-663(1997).
CC -1- CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANOATE +
CC NAD(+) -> 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PRODUCT
CC DECARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
CC -1- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
CC -----
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CC -----
DR EMBL: U78886; AAC45173.1; -.
DR HSP: P00351; 1XAA.
DR InterPro: IPR001804; Isodh.
DR Pfam: PF00180; Isodh. 1.
DR PROSITE: PS00470; IDH_IMDH: 1.
DR OXidoreductase; Leucine biosynthesis; NAD.
DR KM SEQUENCE 336 AA; 35272 MW; 03C95850ACCA51E2 CRC64;
SQ
Query Match 0.6%; Score 7; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 529 VLPDSVY 535
DB 48 VLPDSVY 54
LEU3_MYCTU STANDARD: PRT; 336 AA.
AC P95313;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-Isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)
DE (IMDH) (3-IPM-DH).
GN LEUB OR RV2995C OR MT3073 OR MTV012.09.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97266124; PubMed=9111927;
RA Han M.Y., Son M.Y., Lee S.H., Kim J.K., Huh J.S., Kim J.H., Choe I.S.,
RA Chung T.W., Choe Y.K.;
RT "Molecular cloning of the leub genes from Mycobacterium bovis BCG and
RT Mycobacterium tuberculosis."
RL Biochem. Mol. Biol. Int. 41:657-663(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeller K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Kirog A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sutton J.E., Taylor K., Whitehead S., Barrall B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."

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RL Nature 393:537-544(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Ustebach T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RT Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANOATE +
CC NAD(+) -> 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PRODUCT
CC DECARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
CC -1- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL: U78887; AAC45174.1; -.
DR EMBL: AL021287; CAI16080.1; -.
DR EMBL: AE007127; AKA47402.1; -.
DR HSP: P00351; 1XAA.
DR TIGR: MT3073; -.
DR Tuberculist: RV2995c; -.
DR InterPro: IPR001804; Isodh.
DR Pfam: PF00180; Isodh. 1.
DR PROSITE: PS00470; IDH_IMDH: 1.
DR OXidoreductase; Leucine biosynthesis; NAD; Complete proteome.
DR KM SEQUENCE 336 AA; 35306 MW; E78718100CCASB42 CRC64;
SQ
Query Match 0.6%; Score 7; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 529 VLPDSVY 535
DB 48 VLPDSVY 54
GGH_SOYBN STANDARD: PRT; 342 AA.
AC P93164;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-GLU-X
DE carboxypeptidase) (Conjugase) (GH).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. WILLIAMS 82;
RX MEDLINE=97069645; PubMed=8912628;
RA Huangpu J., Pak J.H., Burkhardt W., Graham M.C., Rickle S.A.,
RA Graham J.S.;
RT "Purification and molecular analysis of an extracellular gamma-
RT glutamyl hydrolase present in young tissues of the soybean plant."

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BL Biochem. Biophys. Res. Commun. 228:1-6(1996).
 CC -1- CATALYTIC ACTIVITY: Cleavage of a gamma-glutamyl bond to release
 CC an unsubstituted C-terminal amino acid.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR OR CELL-MALL BOUND.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN YOUNG (1-15 DAY OLD) LEAF.
 CC STEM AND ROOT TISSUE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C26.
 CC -----
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 CC -----
 DR EMBL: 063726; AAB26960.1; -
 DR Mendel: 12606; GLYMA1806.1;
 KW Hydrolyase; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 342 GAMMA-GLUTAMYL HYDROLASE.
 FT CARBOHD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 342 AA; 37676 MW; 515CBAD1E5BA258C CRC64;

 Query Match 0.6%; Score 7; DB 1; Length 342;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 108 GRTFST 114
 Db 248 GRTFST 254

 RESULT 27
 SOHB_ECOLI
 ID SOHB_ECOLI STANDARD; PRT: 349 AA.
 AC P24213; P77676; 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Possible protease sohb (EC 3.4.21.-).
 GN SOHB OR B1272.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91358368; PubMed=1885549;
 RA Baird L., Lipinska B., Raina S., Georgopoulos C.;
 RT "Identification of the Escherichia coli sohb gene, a multicopy
 RT suppressor of the Htra (DegP) null phenotype.";
 RL J. Bacteriol. 173:5763-5770(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakabe S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Satou N.,
 RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,

Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28,040.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 CC -1- FUNCTION: MULTICOPY SUPPRESSOR OF THE HTRA (DEGP) NULL PHENOTYPE.
 CC IT IS POSSIBLY A PROTEASE, NOT ESSENTIAL FOR BACTERIAL VIABILITY.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S49.
 CC -----
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 CC -----
 DR EMBL: M73320; AAA24639.1; -
 DR EMBL: AE00225; AAC74354.1; -
 DR EMBL: D90764; BAA14809.1; -
 DR EMBL: D90765; BAA14824.1; -
 DR PIR: A38115; A38115.
 DR MEROPS: S49.002; -
 DR Ecocore: E010956; sohb.
 DR InterPro: IPR002142; Peptidase_U7.
 DR Pfam: PF01343; Peptidase_U7; 1.
 DR ProDom: PD02897; Peptidase_U7; 1.
 KW Protease; Hydrolyase; Transmembrane; Complete proteome.
 FT TRANSMEM 9 29 POTENTIAL.
 FT CONFLICT 85 85 A -> R (IN REF. 1).
 FT CONFLICT 90 90 A -> R (IN REF. 1).
 FT CONFLICT 296 296 T -> A (IN REF. 1).
 SQ SEQUENCE 349 AA; 39366 MW; 3362AE74C33C5FC CRC64;

 Query Match 0.6%; Score 7; DB 1; Length 349;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 284 ADKIVSA 290
 Db 187 ADKIVSA 193

 RESULT 28
 SOHB_HAEIN
 ID SOHB_HAEIN STANDARD; PRT: 353 AA.
 AC P45315;
 DT 01-NOV-1995 (Rel. 32, Created).
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Possible protease sohb (EC 3.4.21.-).
 GN SOHB OR H11682.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uiterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georgiades N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL Science 269:496-512(1995).
 RN [1]
 RP FUNCTION: POSSIBLE PROTEASE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S49.
 CC -----
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 CC -----
 CC EMBL: U32841; AAC3328.1; .
 CC MEROPS: S49.002; .
 CC TIGR: H11682; .
 CC InterPro: IPR002142; Peptidase_U7.
 CC Pfam: PF01343; Peptidase_U7; 1.
 CC ProDom: PD002897; Peptidase_U7; 1.
 CC ProScan: Hydrolyase; Transmembrane; Complete proteome.
 CC TRANSMEM 11 31 POTENTIAL
 CC SEQUENCE 353 AA; 39872 MW; 4C2E6D75B0F88070 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 353;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 284 ADKIVSA 290
 |||||
 DB 190 ADKIVSA 196

RESULT 29
 CHSB_PHANT STANDARD; PRT; 363 AA.
 AC P48396;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Chalcone synthase B (Ec 2.3.1.74) (Naringenin-chalcone synthase B)
 DE (CHS-B) (Fragment).
 GN CHSB.
 OS Pharbitis nil (Violet) (Japanese morning glory).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; easterids I; Solanales; Convolvulaceae; Ipomoea.
 OX NCBI_TaxID=35583;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95241498; PubMed=7724563;
 RA Dudin M.L., Leach G.H., Huttley G.A., Clegg M.T.;
 RT "Evolution of the chalcone synthase gene family in the genus
 RT Ipomoea.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:3338-3342(1995).
 CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4',2'',4'',6''-
 CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
 CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
 CC NARINGENIN.
 CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA -> 4 CoA +
 CC naringenin-chalcone + 3 CO(2).
 CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
 CC FLAVONOIDS. A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
 CC OF WHICH ARE BRIGHTLY COLORED.
 CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
 CC -----
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 CC -----
 CC EMBL: U15944; AAC49029.1; .
 CC InterPro: IPR001099; Chal_still_synt.

DR Pfam: PF00195; Chal_still_synt; 1.
 DR Pfam: PF02797; Chal_still_synt; 1.
 DR PROSITE: PS00441; CHALCONE_SYNTH; 1;
 KW Flavonoid biosynthesis; Transferase; Acyltransferase;
 KW Multigene family.
 FT ACT_SITE 170 170 BY SIMILARITY.
 FT NON_TER 363 363
 SQ SEQUENCE 363 AA; 40483 MW; 9349FBA60C7C3FA CRC64;

Query Match 0.6%; Score 7; DB 1; Length 363;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 545 AEITINI 551
 |||||
 DB 197 AEITINI 203

RESULT 30
 RCLL_HUMAN STANDARD; PRT; 373 AA.
 ID RCLL_HUMAN
 AC Q9Y2P8; Q9NY00; Q9P044; Q9H9D0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RNA 3'-terminal phosphate cyclase-like protein (HSPC338).
 DE RNAC OR RPC2 OR RTC2 OR RCLL.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20253086; PubMed=10790377;
 RA Billy E., Meglerki T., Nasr F., Filipowicz W.;
 RT "Rollp, the yeast protein similar to the RNA 3'-phosphate cyclase,"
 RT associates with U3 snRNP and is required for 18S RNA biogenesis.";
 RT EMBO J. 19:2115-2126(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retinoblastoma;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDB databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayaishi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 RA Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y., Oshima A.;
 RT "NEBD human cDNA sequencing project.";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DDB databases.
 RN [4]
 RP SEQUENCE OF 8-373 FROM N.A.
 RA Kan L., Zhang Q.H., Fu G., Zhou J., Ye M., Shen Y., Wu J., He K.,
 RA Chen S.J., Mao M., Chen Z.;
 RT "Human hemopoietic cell derived RNA cyclase (hRNC) homolog.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDB databases.
 RN [5]
 RP SEQUENCE OF 46-373 FROM N.A.
 RC TISSUE=Blood;
 RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
 RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
 RT "Human partial cDS from cd34+ stem cells.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDB databases.
 CC -1- FUNCTION: DOES NOT HAVE CYCLASE ACTIVITY. PLAYS A ROLE IN 40S-
 CC RIBOSOMAL-SUBUNIT BIOGENESIS IN THE EARLY PRE-RNA PROCESSING
 CC STEPS AT SITES A0, A1 AND A2 THAT ARE REQUIRED FOR PROPER
 CC MATURATION OF THE 18S RNA (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RNA 3'-TERMINAL CYCLASE FAMILY.
 CC SUBFAMILY 2.

CC -1- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
 CC IN POSITIONS 13 AND 58.
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 CC -----
 DR EMBL: AJ276894; CAB89811.1; -
 DR EMBL: BC001025; AAH01025.1; -
 DR EMBL: AF022904; BAB1300.1; -
 DR EMBL: AF067172; AAD32456.1; ALT_FRAME.
 DR EMBL: AF161456; AAF29016.1; -
 DR InterPro: IPR000228; RTC.
 DR Pfam: PF01137; RTC; 1.
 DR PROSITE: PS01287; RTC; 1.
 KW Nuclear protein.
 FT CONFLICT 6 6 H -> Y (IN REF. 3).
 FT CONFLICT 46 46 D -> S (IN REF. 5).
 FT CONFLICT 49 49 A -> S (IN REF. 5).
 FT CONFLICT 153 153 K -> N (IN REF. 3).
 FT CONFLICT 310 310 R -> Q (IN REF. 2 AND 3).
 SQ SEQUENCE 373 AA; 40870 MW; 51EFA056F0AF93C8 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 373;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 FSNLSKT 85
 DB 365 FSNLSKT 371

RESULT 31
 RCL1_MOUSE
 ID RCL1_MOUSE STANDARD; PRT; 373 AA.
 AC 09J370;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE RNA 3'-terminal phosphatase cyclase-like protein.
 GN RNAC OR RCL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20253086; PubMed-10790377;
 RA Billy E., Wegierski T., Naar F., Filipowicz W.;
 RT "Rcl1, the yeast protein similar to the RNA 3'-phosphate cyclase,
 RT associates with U3 snRNP and is required for 18S rRNA biogenesis."
 RL EMO J. 19:2115-2126(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; Tissue-Tongue;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arawata T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya W., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Williams L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: DOES NOT HAVE CYCLASE ACTIVITY. PLAYS A ROLE IN 40S-
 CC RIBOSOMAL-SUBUNIT BIOGENESIS IN THE EARLY PRE-RRNA PROCESSING
 CC STEPS AT SITES A0, A1 AND A2 THAT ARE REQUIRED FOR PROPER
 CC MATURATION OF THE 18S RNA (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RNA 3'-TERMINAL CYCLASE FAMILY.
 CC SUBFAMILY 2.
 CC -----
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 CC -----
 DR EMBL: AJ276895; CAB89817.1; -
 DR EMBL: AK009709; BAB26454.1; -
 DR MGD: MGI:1913275; Rnac.
 DR InterPro: IPR000228; RTC.
 DR Pfam: PF01137; RTC; 1.
 DR PROSITE: PS01287; RTC; 1.
 KW Nuclear protein.
 SQ SEQUENCE 373 AA; 40840 MW; 3BE97CA47A8CEFA1 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 373;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 FSNLSKT 85
 DB 365 FSNLSKT 371

RESULT 32
 Y801_METUA
 ID Y801_METUA STANDARD; PRT; 379 AA.
 AC 058211;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Hypothetical ATP-binding protein MJ0801.
 GN MJ0801.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus;
 OX NCBI_Taxid=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE-96337999; PubMed-8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weisslock K.G., Merrick J.M., Glodok A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hirst M.A., Kaine B.P., Botodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii."
 RL Science 273:1058-1073(1996).
 RN [2]
 RP SIMILARITY.

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RX MEDLINE-97197912; PubMed-9045616;
RA Koonin E.V.;
RL "Evidence for a family of archaeal ATPases.";
RL Science 275:1489-1490(1997).
CC -1- SIMILARITY: BELONGS TO THE ARCHAEOAL ATPASE FAMILY.
CC -----
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CC -----
DR EMBL: U67524; AAB98799.1; -
DR TIGR: M0801; -
DR InterPro: IPR002576; Archaeal_ATPase.
DR Pfam: PF01637; Archaeal_ATPase.1.
DR ProDom: PD003808; Archaeal_ATPase.1.
KW Hypothetical protein; ATP-binding; Complete proteome.
FT NP_BIND 29 36 ATP (POTENTIAL).
SQ SEQUENCE 379 AA; 44716 MM; 1BAF2567E0C5D0B4 CRC64;

Query Match 0.68; Score 7; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 VENNINL 1130
DB 243 VENNINL 249

RESULT 33
ID PURT_BACSU STANDARD; PRT; 384 AA.
AC P39771; O31450;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-) (GART 2)
DE (GAR transferase 2) (5'-phosphoribosylglycinamide transferase)
DE 2) (Formate-dependent GAR transferase).
GN PURT.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE-96118702; PubMed-7496533;
RA Saxild H.H., Jacobsen J.H., Nygaard P.;
RT "Functional analysis of the Bacillus subtilis purt gene encoding
RT formate-dependent glycylamide ribonucleotide transferase.";
RL Microbiology 141:2211-2218(1995).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RA Hara K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;
RT "Sequence analysis of the 70kD region between 17 and 23 degree of the
RT Bacillus subtilis chromosome.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES TWO REACTIONS:THE FIRST ONE IS THE PRODUCTION
CC OF BETA-FORMYL GLYCINAMIDE RIBONUCLEOTIDE (GAR) FROM FORMATE, ATP
CC AND BETA GAR. THE SECOND, A SIDE REACTION, IS THE PRODUCTION OF
CC ACETYL PHOSPHATE AND ADP FROM ACETATE AND ATP.
CC -1- CATALYTIC ACTIVITY: FORMATE + ATP + 5'-PHOSPHO-RIBOSYLGLYCINAMIDE
CC = 5'-PHOSPHORIBOSYL-N-FORMYLGLYCINAMIDE + ADP + PYROPHOSPHATE.
CC -1- COFACTOR: MAGNESIUM (BY SIMILARITY).
CC -1- PATHWAY: THIRD STEP (FIRST OF TWO TRANSFORMYLATION REACTIONS)
CC IN DE NOVO PURINE BIOSYNTHESIS. THIS IS AN ALTERNATIVE ENZYME TO
CC THE PURN GAR TRANSFORMYLASE.

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CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PURK / PURT FAMILY.
CC -----
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CC -----
DR EMBL: X78962; CA55557.1; -
DR EMBL: AB006424; BAA33120.1; -
DR EMBL: Z9105; CAB12017.1; -
DR PIR: S47267; S47267.
DR Subtilist; BG10924; PURT.
DR InterPro: IPR003135; ATP-grasp.
DR Pfam: PF02222; ATP-grasp.1.
KW Purine biosynthesis; Transferase; Magnesium; Complete proteome.
FT CONFLICT 240 241 KH -> ND (IN REF. 1).
SQ SEQUENCE 384 AA; 42093 MM; 5E3642C6CA90F7.CRC64;

Query Match 0.68; Score 7; DB 1; Length 384;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1058 DELLKLE 1064
DB 81 DELLKLE 87

RESULT 34
ID RPA2_METVA STANDARD; PRT; 386 AA.
AC P14247;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA-directed RNA polymerase subunit A* (EC 2.7.7.6).
GN RPOA2.
OS Methanococcus vannielii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2187;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1224;
RA Palm P., Arnold-Hammer I., Lechner K.A., Zillig W.;
RT Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 171-386 FROM N.A.
RC STRAIN=DSM 1224;
RX MEDLINE-89362493; PubMed-2475640;
RA Lechner K., Heller G., Boeck A.;
RT "Organization and nucleotide sequence of a transcriptional unit of
RT Methanococcus vannielii comprising genes for protein synthesis
RT elongation factors and ribosomal proteins.";
RL J. Mol. Evol. 29:20-27(1989).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC {RNA}(n).
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----
 DR EMBL: X73293; CAA51729.1;
 DR EMBL: X15970; CAA34086.1;
 DR PIR: S06620; S06620.
 DR InterPro: IPR002879; RNA_pol_A2.
 DR Pfam: PF01854; RNA_pol_A2; 1.
 DR Transbase; Transcription; DNA-directed RNA polymerase; Zinc.
 KW SEQUENCE 386 AA; 42982 MW; 0D26292FB45BA6A7 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 386;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 SEDISVD 925
 |||||
 DB 143 SEDISVD 149

RESULT 35
 CHSB_IPOPU STANDARD: PRT: 396 AA.

AC P48398;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Chalcone synthase B (EC 2.3.1.74) (Naringenin-chalcone synthase B)
 DE (CHS-B).
 GN CHSB.

OS Ipomoea purpurea (Common morning glory).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
 OX NCBI_TaxID=4121;

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE-95241498; PubMed-7724563;
 RA Durbin M.L., Learn G.H., Huttley G.A., Clegg M.T.;
 RT "Evolution of the chalcone synthase gene family in the genus
 Ipomoea."

RL Proc. Natl. Acad. Sci. U.S.A. 92:3338-3342(1995).
 CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4',2',4',6'-
 TETRAHYDROXYCHALONE (ALSO TERMED NARINGENIN-CHALONE OR CHALCONE)

CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
 CC NARINGENIN.
 CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA = 4 CoA +
 CC naringenin-chalcone + 3 CO(2).

CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF
 CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY
 CC OF WHICH ARE BRIGHTLY COLORED.
 CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.

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CC EMBL: U15947; AAC49030.1;
 DR InterPro: IPR001099; Chal_still_synt.
 DR Pfam: PF00195; Chal_still_synt; 1.
 DR Pfam: PF02797; Chal_still_synt; 1.
 DR PROSITE: PS00441; CHALCONE_SYNTH.1.
 KM Flavonoid biosynthesis; Transferrase; Acyltransferase;
 KM Multigene family.
 FT ACT_SITE 170
 SEQUENCE 396 AA; 43926 MW; 352C478C1AF892B6 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 396;
 Best Local Similarity 100.0%; Pred. No. 68;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 545 AETTINI 551
 |||||
 DB 197 AETTINI 203

RESULT 36
 YMS7_YEAST STANDARD: PRT: 420 AA.

AC 003694;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 47.3 kDa protein in TOM40-PRK2 intergenic region.
 GN YMR204C OR YMR325-05C.
 GN Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-S288C / AB972;
 RA Odell C., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

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DR EMBL: Z48755; CAA88645.1;
 DR SGD: S0004817; YMR204C.
 KW Hypothetical protein.

KW SEQUENCE 420 AA; 47314 MW; A11EF5121DEF675 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 420;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1131 GTSKKT 1137
 |||||
 DB 63 GTSKKT 69

RESULT 37
 EXLP_TOBAC STANDARD: PRT: 426 AA.

AC 003211;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Pistil-specific extensin-like protein precursor (PELP).
 DE Nicotiana tabacum (Common tobacco).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. PETITE HAVANA; TISSUE-Pistil;
 RX MEDLINE-93005740; PubMed-1392607;
 RA Goldman M.H., Pezzotti M., Seurinck J., Mariani C.;
 RT "Developmental expression of tobacco pistil-specific genes encoding
 RT novel extensin-like proteins";
 RT Plant Cell 4:1041-1051(1992).

CC -1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN FLORAL BUDS AFTER
 CC PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING

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CC FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE
CC AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER
CC POLLINATION.
CC -----
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CC -----
CC EMBL: Z14019; CA78397.1; -
CC PIR: JQ1696; JQ1696.
CC InterPro: IPR000419; Pollen_Ole_e-1.
CC Pfam: PF01190; Pollen_Ole_e-1.
CC Structural protein; signal; Repeat; Glycoprotein.
CC SIGNAL 1 23
CC CHAIN 24 426 PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN.
CC DOMAIN 69 182 4 X 5 AA REPEATS OF S-P(4).
CC REPEAT 69 73 1.
CC REPEAT 76 80 2.
CC REPEAT 83 87 3.
CC REPEAT 178 182 4.
CC CARBOHD 310 310 N-LINKED (GLCNAc...) (POTENTIAL).
CC SEQUENCE 426 AA; 44278 MW; 51A495C94017812 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 VKPLP 540
|111111|
Db 278 VKPLP 284

RESULT 38
TBB2_PHYPO STANDARD; PRT; 454 AA.
ID TBB2_PHYPO
AC P12458;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tubulin beta-2 chain ('Tubulin beta-major chain').
GN BETA.
OS Physarum polycephalum (Slime mold).
OS Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
CC Physarum.
CC NCBI_TaxID=5791;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=88216603; PubMed=2835667;
RA Burland T.G., Paul E.C.A., Oetliker M., Dove W.F.;
RT Physarum polycephalum plasmodia.
RL Mol. Cell. Biol. 8:1275-1281(1988).
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
CC -1- FUNCTION: THIS IS THE MAJOR BETA TUBULIN OF MITOTIC SPINDLE.
CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
CC -1- SUBCELLULAR LOCATION: MITOSIS IN THE SLIME MOLD PLASMODIUM DIFFERS
CC FROM THE PROCESS IN MANY EUKARYOTES. THE TUBULIN CHAINS MUST BE
CC TRANSPORTED TO THE NUCLEI FOR INTRANUCLEAR ASSEMBLY OF THE
CC SPINDLE.
CC -1- DEVELOPMENTAL STAGE: PREFERENTIALLY EXPRESSED IN PLASMODIUM.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC -----
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CC -----
CC EMBL: M20191; AAA29977.1; -
CC PIR: A33655; A33655.
CC InterPro: IPR002453; Beta.tubulin.
CC InterPro: IPR000217; Tubulin.
CC InterPro: IPR003008; Tubulin_FusZ.
CC Pfam: PF00091; tubulin; 1.
CC PRINTS: PR01161; TUBULIN.
CC PROSITE: PS00227; TUBULIN; 1.
CC PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
CC Microtubules; GTP-binding; Multigene family; Nuclear protein.
CC NP_BIND 140 146 GTP (POTENTIAL).
CC SEQUENCE 454 AA; 50364 MW; A913DA6AF63F1AD4 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 454;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 LGTLIS 863
|111111|
Db 147 LGTLIS 153

RESULT 39
TBB_DICDI STANDARD; PRT; 455 AA.
ID TBB_DICDI
AC P32256;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tubulin beta chain.
GN TUBB.
OS Dictyostelium discoideum (Slime mold).
OS Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
CC NCBI_TaxID=44689;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94043557; PubMed=8227212;
RA Trivinos-Lagos L., Omachi T., Aldrightson C., Burns R.G.,
RA Ennis H.L., Chisholm R.L.;
RT "The highly divergent alpha- and beta-tubulins from Dictyostelium
RT discoideum are encoded by single genes".
RL J. Cell Sci. 105:903-911(1993).
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC -----
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CC -----
CC EMBL: L14000; AAC37344.1; -
CC DICTYD: DD01044; tubB.
CC InterPro: IPR002453; Beta.tubulin.
CC InterPro: IPR000217; Tubulin.
CC InterPro: IPR003008; Tubulin_FusZ.
CC Pfam: PF00091; tubulin; 1.
CC PRINTS: PR01161; TUBULIN.
CC PROSITE: PS00227; TUBULIN; 1.
CC PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
CC Microtubules; GTP-binding.
CC NP_BIND 145 151 GTP (POTENTIAL).

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50 SEQUENCE 455 AA: 51279 MW: EE214EB050285SEC CRC64:

Query Match 0.6%; Score 7; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 857 LGTLLIS 863
|||||||
DB 152 LGTLLIS 158

RESULT 40

ZNT1_MOUSE STANDARD: PRT: 503 AA.

ID ZNT1_MOUSE
AC Q60738;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc transporter 1 (Znt-1).
GN SLC30A1 OR ZNT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=9518868; PubMed=7882967;
RA Palmer R.D., Findley S.D.;
RT "Cloning and functional characterization of a mammalian zinc transporter that confers resistance to zinc."
RL EMO J. 14:639-649(1995).
CC -1- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF THE CELL.
CC LETHALITY OF KNOCKOUT EARLY IN GESTATION SUGGESTS A ROLE OF THE
CC PROTEIN IN FETAL ZINC ACQUISITION AND RETENTION.
CC -1- SUBUNIT: MULTIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS.
CC
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CC
CC EMBL: U17132; AAF79233.1; -
DR MGD; MGI:1345281; SLC30A1.
DR InterPro: IPR002524; Cation_efflux.
KW Pfam: PF01545; Cation_efflux; 1.
KW Zinc; Transport; Transmembrane; Multigene family; Repeat.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 POTENTIAL.
FT DOMAIN 32 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 56 POTENTIAL.
FT DOMAIN 57 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 99 POTENTIAL.
FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 114 134 POTENTIAL.
FT DOMAIN 135 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 264 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 265 303 POTENTIAL.
FT TRANSMEM 304 324 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 325 503 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 294 294 6 X 2 AA APPROXIMATE REPEATS OF H-G.
FT SEQUENCE 503 AA: 54716 MW: 7C4FF93FC13CDA22 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 NTSNSNG 62
|||||||
DB 190 NTSNSNG 196

RESULT 41

G6PD_CHLMU STANDARD: PRT: 507 AA.

ID G6PD_CHLMU
AC Q9PKK8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).
GN ZMF OR TC0457.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mopn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Ulteback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn J., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eelsen J., Fraser C.M.,
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-
CC 1,5-lactone 6-phosphate + NADPH.
CC -1- PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
CC FAMILY.
CC
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CC
CC EMBL: AF002314; AAF73556.1; -
DR TIGR: TC0457;
DR InterPro: IPR001282; G6PD.
DR Pfam: PF00479; G6PD; 1.
DR Pfam: PF02781; G6PD_C; 1.
DR PRINTS: PR00079; G6PDHGNASE.
DR ProDom: PD001129; G6PD; 1.
DR PROSITE: PS00069; G6P_DEHYDROGENASE; 1.
KW Oxidoreductase; NADP; Glucose metabolism; Complete proteome.
KW ACT_SITE 202 BY SIMILARITY.
FT SEQUENCE 507 AA: 58547 MW: C66F3FE1562391A6 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 507;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 963 NFESEAG 969
|||||||
DB 100 NFESEAG 106

RESULT 42
ZNT1_RAT STANDARD: PRT: 507 AA:
ID ZNT1_RAT
AC Q62720;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE zinc transporter 1 (znt-1).
 GN SLC30A1 OR ZNT1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_Taxid=10116;
 RX MEDLINE-9518868; PubMed-7882967;
 RA Palmer R.D., Findley S.D.;
 RT "Cloning and functional characterization of a mammalian zinc
 RT transporter that confers resistance to zinc.";
 RL EMBO J. 14:639-649(1995).
 [2]
 RP INDUCTION BY ZINC.
 RC TISSUE-Intestine;
 RX MEDLINE-98226729; PubMed-9560190;
 RA McMahon R.J., Cousins R.J.;
 RT "Regulation of the zinc transporter ZNT-1 by dietary zinc.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:4841-4846(1998).
 CC -1- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF THE CELL.
 CC -1- SUBUNIT: MULTIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE). LOCALIZED ON THE
 CC LATERAL SURFACE OF THE ENTEROCYTES.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. THE PROTEIN IS DETECTED IN
 CC DODENUM AND JEJUNUM BUT NOT IN ILEUM AND COLON.
 CC -1- INDUCTION: SLIGHTLY BY ZINC IN THE INTESTINE, BUT NOT THE LIVER.
 CC -1- SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL: 017133; AAA9234.1; -
 DR Interpro: IPR002524; Cation_efflux.
 DR Pfam: PF01545; Cation_efflux; 1.
 KW Zinc; Transport; Transmembrane; Multigene family; Repeat.
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1 31 POTENTIAL.
 FT DOMAIN 32 35 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 36 56 POTENTIAL.
 FT DOMAIN 57 78 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 79 99 POTENTIAL.
 FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 114 134 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 135 247 POTENTIAL.
 FT TRANSMEM 248 268 POTENTIAL.
 FT DOMAIN 269 307 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 308 328 POTENTIAL.
 FT DOMAIN 329 507 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 507 515 6 X 2 AA APPROXIMATE REPEATS OF H-G.
 FT CAROHD 298 298 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 507 AA: 55142 MW: 959770017C2455FC CRC64;

Query Match 0.6%; Score 7; DB 1; Length 507;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 NTSNSNG 62
 DB 194 NTSNSNG 200

RESULT 43
 ID SP2A2_STRAU STANDARD; PRI; 508 AA.
 AC P38507;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Immunoglobulin G binding protein A precursor (IGG binding protein A).
 GN SPA.
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Staphylococcus.
 CC NCBI_Taxid=1280;
 RX MEDLINE-78023926; PubMed-913410;
 RA Sjoedahl J.;
 RT "Structural studies on the four repetitive Fc-binding regions in
 RT protein A from Staphylococcus aureus.";
 RL Eur. J. Biochem. 78:471-490(1977).
 [3]
 RP STRUCTURE BY NMR OF 211-270.
 RX MEDLINE-93003122; PubMed-1390743;
 RA Gouda H., Torigoe H., Saito A., Sato M., Arata Y., Shimada I.;
 RT "Three-dimensional solution structure of the B domain of
 RT staphylococcal protein A: comparisons of the solution and crystal
 RT structures.";
 RL Biochemistry 31:9665-9672(1992).
 [4]
 RP STRUCTURE BY NMR OF 37-92.
 RX MEDLINE-97110349; PubMed-8952510;
 RA Starovsniak M.A., Skelton N.J., O'Connell M.P., Kelley R.F.,
 RA Reilly D., Fairbrother W.J.;
 RT "Solution structure of the E-domain of staphylococcal protein A.";
 RL Biochemistry 35:15558-15569(1996).
 [5]
 RP STRUCTURE BY NMR OF 212-269.
 RX MEDLINE-97467196; PubMed-9325113;
 RA Tashiro M., Tejero R., Zimmerman D.E., Cejda B., Nilsson B.,
 RA Montellone G.T.;
 RT "High-resolution solution NMR structure of the z domain of
 RT staphylococcal protein A.";
 RL J. Mol. Biol. 272:573-590(1997).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
 CC -1- DOMAIN: THE N-TERMINAL HALF CONTAINS THE IGG-BINDING REGION
 CC WHILST THE C-TERMINAL HALF IS THE CELL-WALL-BINDING DOMAIN.
 CC -1- MISCELLANEOUS: IMPORTANT IMMUNODIAGNOSTIC REAGENT BECAUSE OF ITS
 CC ABILITY TO BIND THE FC FRAGMENT OF A WIDE RANGE OF MAMMALIAN
 CC IMMUNOGLOBULINS.
 CC -1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
 CC IN THE REGION OF THE MEMBRANE ANCHOR.
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 CC -----
 DR EMBL: M18264; AAA2677.1; -
 DR PIR: A29605; A29605.


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FT DOMAIN 490 495 CONSERVED IN GRAM-POSITIVE COCCI SURFACE
FT PROTEINS.
FT CONFLICT 101 101 N -> D (IN REF. 3).
SQ SEQUENCE 524 AA; 57320 MW; 0A615C73C61316FE CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 524;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 LGTLLIS 863
DB 21 LGTLLIS 27

RESULT 45
IL2B_MOUSE
ID IL2B_MOUSE STANDARD; PRT; 539 AA.
AC P16297;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
DE (High affinity IL-2 receptor beta subunit) (CD122).
GN IL2RB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90175385; PubMed=2155425;
RA Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Tsudo M.,
RA Miyasaka M., Miyata T., Taniguchi T.;
RT "Murine interleukin 2 receptor beta chain: dysregulated gene,
RT expression in lymphoma line EL-4 caused by a promoter insertion.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:1806-1810(1990).
RL
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
CC INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
CC MITOGENIC SIGNALS OF IL-2.
CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC WITH A GAMMA CHAIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL: M28052; AAA39283.1; -
DR PIR: A35052; A35052.
DR HSSP: P14784; I11N.
DR MGD: MGI:96550; I12rb.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003531; FN_III.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; fn3; 1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
DR Receptor: Transmembrane; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 26
FT DOMAIN 27 539 INTERLEUKIN-2 RECEPTOR BETA CHAIN.
FT DOMAIN 27 240 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 241 268 POTENTIAL.
FT DOMAIN 269 539 CYTOPLASMIC (POTENTIAL).
FT DISULFID 36 46 BY SIMILARITY.

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FT DISULFID 74 86 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 539 AA; 60538 MW; 365C9D206E86FE14 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 539;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 SYEVQVR 309
DB 204 SYEVQVR 210

RESULT 46
C166_CARAU
ID C166_CARAU STANDARD; PRT; 555 AA.
AC O90304.
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CD166 antigen homolog precursor (Neuroilin) (DM-GRASP homolog).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Actinopterygii; Neopterygii; Teleostei; Osteichthys;
DE Cypriniformes; Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue-Retina.
RA Laessing U.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
CC SEQUENCE OF 30-552 FROM N.A., AND PARTIAL SEQUENCE.
CC TISSUE-Retina;
CC MEDLINE=94299040; PubMed=8026643;
CC Laessing U., Giordano S., Stecher B., Lottspeich F., Stuermer C.A.O.;
CC "Molecular characterization of fish neuroilin: a growth-associated
CC cell surface protein and member of the immunoglobulin superfamily in
CC the fish retinotectal system with similarities to chick protein
CC DM-GRASP/SC-1/BEN.";
CC Differentiation 56:21-29(1994).
CC -1- FUNCTION: CELL ADHESION MOLECULE. INVOLVED IN NEURITE EXTENSION BY
CC NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PRESENT ON ALL RETINAL GANGLION CELLS (RGCs)
CC AND THEIR AXONS (IN EMBRYO). ABSENT FROM MATURE AXONS ALONG MOST
CC OF THEIR LENGTH, BUT IS PRESENT ON NEW AND GROWING AXONS DERIVED
CC FROM THE RGCs AT THE RETINAL MARGIN. REMAINS ON ADULT RGCs ONLY AT
CC CELL-CELL CONTACT SITES AND IS CONTINUOUSLY FOUND IN THE RETINAL
CC AXON TERMINAL AXON LAYERS OF THE ADULT TECTUM.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL: U25056; AAC38015.2; -
DR HSSP: Q13740; IKIC.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003596; IG_V.

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DR MIM: 602019; NAD_binding.
DR InterPro: IPR000205; NAD_binding.
DR InterPro: IPR003042; NAD_binding.
DR InterPro: IPR000733; Flavomonooxygenase.
DR Pfam: PF01360; Monooxygenase: 1.
DR PRINTS: PR00420; RINGMONOXNASE.
KW Oxidoreductase; Flavoprotein; FAD; Transmembrane.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 61 81 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
FT TRANSMEM 546 566 POTENTIAL.
FT NP_BIND 126 153 POTENTIAL.
FT NP_BIND 247 247 FAD (ADP PART) (POTENTIAL).
FT CONFLICT 336 336 E -> G (IN REF. 2).
FT CONFLICT 389 389 R -> Q (IN REF. 2).
FT CONFLICT 451 451 L -> P (IN REF. 2).
FT CONFLICT 518 518 N -> K (IN REF. 2).
FT CONFLICT 518 518 A -> V (IN REF. 2).
SQ SEQUENCE 574 AA; 63939 MW; DD4F9530864FD09 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 574;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 538 LPPSSVK 544
DB 393 LPPSSVK 399

RESULT 50

GTBL_MOUSE

ID GTBL_MOUSE STANDARD; PRT: 583 AA.

AC 008582;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE GTP-binding protein 1 (G-protein 1) (GP-1).

GN GTPBP1 OR GTPBP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_Taxid=10090;

RN NCI_Taxid=10090;

RP SEQUENCE FROM N.A.

RX MEDLINE-97223458; PubMed-9070279;

RA Senju S.; Nishimura Y.;

RT "Identification of human and mouse GP-1, a putative member of a novel

RT G-protein family.";

RL Blochem Biophys. Res. Commun. 231:360-364(1997).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, THYMUS, LUNG, AND KIDNEY.

CC -1- SIMILARITY: BELONGS TO THE AGPI/GTPBP1 FAMILY OF GTP-BINDING

CC PROTEINS.

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CC -----

CC EMBL: U87965; AAB51274.1; -.

DR MGD: MGI:109443; Gtpbp1.

DR InterPro: IPR000795; GTP_EFTU.

DR InterPro: IPR004161; GTP_EFTU_D2.

DR InterPro: IPR004160; GTP_EFTU_D3.

DR Pfam: PF00009; GTP_EFTU_1.

DR Pfam: PF03144; GTP_EFTU_D2; 1.

DR Pfam: PF03143; GTP_EFTU_D3; 1.

KW GTP-binding.

FT NP_BIND 82 89 GTP (POTENTIAL).

FT NP_BIND 167 171 GTP (POTENTIAL).

FT NP_BIND 223 226 GTP (POTENTIAL).

SQ SEQUENCE 583 AA; 63329 MW; A17F297D214247F9 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 583;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 204 KINTTLL 210
DB 337 KINTTLL 343

Search completed: May 18, 2002, 07:08:25
Job time: 248 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 07:04:02 ; Search time 37.5 Seconds
(without alignments)
5374.376 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 1165
Sequence: 1 MICQKFCVVLHMEFLIVT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size: 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database:

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1165	100.0	1165	4	Q92921 homo sapien
2	891	76.5	896	4	Q92919 homo sapien
3	891	76.5	958	4	Q92920 homo sapien
4	681	58.5	896	4	Q13594 homo sapien
5	681	58.5	906	4	Q13593 homo sapien
6	681	58.5	958	4	Q13592 homo sapien
7	84	7.2	925	6	Q9MYL1 macaca mulla
8	84	7.2	925	6	Q9MYK9 macaca mulla
9	84	7.2	1163	6	Q9MYI2 macaca mulla
10	84	7.2	1194	6	Q9MYL0 macaca mulla
11	53	4.5	848	6	Q9MZS2 sus scrofa
12	53	4.5	1165	6	Q02671 sus scrofa
13	43	3.7	57	6	Q97778 elaphas max
14	43	3.7	57	6	Q97779 loxodonta a
15	42	3.6	1162	11	Q9QW63 mus musculu
16	41	3.5	893	11	Q62960 rattus norv

17	26	2.2	203	6	Q28604	Q28604 ovis aries
18	20	1.7	152	6	P79115	P79115 bos taurus
19	18	1.5	74	11	Q9ER14	Q9ER14 rattus norv
20	18	1.5	173	6	Q9XSN9	Q9XSN9 sus scrofa
21	18	1.5	246	11	Q35773	Q35773 rattus norv
22	17	1.5	102	6	Q9XSH3	Q9XSH3 equus caball
23	17	1.5	145	13	Q91A32	Q91A32 gallus gall
24	17	1.5	1146	13	Q91B86	Q91B86 gallus gall
25	17	1.5	1147	13	Q9DDK1	Q9DDK1 meleagris g
26	17	1.5	1148	13	Q91BA7	Q91BA7 gallus gall
27	13	1.1	123	6	Q9N1P9	Q9N1P9 sus scrofa
28	13	1.1	161	6	Q28605	Q28605 ovis aries
29	13	1.1	273	11	Q9QWV5	Q9QWV5 mus musculu
30	10	0.9	147	6	Q95257	Q95257 sus scrofa
31	9	0.8	26	11	Q9WV88	Q9WV88 mus musculu
32	9	0.8	121	6	Q18980	Q18980 bos taurus
33	9	0.8	901	4	Q9HCE2	Q9HCE2 homo sapien
34	9	0.8	919	4	Q9BDK8	Q9BDK8 homo sapien
35	9	0.8	919	4	Q9BHT7	Q9BHT7 homo sapien
36	8	0.7	30	11	Q9JHF4	Q9JHF4 rattus norv
37	8	0.7	103	12	Q91D21	Q91D21 respiratory
38	8	0.7	104	12	Q91D20	Q91D20 respiratory
39	8	0.7	104	12	Q91D01	Q91D01 respiratory
40	8	0.7	107	12	Q91D00	Q91D00 respiratory
41	8	0.7	124	3	Q13894	Q13894 schizosach
42	8	0.7	184	5	Q9BHD6	Q9BHD6 trypanosoma
43	8	0.7	217	13	P70016	P70016 xenopus lae
44	8	0.7	222	16	Q97185	Q97185 clostridium
45	8	0.7	236	17	P95945	P95945 sulfolobus
46	8	0.7	322	13	Q91B64	Q91B64 xenopus lae
47	8	0.7	325	13	Q91B62	Q91B62 xenopus lae
48	8	0.7	326	13	Q91B62	Q91B62 xenopus lae
49	8	0.7	326	13	Q91B62	Q91B62 xenopus lae
50	8	0.7	335	12	Q9DH41	Q9DH41 meleagris h
51	8	0.7	383	8	Q9B205	Q9B205 calman croc
52	8	0.7	425	16	Q9K9C3	Q9K9C3 bacillus ha
53	8	0.7	459	16	Q91E92	Q91E92 pseudomonas
54	8	0.7	498	12	Q88525	Q88525 turkey herp
55	8	0.7	850	16	Q9CKA8	Q9CKA8 pasteurella
56	8	0.7	864	10	Q9L219	Q9L219 arabidopsis
57	8	0.7	937	16	Q9A3P1	Q9A3P1 caulobacter
58	8	0.7	952	5	Q9P9T5	Q9P9T5 haloarcula
59	8	0.7	1270	5	Q19736	Q19736 caenorhabdi
60	8	0.7	1291	5	Q19734	Q19734 caenorhabdi
61	8	0.7	1318	5	Q19733	Q19733 caenorhabdi
62	8	0.7	1327	5	Q19735	Q19735 caenorhabdi
63	7	0.6	47	11	Q63139	Q63139 rattus norv
64	7	0.6	64	16	Q9PH48	Q9PH48 xyella fas
65	7	0.6	78	5	Q9N1E5	Q9N1E5 leishmania
66	7	0.6	94	2	Q9AGE7	Q9AGE7 listeria mo
67	7	0.6	94	16	Q92909	Q92909 listeria in
68	7	0.6	101	3	Q07236	Q07236 saccharomyc
69	7	0.6	104	16	Q92DX8	Q92DX8 listeria in
70	7	0.6	111	4	Q9H4W3	Q9H4W3 homo sapien
71	7	0.6	120	8	Q9BBT8	Q9BBT8 lotus japon
72	7	0.6	120	13	Q9UADI	Q9UADI epitelretus
73	7	0.6	125	2	Q47664	Q47664 escherichia
74	7	0.6	127	16	Q92FK4	Q92FK4 listeria in
75	7	0.6	128	2	Q53089	Q53089 rhodobacter

ALIGNMENTS

RESULT 1
ID Q92921 PRELIMINARY: PRT: 1165 AA.
AC Q92921;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96398968; PubMed=8803376;
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
 RA Matthews W.;
 RT "A role for leptin and its cognate receptor in hematopoiesis.";
 RL Curr. Biol. 6:1170-1180(1996).
 DR EMBL: U66497; AAB07497.1; -;
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CRC64;

Query Match 100.0%; Score 1165; DB 4; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCOQFCVLLHMERITYTAFNLSTPTPMRFKLSMPNSTYQYFLPAGLSKNTS 60
 DB 1 MCOQFCVLLHMERITYTAFNLSTPTPMRFKLSMPNSTYQYFLPAGLSKNTS 60
 OY 61 NGHYETAEPKNSSGTHFSNLSKTTFHCCFSEODRNCSLCADNIEGTFSTNSLVF 120
 DB 61 NGHYETAEPKNSSGTHFSNLSKTTFHCCFSEODRNCSLCADNIEGTFSTNSLVF 120
 OY 121 COIDANNNIQCGLKGDLLKFLCYVESLEKNLFRNRYKXHLLYLPEVLEDSPLYPQKS 180
 DB 121 COIDANNNIQCGLKGDLLKFLCYVESLEKNLFRNRYKXHLLYLPEVLEDSPLYPQKS 180
 OY 121 COIDANNNIQCGLKGDLLKFLCYVESLEKNLFRNRYKXHLLYLPEVLEDSPLYPQKS 180
 DB 121 COIDANNNIQCGLKGDLLKFLCYVESLEKNLFRNRYKXHLLYLPEVLEDSPLYPQKS 180
 OY 181 FOMVHCNCSVHECCCLVNPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMKPDP 240
 DB 181 FOMVHCNCSVHECCCLVNPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMKPDP 240
 OY 181 FOMVHCNCSVHECCCLVNPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMKPDP 240
 DB 181 FOMVHCNCSVHECCCLVNPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMKPDP 240
 OY 241 LGLHNETDDGMLKISWSSPLVPEPLQYQVYKXSENSSTVIREADKIYATSILVDSILP 300
 DB 241 LGLHNETDDGMLKISWSSPLVPEPLQYQVYKXSENSSTVIREADKIYATSILVDSILP 300
 OY 241 LGLHNETDDGMLKISWSSPLVPEPLQYQVYKXSENSSTVIREADKIYATSILVDSILP 300
 DB 241 LGLHNETDDGMLKISWSSPLVPEPLQYQVYKXSENSSTVIREADKIYATSILVDSILP 300
 OY 301 GSSYEVQVGRKRLDGPGLMSDMSTPRVFTQVYIFPPKILTSVGSNVSFHCITYKKNKI 360
 DB 301 GSSYEVQVGRKRLDGPGLMSDMSTPRVFTQVYIFPPKILTSVGSNVSFHCITYKKNKI 360
 OY 301 GSSYEVQVGRKRLDGPGLMSDMSTPRVFTQVYIFPPKILTSVGSNVSFHCITYKKNKI 360
 DB 301 GSSYEVQVGRKRLDGPGLMSDMSTPRVFTQVYIFPPKILTSVGSNVSFHCITYKKNKI 360
 OY 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSKYTFPMNLNETKPGKTYDAVYCNHECHH 420
 DB 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSKYTFPMNLNETKPGKTYDAVYCNHECHH 420
 OY 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSKYTFPMNLNETKPGKTYDAVYCNHECHH 420
 DB 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSKYTFPMNLNETKPGKTYDAVYCNHECHH 420
 OY 421 RYAEELVIDVNNINISCEIDGYLTMTKTCMSSTIQTSLAESTLQRLYHRSSLYCSDIPSIH 480
 DB 421 RYAEELVIDVNNINISCEIDGYLTMTKTCMSSTIQTSLAESTLQRLYHRSSLYCSDIPSIH 480
 OY 421 RYAEELVIDVNNINISCEIDGYLTMTKTCMSSTIQTSLAESTLQRLYHRSSLYCSDIPSIH 480
 DB 421 RYAEELVIDVNNINISCEIDGYLTMTKTCMSSTIQTSLAESTLQRLYHRSSLYCSDIPSIH 480
 OY 481 PISEKDCYLOSDFEYECIFQPIFLSGTYMKIRINHSIGSLDSPCTVCLPDSVYKPLPP 540
 DB 481 PISEKDCYLOSDFEYECIFQPIFLSGTYMKIRINHSIGSLDSPCTVCLPDSVYKPLPP 540
 OY 481 PISEKDCYLOSDFEYECIFQPIFLSGTYMKIRINHSIGSLDSPCTVCLPDSVYKPLPP 540
 DB 481 PISEKDCYLOSDFEYECIFQPIFLSGTYMKIRINHSIGSLDSPCTVCLPDSVYKPLPP 540
 OY 541 SSVKKEITINIGLKTISMEKPVPEPNNLOFOIRVGLSGKEVOMKVEYVDKSKSVSLPV 600
 DB 541 SSVKKEITINIGLKTISMEKPVPEPNNLOFOIRVGLSGKEVOMKVEYVDKSKSVSLPV 600
 OY 541 SSVKKEITINIGLKTISMEKPVPEPNNLOFOIRVGLSGKEVOMKVEYVDKSKSVSLPV 600
 DB 541 SSVKKEITINIGLKTISMEKPVPEPNNLOFOIRVGLSGKEVOMKVEYVDKSKSVSLPV 600
 OY 601 PDLCAVAVVQVGRKRLDGLGYWSNNSNPATYVMDIKYPMKGPPEWRRIINGTMMKKNV 660
 DB 601 PDLCAVAVVQVGRKRLDGLGYWSNNSNPATYVMDIKYPMKGPPEWRRIINGTMMKKNV 660
 OY 601 PDLCAVAVVQVGRKRLDGLGYWSNNSNPATYVMDIKYPMKGPPEWRRIINGTMMKKNV 660
 DB 601 PDLCAVAVVQVGRKRLDGLGYWSNNSNPATYVMDIKYPMKGPPEWRRIINGTMMKKNV 660
 OY 661 TLLMKPLMKNDLSGVQRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHVTYVLAINSI 720
 DB 661 TLLMKPLMKNDLSGVQRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHVTYVLAINSI 720

DB 661 TLLMKPLMKNDLSGVQRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHVTYVLAINSI 720
 OY 721 GASVANFNLTFEWPMSKNIYOSLSAYPLNSCIVSNLSPDYKLYFTIEMKLNLD 780
 DB 721 GASVANFNLTFEWPMSKNIYOSLSAYPLNSCIVSNLSPDYKLYFTIEMKLNLD 780
 OY 781 GEIKMLRISSSVKKYIHDHFIPIEKYQSLPIFMEGVKPKIINSFTODDIEKHQSDA 840
 DB 781 GEIKMLRISSSVKKYIHDHFIPIEKYQSLPIFMEGVKPKIINSFTODDIEKHQSDA 840
 OY 841 GLYIVPVYIISSTILLGTLISHORMKLFWEDVYPNPKNCWAGLNFQKETFHEHLFI 900
 DB 841 GLYIVPVYIISSTILLGTLISHORMKLFWEDVYPNPKNCWAGLNFQKETFHEHLFI 900
 OY 901 KHTASVTCGPLLPEPTISEDIVSTSMKNKDEMPPTVYSLSTTDEKGSVCISDQFN 960
 DB 901 KHTASVTCGPLLPEPTISEDIVSTSMKNKDEMPPTVYSLSTTDEKGSVCISDQFN 960
 OY 901 KHTASVTCGPLLPEPTISEDIVSTSMKNKDEMPPTVYSLSTTDEKGSVCISDQFN 960
 DB 901 KHTASVTCGPLLPEPTISEDIVSTSMKNKDEMPPTVYSLSTTDEKGSVCISDQFN 960
 OY 961 SVNFSEADQTEVYDESOQROPFVKYATLISNKSKEGEGGLINSSVTKCFSSKNSPL 1020
 DB 961 SVNFSEADQTEVYDESOQROPFVKYATLISNKSKEGEGGLINSSVTKCFSSKNSPL 1020
 OY 1021 KDSENSSWETBQAQFFILSDQHPNIIISPHTLFSGLDELKLEGNFPEENNDRKSIYLL 1080
 DB 1021 KDSENSSWETBQAQFFILSDQHPNIIISPHTLFSGLDELKLEGNFPEENNDRKSIYLL 1080
 OY 1081 GYTSIKKRESGYLLDKNRSCPPAPCLFTDIRVLQDSCSHFVNNINLGTSSKRTAS 1140
 DB 1081 GYTSIKKRESGYLLDKNRSCPPAPCLFTDIRVLQDSCSHFVNNINLGTSSKRTAS 1140
 OY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
 DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 2
 OY 929219 PRELIMINARY; PRG: 896 AA.
 AC 929219;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE LEPTIN RECEPTOR.
 GN DB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
 RA Matthews W.;
 RL Curr. Biol. 6:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9721244; PubMed=9061609;
 RA Luch S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
 RA Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;
 RT "Cloning and characterization of a human leptin receptor using a
 biologically active leptin immunoadhesin.";
 RL J. Mol. Endocrinol. 18:77-85(1997).
 DR EMBL: U66495; AAB07495.1; -;
 DR EMBL: U50748; AAC23650.1; -;
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.

50 'SEQUENCE 896 AA: 102489 MW: D371C7A186DEER3 CRC64;

Query Match 76.5%; Score 891; DB 4; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYITAFNLSTPTTPMRFKLSCLMPNSTYDFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHMEFIYITAFNLSTPTTPMRFKLSCLMPNSTYDFLLPAGLSKNTSNS 60
QY 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCCEFRSEODRNCSCADNIEGTFYSTNSLVF 120
DB 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCCEFRSEODRNCSCADNIEGTFYSTNSLVF 120
QY 121 QOIDANMNIQCMKGLDKLFICYVESLEKRLFRNRYNYKHLVLYPEVLEDSPLVPQKGS 180
DB 121 QOIDANMNIQCMKGLDKLFICYVESLEKRLFRNRYNYKHLVLYPEVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCCECLVPPVPAKLNDTLMLCKLITSGGVIFQSPPLMSVQPINMKYKDDP 240
DB 181 FQWVHCNCSVHECCCECLVPPVPAKLNDTLMLCKLITSGGVIFQSPPLMSVQPINMKYKDDP 240
QY 241 LGLHMEITDDGNLKITSMSSPPLVPPLOQVAKYSENSTTVIREAKIVASATSLVDSTLP 300
DB 241 LGLHMEITDDGNLKITSMSSPPLVPPLOQVAKYSENSTTVIREAKIVASATSLVDSTLP 300
QY 301 GSSYEVOVGRKRLDGPGLMSDMSTPRVFTTQDVIYFPPKILTVSGSNSVFCIYKREKNI 360
DB 301 GSSYEVOVGRKRLDGPGLMSDMSTPRVFTTQDVIYFPPKILTVSGSNSVFCIYKREKNI 360
QY 361 VPSKEITVMMNLAEKIPQSQDYVSDHVSQVTFENLNETKPRGKTTYDAVYCCNEHECH 420
DB 361 VPSKEITVMMNLAEKIPQSQDYVSDHVSQVTFENLNETKPRGKTTYDAVYCCNEHECH 420
QY 421 RYAEIYDIVNINISCEIDGYLTMTGCRNSTSTIOSLAESTLOLRHRSLSLCSIDPSIH 480
DB 421 RYAEIYDIVNINISCEIDGYLTMTGCRNSTSTIOSLAESTLOLRHRSLSLCSIDPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFOPILFLSGYTMIRINHSLSLSDSPPTCVLPDSVYKPLPP 540
DB 481 PISEPKDCYLOSDGFYECIFOPILFLSGYTMIRINHSLSLSDSPPTCVLPDSVYKPLPP 540
QY 541 SSVKAEITINIGLKITSMKRPVFPENNLOFOIRYGLSGKEVQMKIYEVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLKITSMKRPVFPENNLOFOIRYGLSGKEVQMKIYEVDAKSKSVSLPV 600
QY 601 PDLCAVYAVOVACRKLDDGLGYSNMSNPATVYVMDIKVPMRGPEFRRIINSGTMRKKNV 660
DB 601 PDLCAVYAVOVACRKLDDGLGYSNMSNPATVYVMDIKVPMRGPEFRRIINSGTMRKKNV 660
QY 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLTEQAHTVYLAINSI 720
DB 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLTEQAHTVYLAINSI 720
QY 721 GASVANFNLTFSWPSKKNIVOSLSAYPLNNSCVYSLWSLSDYKLMYFIIEKKNLND 780
DB 721 GASVANFNLTFSWPSKKNIVOSLSAYPLNNSCVYSLWSLSDYKLMYFIIEKKNLND 780
QY 781 GIKMLRISSSVKKYIYIDHFIPIEKYQSLPIFMEGGRKLIINSFQODDIERKQSDA 840
DB 781 GIKMLRISSSVKKYIYIDHFIPIEKYQSLPIFMEGGRKLIINSFQODDIERKQSDA 840
QY 841 GLYIVIVPVISSIIILGTLISHRMKKLFWEDVYVNPKNCSMAOGLNFK 891
DB 841 GLYIVIVPVISSIIILGTLISHRMKKLFWEDVYVNPKNCSMAOGLNFK 891

RESULT 3
Q92920 PRELIMINARY; PRT: 958 AA.
AC Q92920:
DT 01-FEB-1997 (TREMblrel. 02, Created)

DT 01-FEB-1997 (TREMblrel. 02, last sequence update)
DT 01-DEC-2001 (TREMblrel. 13, last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96398968; PubMed=8805376;
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RT "A role for leptin and its cognate receptor in hematopoiesis.";
RL Curr. Biol. 6:1170-1180(1996).
DR EMBL: U66496; AB07496.1;
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003529; Hematopo_receptor_L.F2.
DR InterPro: IPR003531; Hematopo_receptor_S.F1.
DR Pfam: PF00041; In3; 2.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L.F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S.F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 958 AA: 109392 MW: 3F65BC5A187E803A CRC64;

Query Match 76.5%; Score 891; DB 4; Length 958;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYITAFNLSTPTTPMRFKLSCLMPNSTYDFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHMEFIYITAFNLSTPTTPMRFKLSCLMPNSTYDFLLPAGLSKNTSNS 60
QY 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCCEFRSEODRNCSCADNIEGTFYSTNSLVF 120
DB 61 NGHYETAEPKFNSSGTHFSNLSTKTFHCCEFRSEODRNCSCADNIEGTFYSTNSLVF 120
QY 121 QOIDANMNIQCMKGLDKLFICYVESLEKRLFRNRYNYKHLVLYPEVLEDSPLVPQKGS 180
DB 121 QOIDANMNIQCMKGLDKLFICYVESLEKRLFRNRYNYKHLVLYPEVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCCECLVPPVPAKLNDTLMLCKLITSGGVIFQSPPLMSVQPINMKYKDDP 240
DB 181 FQWVHCNCSVHECCCECLVPPVPAKLNDTLMLCKLITSGGVIFQSPPLMSVQPINMKYKDDP 240
QY 241 LGLHMEITDDGNLKITSMSSPPLVPPLOQVAKYSENSTTVIREAKIVASATSLVDSTLP 300
DB 241 LGLHMEITDDGNLKITSMSSPPLVPPLOQVAKYSENSTTVIREAKIVASATSLVDSTLP 300
QY 301 GSSYEVOVGRKRLDGPGLMSDMSTPRVFTTQDVIYFPPKILTVSGSNSVFCIYKREKNI 360
DB 301 GSSYEVOVGRKRLDGPGLMSDMSTPRVFTTQDVIYFPPKILTVSGSNSVFCIYKREKNI 360
QY 361 VPSKEITVMMNLAEKIPQSQDYVSDHVSQVTFENLNETKPRGKTTYDAVYCCNEHECH 420
DB 361 VPSKEITVMMNLAEKIPQSQDYVSDHVSQVTFENLNETKPRGKTTYDAVYCCNEHECH 420
QY 421 RYAEIYDIVNINISCEIDGYLTMTGCRNSTSTIOSLAESTLOLRHRSLSLCSIDPSIH 480
DB 421 RYAEIYDIVNINISCEIDGYLTMTGCRNSTSTIOSLAESTLOLRHRSLSLCSIDPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFOPILFLSGYTMIRINHSLSLSDSPPTCVLPDSVYKPLPP 540
DB 481 PISEPKDCYLOSDGFYECIFOPILFLSGYTMIRINHSLSLSDSPPTCVLPDSVYKPLPP 540
QY 541 SSVKAEITINIGLKITSMKRPVFPENNLOFOIRYGLSGKEVQMKIYEVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLKITSMKRPVFPENNLOFOIRYGLSGKEVQMKIYEVDAKSKSVSLPV 600
QY 601 PDLCAVYAVOVACRKLDDGLGYSNMSNPATVYVMDIKVPMRGPEFRRIINSGTMRKKNV 660

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Db 601 PDLCAVYAQVORCKRLDGLGYWMSNMSNPAYTVVMDIKVPMRGPEFMRINNGDTMKKEKXV 660
QY 661 TLLMPPLMKNDLSCSVQRYVINHHTSCNGTMSBDVGNHRTKFTFLMTEQAHVTAIINSI 720
Db 661 TLLMPPLMKNDLSCSVQRYVINHHTSCNGTMSBDVGNHRTKFTFLMTEQAHVTAIINSI 720
QY 721 GASVANFNLFSPMPSKVNIVOSLSAYPLNSSCVIYSWILSPSDYKLMFIETKKNLND 780
Db 721 GASVANFNLFSPMPSKVNIVOSLSAYPLNSSCVIYSWILSPSDYKLMFIETKKNLND 780
QY 781 GEIKMLRISSSVKYYIHDFPIEKYOPSLPIFMEGVGAKKIINSFTQDITEKHQSDA 840
Db 781 GEIKMLRISSSVKYYIHDFPIEKYOPSLPIFMEGVGAKKIINSFTQDITEKHQSDA 840
QY 841 GLYVIVPVISSILLGLTLLISHORMKLFMEDVNPNCMAOGLNFK 891
Db 841 GLYVIVPVISSILLGLTLLISHORMKLFMEDVNPNCMAOGLNFK 891

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RESULT 4
ID 013594 PRELIMINARY: PRT: 896 AA.
AC 013594:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
DR EMBL: U52914; AAC50511.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 896 B219/OB RECEPTOR ISOFORM HUB219.3.
SQ SEQUENCE 896 AA: 102516 MW: 73C431F8C578CD07 CRC64;

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Query Match 58.5%; Score 681; DB 4; Length 896;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 110 TFSVTVNSLIVFOQIDANNMNIQCMKGLDKLFTCYVESLTKNLFRRNKKVHLVLEPEVL 169
Db 110 TFSVTVNSLIVFOQIDANNMNIQCMKGLDKLFTCYVESLTKNLFRRNKKVHLVLEPEVL 169
QY 170 EDSPLVPQKSGQWVHCNCSVHECCCECLVPVPTAKLNTDMLKLTISGCVTFQSPMSV 229
Db 170 EDSPLVPQKSGQWVHCNCSVHECCCECLVPVPTAKLNTDMLKLTISGCVTFQSPMSV 229
QY 230 QPINNVKDPPLGLHMETIDGNTLKISWSSPLVFPPLQYQVYSENSITVIREADKIYS 289
Db 230 QPINNVKDPPLGLHMETIDGNTLKISWSSPLVFPPLQYQVYSENSITVIREADKIYS 289

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QY 290 ATSLVLDLSILPSSSYEVQGRKRLDGPGLMSDMSPRFFTTODVYIFPKILITVSGSNVS 349
Db 290 ATSLVLDLSILPSSSYEVQGRKRLDGPGLMSDMSPRFFTTODVYIFPKILITVSGSNVS 349
QY 350 FHCITRKKNKIYPSKEIYWMNLAEKIPQSOYDVYSDHYSKTFIRNLNTRKRGFTYDA 409
Db 350 FHCITRKKNKIYPSKEIYWMNLAEKIPQSOYDVYSDHYSKTFIRNLNTRKRGFTYDA 409
QY 410 VYCCNEHECHHRYAEIYADVNIINISCEPDDGYLTNKTCSMTSTIOSLAESTIOLRYHS 469
Db 410 VYCCNEHECHHRYAEIYADVNIINISCEPDDGYLTNKTCSMTSTIOSLAESTIOLRYHS 469
QY 470 SLVCSIDIPSINHISEPKDCYIOSDGFYECIFQPIFLLSGYTWMIRINHSLSGLSDSPPCV 529
Db 470 SLVCSIDIPSINHISEPKDCYIOSDGFYECIFQPIFLLSGYTWMIRINHSLSGLSDSPPCV 529
QY 530 LPDSVVKPLPPSSVKAETININGLAKISWEKVFPEPNNQFOIRIGLSGEVQMKMEYV 589
Db 530 LPDSVVKPLPPSSVKAETININGLAKISWEKVFPEPNNQFOIRIGLSGEVQMKMEYV 589
QY 590 DAKSKSVSLPVPDLCAYVAVQVRCRRLDGLGYWMSNMSNPAYTVVMDIKVPMRGPEFMRIT 649
Db 590 DAKSKSVSLPVPDLCAYVAVQVRCRRLDGLGYWMSNMSNPAYTVVMDIKVPMRGPEFMRIT 649
QY 650 NEDTKKKEKNVTLMLKPLMKNDLSCSVQRYVINHHTSCNGTMSBDVGNHRTKFTFLMTEQA 709
Db 650 NEDTKKKEKNVTLMLKPLMKNDLSCSVQRYVINHHTSCNGTMSBDVGNHRTKFTFLMTEQA 709
QY 710 HTVYTAIINISGASVANFNLFSPMPSKVNIVOSLSAYPLNSSCVIYSWILSPSDYKLMY 769
Db 710 HTVYTAIINISGASVANFNLFSPMPSKVNIVOSLSAYPLNSSCVIYSWILSPSDYKLMY 769
QY 770 FIETKKNLNEDEIKMLRISSSVKYYIHDFPIEKYOPSLPIFMEGVGAKKIINSFT 829
Db 770 FIETKKNLNEDEIKMLRISSSVKYYIHDFPIEKYOPSLPIFMEGVGAKKIINSFT 829
QY 830 QDDITEKHQSDAGLYVIVPVISSILLGLTLLISHORMKLFMEDVNPNCMAOGLNFK 889
Db 830 QDDITEKHQSDAGLYVIVPVISSILLGLTLLISHORMKLFMEDVNPNCMAOGLNFK 889
QY 890 OK 891
Db 890 OK 891

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RESULT 5
ID 013593 PRELIMINARY: PRT: 906 AA.
AC 013593:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.2 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
DR EMBL: U52913; AAC50510.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.

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DR SMART: SM00060; FN3; 1
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Signal; Receptor.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 906 B219/OB RECEPTOR ISOFORM HUB219.2.
 SQ SEQUENCE 906 AA; 103487 MW; 6D51126F33076626 CRC64;

Query Match 58.5%; Score 681; DB 4; Length 906;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVFQOQIDANNIQCMLKGLDKLFLCYVESLEFKLFRNRYNKHLLYLPEVL 169
 DB 110 TFEVSTVNSLVFQOQIDANNIQCMLKGLDKLFLCYVESLEFKLFRNRYNKHLLYLPEVL 169
 QY 170 EDSPLVPQKGSFQWYHNCNSVHECCCECLVPPTAKLNDTLMLCKLITSGGVIFRSPLSMV 229
 DB 170 EDSPLVPQKGSFQWYHNCNSVHECCCECLVPPTAKLNDTLMLCKLITSGGVIFRSPLSMV 229
 QY 230 QPINWVKPDPPLGLMELTDGDKLISMSPPPLVPEPLQYQKYSNSTTVREADKIVS 289
 DB 230 QPINWVKPDPPLGLMELTDGDKLISMSPPPLVPEPLQYQKYSNSTTVREADKIVS 289
 QY 290 ATSLVSDILPGSSYEVOYGRKRLDGPGLWSDWSTPRVFTTQDVLYFPFKILTSVGSNVS 349
 DB 290 ATSLVSDILPGSSYEVOYGRKRLDGPGLWSDWSTPRVFTTQDVLYFPFKILTSVGSNVS 349
 QY 350 FHCITKRNKIVPSKEIYVMMMLAEKIPQSOYDVSDHVSKTFFPNLNETKRGKFTYDA 409
 DB 350 FHCITKRNKIVPSKEIYVMMMLAEKIPQSOYDVSDHVSKTFFPNLNETKRGKFTYDA 409
 QY 410 VYCCNEHECHHRYALYIVDVNINISCEFDGTLTKTCRMSTSTIOSLAESTLOLRHRS 469
 DB 410 VYCCNEHECHHRYALYIVDVNINISCEFDGTLTKTCRMSTSTIOSLAESTLOLRHRS 469
 QY 470 SLVCSDFPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTWIRINSHLSGLSDSPPTCV 529
 DB 470 SLVCSDFPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTWIRINSHLSGLSDSPPTCV 529
 QY 530 LPDSVYVKPLPSSVKAETITINIGLTKISWEKVPFPENNLOFOIRYGLSKEVQMKWEYV 589
 DB 530 LPDSVYVKPLPSSVKAETITINIGLTKISWEKVPFPENNLOFOIRYGLSKEVQMKWEYV 589
 QY 590 DAKSKSVSLPVPDLCAYAVQYRCKRLDGLGYWNSNPNATYVMDIKYPMGPEFWRII 649
 DB 590 DAKSKSVSLPVPDLCAYAVQYRCKRLDGLGYWNSNPNATYVMDIKYPMGPEFWRII 649
 QY 650 NGDTMKKKENVTLLMKPLMKNDSLCSVORYVINHTSCNGTSEDEVGNHTKFTPLMTEQA 709
 DB 650 NGDTMKKKENVTLLMKPLMKNDSLCSVORYVINHTSCNGTSEDEVGNHTKFTPLMTEQA 709
 QY 710 HTVYPLAINSTIGASVANNLTFSPMSKVNIVOSLSAYPLNSCVIVSIIISPSOYKLMY 769
 DB 710 HTVYPLAINSTIGASVANNLTFSPMSKVNIVOSLSAYPLNSCVIVSIIISPSOYKLMY 769
 QY 770 FLEKRNINDEDEIMLRISSSVKKYIYHDHPIPIEKYOFSLYPIFMEVGKPKIINST 829
 DB 770 FLEKRNINDEDEIMLRISSSVKKYIYHDHPIPIEKYOFSLYPIFMEVGKPKIINST 829
 QY 830 QDDIKRHOSDAGLYIVYVYIISSTILLGLTLISHQRMKLLFWEDVPNPKNCNMAOGLNF 889
 DB 830 QDDIKRHOSDAGLYIVYVYIISSTILLGLTLISHQRMKLLFWEDVPNPKNCNMAOGLNF 889
 QY 890 OK 891
 DB 890 OK 891

RESULT 6
 Q13592 PRELIMINARY: PRT: 958 AA.

AC Q13592;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=96206286; PubMed=8616721;
 RA Clifton J.A., Shaler A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
 RA Platika D., Snodgrass H.R.;
 RT "Novel B219/OB receptor isoforms: possible role of leptin in
 hematopoiesis and reproduction."
 RL Nat. Med. 2:585-589(1996).
 DR EMBL; U52912; AAC50509.1; -;
 DR HSSP; P16471; 1BP3.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR003961; FN.III.
 DR InterPro; IPR003529; Hematopo_receptor_L_F2.
 DR InterPro; IPR003531; Hematopo_receptor_S_F1.
 DR Pfam; PF00041; I03; 2.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Signal; Receptor.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 958 B219/OB RECEPTOR ISOFORM HUB219.1.
 SQ SEQUENCE 958 AA; 109419 MW; C7E0B8D18428677B CRC64;

Query Match 58.5%; Score 681; DB 4; Length 958;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVFQOQIDANNIQCMLKGLDKLFLCYVESLEFKLFRNRYNKHLLYLPEVL 169
 DB 110 TFEVSTVNSLVFQOQIDANNIQCMLKGLDKLFLCYVESLEFKLFRNRYNKHLLYLPEVL 169
 QY 170 EDSPLVPQKGSFQWYHNCNSVHECCCECLVPPTAKLNDTLMLCKLITSGGVIFRSPLSMV 229
 DB 170 EDSPLVPQKGSFQWYHNCNSVHECCCECLVPPTAKLNDTLMLCKLITSGGVIFRSPLSMV 229
 QY 230 QPINWVKPDPPLGLMELTDGDKLISMSPPPLVPEPLQYQKYSNSTTVREADKIVS 289
 DB 230 QPINWVKPDPPLGLMELTDGDKLISMSPPPLVPEPLQYQKYSNSTTVREADKIVS 289
 QY 290 ATSLVSDILPGSSYEVOYGRKRLDGPGLWSDWSTPRVFTTQDVLYFPFKILTSVGSNVS 349
 DB 290 ATSLVSDILPGSSYEVOYGRKRLDGPGLWSDWSTPRVFTTQDVLYFPFKILTSVGSNVS 349
 QY 350 FHCITKRNKIVPSKEIYVMMMLAEKIPQSOYDVSDHVSKTFFPNLNETKRGKFTYDA 409
 DB 350 FHCITKRNKIVPSKEIYVMMMLAEKIPQSOYDVSDHVSKTFFPNLNETKRGKFTYDA 409
 QY 410 VYCCNEHECHHRYALYIVDVNINISCEFDGTLTKTCRMSTSTIOSLAESTLOLRHRS 469
 DB 410 VYCCNEHECHHRYALYIVDVNINISCEFDGTLTKTCRMSTSTIOSLAESTLOLRHRS 469
 QY 470 SLVCSDFPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTWIRINSHLSGLSDSPPTCV 529
 DB 470 SLVCSDFPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTWIRINSHLSGLSDSPPTCV 529
 QY 530 LPDSVYVKPLPSSVKAETITINIGLTKISWEKVPFPENNLOFOIRYGLSKEVQMKWEYV 589
 DB 530 LPDSVYVKPLPSSVKAETITINIGLTKISWEKVPFPENNLOFOIRYGLSKEVQMKWEYV 589
 QY 590 DAKSKSVSLPVPDLCAYAVQYRCKRLDGLGYWNSNPNATYVMDIKYPMGPEFWRII 649
 DB 590 DAKSKSVSLPVPDLCAYAVQYRCKRLDGLGYWNSNPNATYVMDIKYPMGPEFWRII 649

Qy	650	NGTWMKKKKKXNTLLMKPKLPMKNDISCXVQRYVINHHHTGONGWASDVCXGNHKTFTFLWTEQA	7039
Db	650	NGDTMKKKKXNTLLMKPKLPMKNDISCXVQRYVINHHHTGONGWASDVCXGNHKTFTFLWTEQA	7099
Qy	710	HTVTVLAINSIGASVAVNENLTFSPMPSKVNTVQSLAVPLNSSCVIYSWILSPSDYKLMY	7699
Db	710	HTVTVLAINSIGASVAVNENLTFSPMPSKVNTVQSLAVPLNSSCVIYSWILSPSDYKLMY	7699
Qy	770	FIIEKKNLNEDGETKMLPIEISSVKKRYIHDHFIPIEKVQSLYPIEMEGGPKPIINSFT	8299
Db	770	FIIEKKNLNEDGETKMLPIEISSVKKRYIHDHFIPIEKVQSLYPIEMEGGPKPIINSFT	8299
Qy	830	QDDIERHQSDAGLYVIYVPIIISSTILLGLTLLISHQRAKKLFWEDVNPKNCSMAOGLNF	8899
Db	830	QDDIERHQSDAGLYVIYVPIIISSTILLGLTLLISHQRAKKLFWEDVNPKNCSMAOGLNF	8899
Qy	890	QK 891	
Db	890	QK 891	

RESULT	7
ID	Q9MYL1
AC	Q9MYL1; PRELIMINARY; PRT; 894 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT	01-DEC-2001 (TREMBLrel. 15, last annotation update)
DE	LEPTIN RECEPTOR SHORT ISOFORM.
OS	Macaque mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Choriata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
CC	Cercopithecinae; Macaca.
NCBI_Taxid=9544;	[1]
RN	
RP	SEQUENCE FROM N.A.
RC	TISSUE=ADIPOSE TISSUE;
RX	MEDLINE=98408931; PubMed=9738551;
RA	Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT	"Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT	expression in the adipose tissue of normal, hyperinsulinemic, and type
RT	2 diabetic rhesus monkeys."
RL	Obes. Res. 6:353-360(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=ADIPOSE TISSUE;
RA	Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL	Submitted (JAN-2000) to the EMBL/genbank/DBJ databases.
DR	HMLP; AF225873; AAF3587.1; -
DR	HSSP; PI6471; IBP3.
DR	InterPro: IPR002996; CRIA.
DR	InterPro: IPR003961; FN.III.
DR	InterPro: IPR003529; Hematopo_receptor_L_F2.
DR	InterPro: IPR003531; Hematopo_receptor_S_F1.
DR	Pfam; PF00041; fn3; 2.
DR	SMART; SM00060; FN3; 1.
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW	Receptor.
GO	SEQUENCE 894 AA; 102191 MW; B3CAF032238BAF99 CRC64;

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DB          730 SMPMSKVNIYQSLAYPLNSSCVI 753

RESULT      8
Q9MYK9
AC          09MYK9          PRELIMINARY;      PRT;      925 AA.
DT          01-OCT-2000 (TREMBLrel. 15, Created)
DT          01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT          01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE          LEPTIN RECEPTOR SHORT INSERT ISOFORM.
OS          Macaca mulatta (Rhesus macaque) ;
OC          Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
OC          Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea;
OC          Cercopithecoinae: Macaca.
OX          NCBI_TaxID=9544;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE=ADIPOSE TISSUE.
RX          MEDLINE=98408931; PubMed=9738551;
RA          Hotta K., Gustafsson T.A., Ortmeayer H.K., Bockin N.L., Hansen B.C.;
RT          "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT          expression in the adipose tissue of normal, hyperinsulinemic, and type
RT          2 diabetic rhesus monkeys."
RL          Obes. Res. 6:353-360(1998).

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Query Match	7.2%	Score 84	DB 6	Length 894
Best Local Similarity	100.0%	Pred. No. 2,96-80		
Matches 84	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	672	SLCSQRYVYINHTSCNGTSGEDYVGNHTKFTPLMEQATVTYVLAINSTGASVAFNLTFF	731	
Db	670	SLCSQRYVYINHTSCNGTSGEDYVGNHTKFTPLMEQATVTYVLAINSTGASVAFNLTFF	729	
QY	732	SNPMKVNIVOSLSAYPLNNSCVI	755	

RESULT	9
Q9MYL2	
ID	Q9MYL2
AC	Q9MYL2;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	LEPTIN RECEPTOR LONG FORM.
OS	Macaca mulatta (Rhesus macaque).
CC	Eukaryota; Metazoa; Chordata; Crinata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC	Cercopitheciinae; Macaca.
OX	NCBI_TaxID:9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE:98408931; PubMed:9738551;

RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
 RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
 expression in the adipose tissue of normal, hyperinsulinemic, and type
 RT 2 diabetic rhesus monkeys.";
 RL Obes. Res. 6:353-360(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF222960; AAF34683.1; -
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003861; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 1163 AA; 132295 MW; 6B7B89108F851895 CRC64;

Query Match 7.2%; Score 84; DB 6; Length 1163;
 Best Local Similarity 100.0%; Pred. No. 3.6e-80;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 672 SICSVQRYVINHTSCNGTWSGSDVGNHTKFTFLMTGQATVTVLAINSIGASVAFNLTFF 731
 DB 670 SICSVQRYVINHTSCNGTWSGSDVGNHTKFTFLMTGQATVTVLAINSIGASVAFNLTFF 729
 OY 732 SWPMSKVNIVOSLSAYPLNMSCVI 755
 DB 730 SWPMSKVNIVOSLSAYPLNMSCVI 753

RESULT 10
 OYMYL0 PRELIMINARY: PRT; 1194 AA.
 AC OYMYL0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LEPTIN RECEPTOR LONG INSERT ISOFORM.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ADIPOSE TISSUE;
 RX MEDLINE=98408931; PubMed=9738551;
 RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
 RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
 expression in the adipose tissue of normal, hyperinsulinemic, and type
 RT 2 diabetic rhesus monkeys.";
 RL Obes. Res. 6:353-360(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ADIPOSE TISSUE;
 RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF225874; AAF35388.1; -
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003861; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.

KW Receptor.
 SQ SEQUENCE 1194 AA; 135824 MW; 76D023B659911AA9 CRC64;
 Query Match 7.2%; Score 84; DB 6; Length 1194;
 Best Local Similarity 100.0%; Pred. No. 3.7e-80;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 672 SICSVQRYVINHTSCNGTWSGSDVGNHTKFTFLMTGQATVTVLAINSIGASVAFNLTFF 731
 DB 670 SICSVQRYVINHTSCNGTWSGSDVGNHTKFTFLMTGQATVTVLAINSIGASVAFNLTFF 729
 OY 732 SWPMSKVNIVOSLSAYPLNMSCVI 755
 DB 730 SWPMSKVNIVOSLSAYPLNMSCVI 753

RESULT 11
 OYMS2 PRELIMINARY: PRT; 848 AA.
 AC OYMS2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TRANSMEMBRANE LEPTIN RECEPTOR (FRAGMENT).
 GN OBR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=96823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Hu X., Dai R., Li N., Wu C.;
 RT "Expression, Detection, and Partial Cloning of Porcine Leptin Receptor
 (OBR) Gene.";
 RT Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF167719; AAF89633.1; -
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 848 848
 SQ SEQUENCE 848 AA; 96372 MW; 0C5AD3B40B278FAB CRC64;

Query Match 4.5%; Score 53; DB 6; Length 848;
 Best Local Similarity 100.0%; Pred. No. 3.9e-47;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 399 TRPRGKFTYDAVCCNEHCNHRAYALYIVDYNINISCTDGYLLKMYCRWST 451
 DB 393 TRPRGKFTYDAVCCNEHCNHRAYALYIVDYNINISCTDGYLLKMYCRWST 445

RESULT 12
 OYMS2 PRELIMINARY: PRT; 1165 AA.
 AC OYMS2;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE TRANSMEMBRANE LEPTIN RECEPTOR.
 GN LEPR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCB1_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Men T.Y., Lacroix D.A., Ruiz-Cortes Z.T., Song J.H., Palin M.F.,
 RA Murphy B.D.;
 RT "Porcine Leptin (Ob) receptor complete coding sequence."
 RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 408-470 FROM N.A.
 RX MEDLINE=97222487; PubMed=9069130;
 RA Ernst C.W., Kapke P.A., Verle M., Rothschild M.F.;
 RT "The Leptin receptor gene (LEPR) maps to porcine chromosome 6."
 RL Mamm. Genome 8:226-226(1997).
 DR EMBL: AF092422; AAC61766.1; -
 DR EMBL: U72070; AAC48707.1; -
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002896; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KM Transmembrane.
 SQ SEQUENCE 1165 AA; 132548 MW; 1BEH562FEA282F12 CRC64;

Query Match 4.5%; Score 53; DB 6; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 5.2e-47;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 399 TPKRGKFTYDAYCCNEHCCHRYALVYDVNINISCTDGYLTRKTCRMST 451
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 399 TPKRGKFTYDAYCCNEHCCHRYALVYDVNINISCTDGYLTRKTCRMST 451

RESULT 13
 O97778 PRELIMINARY; PRT; 57 AA.
 AC O97778;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE LEPTIN RECEPTOR (FRAGMENT).
 GN LEPR.
 OS Elephas maximus (Indian elephant).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
 OX NCB1_TaxID=9783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Elavsky N.E., Ernst C.W., Messer L.A., Rothschild M.F.;
 RT "Identification of Sequence Tagged Sites in the Asian Elephant
 (Elephas maximus) and the African Elephant (Loxodonta africana)."
 RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U95048; AAD00769.1; -
 DR HSSP: P16471; 1BP3.
 DR MGD: MGI:104993; LEPR.
 DR InterPro: IPR002896; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 3.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KM Receptor.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SO SEQUENCE 57 AA; 6605 MW; 667857030937BA26 CRC64;

Query Match 3.7%; Score 43; DB 6; Length 57;
 Best Local Similarity 100.0%; Pred. No. 1.8e-37;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 409 AVYCCNEHCCHRYALVYDVNINISCTDGYLTRKTCRMST 451
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3 AVYCCNEHCCHRYALVYDVNINISCTDGYLTRKTCRMST 45

RESULT 14
 O97779 PRELIMINARY; PRT; 57 AA.
 AC O97779;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE LEPTIN RECEPTOR (FRAGMENT).
 GN LEPR.
 OS Loxodonta africana (African elephant).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Proboscidea; Elephantidae; Loxodonta.
 OX NCB1_TaxID=9785;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Elavsky N.E., Ernst C.W., Messer L.A., Rothschild M.F.;
 RT "Identification of Sequence Tagged Sites in the Asian Elephant
 (Elephas maximus) and the African Elephant (Loxodonta africana)."
 RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U95049; AAD00770.1; -
 DR HSSP: P16471; 1BP3.
 DR MGD: MGI:104993; LEPR.
 DR InterPro: IPR002896; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 3.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KM Receptor.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SO SEQUENCE 57 AA; 6605 MW; 667857030937BA26 CRC64;

Query Match 3.7%; Score 43; DB 6; Length 57;
 Best Local Similarity 100.0%; Pred. No. 1.8e-37;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 409 AVYCCNEHCCHRYALVYDVNINISCTDGYLTRKTCRMST 451
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3 AVYCCNEHCCHRYALVYDVNINISCTDGYLTRKTCRMST 45

RESULT 15
 O90WG3 PRELIMINARY; PRT; 1162 AA.
 AC O90WG3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LEPTIN RECEPTOR B.
 GN LEPR OR LEPRB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K OBESE; TISSUE=BRAIN, HYPOTHALAMUS;
 RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
 RA Joost H.G.;
 RT "Hypertension and Leptin receptor variant Asp600Asn in the obese,
 hyperinsulinemic KK mouse strain."
 RL J. Endocrinol. 21:337-345(1998).
 DR EMBL: Y10296; CAA71342.1; -
 DR HSSP: P16471; 1BP3.
 DR MGD: MGI:104993; LEPR.
 DR InterPro: IPR002896; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 3.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KM Receptor.
 FT VARIANT 600 600 N -> D.
 SO SEQUENCE 1162 AA; 130787 MW; 541E77CBA46EC00D CRC64;

Query Match 3.6%; Score 42; DB 11; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 3e-35;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FOPFLSGYTMWIRINHSLSGSDPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||
 DB 498 FOPFLSGYTMWIRINHSLSGSDPPTCVLPDSVVKPLPPS 539

RESULT 16
 ID 062960 PRELIMINARY: PRT: 895 AA.
 AC 062960.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LEPTIN RECEPTOR.
 GN BOB-R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RT Wang M.-Y., Unger R.H.;
 RT "Characterization of Leptin receptors in normal and Zucker diabetic
 RT fatty rats."
 RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U53144; AAB03088.1; -
 DR HSSP; P16471; 1BP3.
 DR InterPro; IPR002936; CRIA.
 DR InterPro; IPR003361; FM_III.
 DR InterPro; IPR003529; Hematopo_receptor_L_F2.
 DR InterPro; IPR003531; Hematopo_receptor_S_F1.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 DR Receptor.
 KW SEQUENCE 895 AA; 101324 MW; 3C93F018A737CC07 CRC64;
 SQ

Query Match 3.5%; Score 41; DB 11; Length 895;
 Best Local Similarity 100.0%; Pred. No. 2.8e-34;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 501 OPFLSGYTMWIRINHSLSGSDPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||
 DB 499 OPFLSGYTMWIRINHSLSGSDPPTCVLPDSVVKPLPPS 539

RESULT 17
 ID 028604 PRELIMINARY: PRT: 203 AA.
 AC 028604.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LEPTIN RECEPTOR LONG FORM (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=HYPOPHALAMUS;
 RA MEDLINE=97217693; PubMed=9063654;
 RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.;
 RT "Leptin receptor mRNA is expressed in ewe anterior pituitary and
 RT adipose tissues and is differentially expressed in hypothalamic
 RT regions of well-fed and feed-restricted ewes."

RL Domest. Anim. Endocrinol. 14:119-128(1997).
 DR EMBL: U62124; AAC48708.1; -
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 203 203
 SQ SEQUENCE 203 AA; 22398 MW; 94CAC2852950AD03 CRC64;

Query Match 2.2%; Score 26; DB 6; Length 203;
 Best Local Similarity 100.0%; Pred. No. 8.3e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 909 GPLLEPETISDISVDSWKKNDEM-934
 ||||||||||||||||||||||||||||||||||||
 DB 18 GPLLEPETISDISVDSWKKNDEM 43

RESULT 18
 ID P79115 PRELIMINARY: PRT: 152 AA.
 AC P79115.
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OBES RECEPTOR (FRAGMENT).
 GN OB-R.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfister-Genskow M., Eggen A., Hayes H., Bishop M.D.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U62385; AAB40624.1; -
 DR Receptor.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 152 152
 SQ SEQUENCE 152 AA; 16749 MW; 1B58BF0D5EBD8B CRC64;
 SQ

Query Match 1.7%; Score 20; DB 6; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.7e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1053 FSEGLDELKLGKGNFPEENN 1072
 ||||||||||||||||||||||||||||||||||||
 DB 120 FSEGLDELKLGKGNFPEENN 139

RESULT 19
 ID 09ER14 PRELIMINARY: PRT: 74 AA.
 AC 09ER14.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE LEPTIN RECEPTOR OB-RA (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=MUNICH-WISTAR; TISSUE=KIDNEY;
 RA Totsune K., Takahashi K., Mackenzie H.S., Murakami O., Aihara Z.,
 RA Sone M., Satoh F., Mouri T., Brenner B.M., Ito S.;
 RT "Leptin receptor gene expression in rat kidney."
 RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF304191; AAG22823.1; -
 DR Receptor.
 KW NON_TER 1 1
 KW NON_TER 1 1

SEQ SEQUENCE 74 AA; 8357 MW; E6ABC5C4FA/CE3D6 CRC64;

Query Match 1.5%; Score 18; DB 11; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.2e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 855 LLLGTLISHQRMKRLFW 872
 DB 33 LLLGTLISHQRMKRLFW 50

RESULT 20

O9XSN9 PRELIMINARY; PRT; 173 AA.

ID O9XSN9
 AC O9XSN9;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE LEPTIN RECEPTOR (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOTHALAMUS;
 RA Materl R.L.;
 RT "Partial cDNA sequence of the porcine leptin receptor."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF036908; AAB88825.1; -.
 KW Receptor.
 FT NON-TER
 FT NON-TER
 SQ SEQUENCE 173 AA; 19539 MW; 678897C04BFDD842 CRC64;

Query Match 1.5%; Score 18; DB 6; Length 173;

Best Local Similarity 100.0%; Pred. No. 2.6e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 917 TISEDISVDTSMKNDKM 934
 DB 1 TISEDISVDTSMKNDKM 18

RESULT 21

O35773 PRELIMINARY; PRT; 246 AA.

ID O35773
 AC O35773;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LEPTIN RECEPTOR OB-RE (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Chien E.K., Hara M., Rouard M., Yano H., Phillippe M., Polonsky K.S.,
 RA Bell G.I.;
 RT "Rat leptin splice variant Ob-Re."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF007819; AAB63202.1; -.
 DR HSSP; P40189; 180U.
 DR InterPro; IPR003529; Hematopo_receptor_L_F2.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 KW Receptor.
 FT NON-TER
 FT NON-TER
 SQ SEQUENCE 246 AA; 28085 MW; 4A469748F2B6ED8E CRC64;

Query Match 1.5%; Score 18; DB 11; Length 246;

Best Local Similarity 100.0%; Pred. No. 3.5e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 559 EKVPFENNLOFOIRYGL 576
 DB 1 EKVPFENNLOFOIRYGL 18

RESULT 22

O9XSH3 PRELIMINARY; PRT; 102 AA.

ID O9XSH3
 AC O9XSH3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE LEPTIN RECEPTOR (FRAGMENT).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dodds A.C., Whitley N.C., Keisler D.H.;
 RT "Equine leptin receptor."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF139663; AAD31284.1; -.
 KW Receptor.
 FT NON-TER
 FT NON-TER
 SQ SEQUENCE 102 AA; 11025 MW; 6AB008D11B6CE783 CRC64;

Query Match 1.5%; Score 17; DB 6; Length 102;

Best Local Similarity 100.0%; Pred. No. 1.9e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1034 QAFILSDQHPNITSPH 1050
 DB 86 QAFILSDQHPNITSPH 102

RESULT 23

O9IA32 PRELIMINARY; PRT; 145 AA.

ID O9IA32
 AC O9IA32;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LEPTIN RECEPTOR (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20539125; PubMed-11086550;
 RA Dunn I.C., Boswell T., Friedman-Einat M., Eshdat Y., Burt D.W.,
 RA Paton I.R.;
 RT "Mapping of the leptin receptor gene (LEPR) to chicken chromosome 8."
 RL Anim. Genet. 31:290-290(2000).
 DR EMBL; AF222783; AAF63467.1; -.
 KW Receptor.
 FT NON-TER
 FT NON-TER
 SQ SEQUENCE 145 AA; 16684 MW; 71CF3A3A2AE942DAD CRC64;

Query Match 1.5%; Score 17; DB 13; Length 145;

Best Local Similarity 100.0%; Pred. No. 2.6e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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OY 339 KILTSVGSNVSFHCITYK 355
    |||||||
DB 55 KILTSVGSNVSFHCITYK 71

RESULT 24
O918V6 PRELIMINARY; PRT: 1146 AA.
AC O918V6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LEPTIN RECEPTOR.
GN LEPR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
XX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=20314392; PubMed=10854702;
RA Horev G., Eliaf P., Aharoni T., Eshdat Y., Friedman-Eliaf M.;
RT "Molecular cloning and properties of the chicken leptin-receptor
(CLEPR) gene."
RL Mol. Cell. Endocrinol. 162:95-106(2000).
DR HSSP; P40189; 180U.
DR InterPro; IPR002896; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1146 AA; 129036 MW; 4031612670437BE4 CRC64;

Query Match 1.5%; Score 17; DB 13; Length 1146.
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 339 KILTSVGSNVSFHCITYK 355
    |||||||
DB 329 KILTSVGSNVSFHCITYK 345

RESULT 25
O9DDK1 PRELIMINARY; PRT: 1147 AA.
AC O9DDK1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LEPTIN RECEPTOR.
GN OB-R.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
XX NCBI_TaxID=9103;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Richards M.P., Poch S.M., Ashwell C.M.;
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF321982; AAG40323.1; -.
DR HSSP; P40189; 180U.
DR InterPro; IPR002896; CR1A.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 4.
KW Receptor.

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FT VARIANT 1133 1133 Q -> R
SQ SEQUENCE 1147 AA; 129131 MW; 34197B7908F734F4 CRC64;

Query Match 1.5%; Score 17; DB 13; Length 1147.
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 339 KILTSVGSNVSFHCITYK 355
    |||||||
DB 330 KILTSVGSNVSFHCITYK 346

RESULT 26
O91BA7 PRELIMINARY; PRT: 1148 AA.
AC O91BA7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LEPTIN RECEPTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
XX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=20225474; PubMed=10760595;
RA Okubo T., Tanaka M., Nakashima K.;
RT "Structure and tissue distribution of chicken leptin receptor (cOb-R)
mRNA."
RL Biochim. Biophys. Acta 1491:303-308(2000).
DR EMBL; AB033383; BAA94292.1; -.
DR HSSP; P40189; 180U.
DR InterPro; IPR002896; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1148 AA; 129195 MW; 06Q13EF295D7CEDE CRC64;

Query Match 1.5%; Score 17; DB 13; Length 1148;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 339 KILTSVGSNVSFHCITYK 355
    |||||||
DB 330 KILTSVGSNVSFHCITYK 346

RESULT 27
O9N1F9 PRELIMINARY; PRT: 123 AA.
AC O9N1F9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE LEPTIN RECEPTOR (FRAGMENT).
GN LEPR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
XX NCBI_TaxID=9823;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BRED YORKSHIRE/MEISHAN;
RA Lacroix D.A., Gevry N.Y., Ruiz-Cortes Z.T., Murphy B.D.;
RT "Porcine leptin receptor intron 3, partial."
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

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DR EMBL: AF184173; AAF66822.1; -.
 DR EMBL: AF184172; AAF66822.1; JOINED.
 KM Receptor.
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13696 MW; 91C8ED51BCCA7B5B CRC64;

Query Match 1.1%; Score 13; DB 6; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LHMFEIVITAF 22
 |||||
 DB 10 LHMFEIVITAF 22

RESULT 28
 ID Q28606 PRELIMINARY; PRT: 161 AA.
 AC Q28606.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE LEPIN RECEPTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID:9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOTHALAMUS;
 RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.;
 RT "Ovine partial leptin receptor cDNA."
 RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U63719; AAB51695.1; -.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 161 161
 SQ SEQUENCE 161 AA; 18678 MW; 308DFC03621E6A19 CRC64;

Query Match 1.1%; Score 13; DB 6; Length 161;
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FCVLLHMEFIV 18
 |||||
 DB 1 FCVLLHMEFIV 13

RESULT 29
 ID Q9QWV5 PRELIMINARY; PRT: 273 AA.
 AC Q9QWV5.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE LEPIN RECEPTOR LONG ISOFORM RB (FRAGMENT).
 GN LEPR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129;
 RA Banks A.S., Myers M.G.Jr.;
 RT "Murine Leptin Receptor Genomic Exon 18b and Surrounding Sequence."
 RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF098792; AAD13218.1; -.
 KW Receptor.

FT NON_TER 1 1
 SQ SEQUENCE 273 AA; 30335 MW; A800AE611EB85F96 CRC64;

Query Match 1.1%; Score 13; DB 11; Length 273;
 Best Local Similarity 100.0%; Pred. No. 8.6e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1153 HKIMENKMDLTV 1165
 |||||
 DB 261 HKIMENKMDLTV 273

RESULT 30
 ID Q95257 PRELIMINARY; PRT: 147 AA.
 AC Q95257.
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
 DE LEPIN RECEPTOR (FRAGMENT).
 GN LEPR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID:9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOTHALAMUS;
 RA Matteri R.L., Carroll J.A.;
 RL Submitted (AUG-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 97-111 FROM N.A.
 RA Striell A., Kopecky M., Moser G., Schroff J., Cepica S.;
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U67739; AAB07892.1; -.
 DR EMBL: AJ223162; CA11142.1; -.
 DR EMBL: AJ223163; CA11143.1; -.
 FT NON_TER 1 1
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16811 MW; 96AC8E929D0FED2F CRC64;

Query Match 0.9%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 WEIVITAF 22
 |||||
 DB 1 WEIVITAF 10

RESULT 31
 ID Q9WV88 PRELIMINARY; PRT: 26 AA.
 AC Q9WV88.
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE LEPIN RECEPTOR (FRAGMENT).
 GN LEPR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1;
 RA Brown J.A., Chua S.C., Liu S.M., Andrews M.T., Vandenbergh J.G.;
 RT "A spontaneous mutation in the db gene results in obesity and diabetes in CD-1 outbred mice."
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF152957; AAD41084.1; -.

KM Receptor.
 FT NON_TER 1
 FT NON_TER 26
 SQ SEQUENCE 26 AA; 3087 MW; AA471248894FCBH CRC64;

Query Match
 Best Local Similarity 100.0%; Score 9; DB 11; Length 26;
 Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 639 PMRGPFW 647
 |||||
 Db 1 PMRGPFW 9

RESULT 32
 018980 PRELIMINARY: PRT; 121 AA.
 AC 018980;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LEPIN RECEPTOR (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RA Morrison C., Yan X., Ramsay T.G.;
 RT Bovine ovarian lepton receptor partial cDNA sequence and mRNA
 expression in response to stimuli."
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U83512; AAB62399.1;
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13823 MW; 1C675E2783FE373 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 9; DB 6; Length 121;
 Pred. No. 0.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 TVNSLVFOQ 122
 |||||
 Db 84 TVNSLVFOQ 92

RESULT 33
 09HCE2 PRELIMINARY: PRT; 901 AA.
 AC 09HCE2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KIAI1630 PROTEIN (FRAGMENT).
 GN KIAI1630.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-20450683; PubMed-10997877;
 RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;
 RT Prediction of the coding sequences of unidentified human genes.
 RT XVIII. The complete sequences of 100 new cDNA clones from brain which
 code for large proteins in vitro."
 RL DNA Res. 7:273-281(2000).
 DR EMBL: AB046850; BAB13456.1; -.

DR InterPro; IPR001017; El_dh.
 DR Pfam; PF00676; El_dehydrog; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 901 AA; 101085 MW; B32C84628EDCC2F6 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 9; DB 4; Length 901;
 Pred. No. 4.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 RSSLYCSDI 476
 |||||
 Db 390 RSSLYCSDI 398

RESULT 34
 09BUM8 PRELIMINARY: PRT; 919 AA.
 AC 09BUM8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 103.0 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY, RENAL CELL ADENOCARCINOMA;
 RA Strausberg R.;
 RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC002477; AAH02477.1;
 DR InterPro: IPR001017; El_dh.
 DR InterPro: IPR000360; Transketolase.
 DR Pfam: PF00676; El_dehydrog; 1.
 DR Pfam: PF02779; transket_pyr; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 919 AA; 102969 MW; 938716BD65A1D605 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 9; DB 4; Length 919;
 Pred. No. 4.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 RSSLYCSDI 476
 |||||
 Db 378 RSSLYCSDI 386

RESULT 35
 096HY7 PRELIMINARY: PRT; 919 AA.
 AC 096HY7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 103.0 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-UTERUS, AND LEIOMYOSARCOMA;
 RA Strausberg R.;
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC000795; AAH07955.1;
 KW Hypothetical protein.
 SQ SEQUENCE 919 AA; 103042 MW; E07A3137BDD2C8D4 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 9; DB 4; Length 919;

Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 RSLYCSOI 476
11111111
DB 378 RSLYCSOI 386

RESULT 36
O9JHF4 PRELIMINARY; PRT: 30 AA.

AC O9JHF4: 01-DEC-2000 (TREMBLrel. 15, Created)
DT 01-DEC-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2000 (TREMBLrel. 15, Last annotation update)
DE LEPTIN RECEPTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Lindell K., Bennett P.A., Itoh Y., Robinson I.C.A.F., Carlsson L.M.S.,
Carlsson B.;
RT Submitted (Mar-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Lindell K., Bennett P.A., Itoh Y., Robinson I.C.A.F., Carlsson L.M.S.,
Carlsson B.;
RT "5' Alternate splicing of leptin receptor transcripts.";
RL Submitted (Jan-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF139208; AAF63410.1; -;
DR EMBL: AF121331; AAF61190.1; -;
DR EMBL: AF121332; AAF61191.1; -;
DR EMBL: AF121333; AAF61192.1; -;
KW Receptor.
FT NON_TER 30
SQ SEQUENCE 30 AA; 3562 MW; E99F8168A5A7AB67 CRC64;

Query Match 0.7%; Score 8; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 VYLLHMEP 15
11111111
DB 8 VYLLHMEP 15

RESULT 37
O9IDZ1 PRELIMINARY; PRT: 103 AA.

AC O9IDZ1: 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
OS respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A965C;
RA Zambon M.C., Stockton J.D., Clewley J.P., Fleming D.M.;
RT "Influenza and RSV.";
RN Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A965C;
RA Stockton J.D.;

RL Thesis (2000), Department of Life Sciences, Open University, London,
RL United Kingdom.
DR EMBL: AJ410801; CAC44814.1; -;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 103 AA; 11018 MW; 1FDPCAAC99CA92C1 CRC64;

Query Match 0.7%; Score 8; DB 12; Length 103;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 FSNLSKTT 86
11111111
DB 43 FSNLSKTT 50

RESULT 38
O9IDZ0 PRELIMINARY; PRT: 104 AA.

AC O9IDZ0: 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
OS respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A966C;
RA Zambon M.C., Stockton J.D., Clewley J.P., Fleming D.M.;
RT "Influenza and RSV.";
RN Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A966C;
RA Stockton J.D.;
RL Thesis (2000), Department of Life Sciences, Open University, London,
United Kingdom.
DR EMBL: AJ410802; CAC44815.1; -;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 104 AA; 11036 MW; 6AC87C99F92FE34 CRC64;

Query Match 0.7%; Score 8; DB 12; Length 104;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 FSNLSKTT 86
11111111
DB 45 FSNLSKTT 52

RESULT 39
O9IDU1 PRELIMINARY; PRT: 104 AA.

AC O9IDU1: 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
OS respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BIRM/12291/96;
RA Zambon M.C., Stockton J.D., Clewley J.P., Fleming D.M.;
RT "Influenza and RSV.";

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BIRM/12291/96;
 RA Stockton J.D.;
 RL Thesis (2000). Department of Life Sciences, Open University, London.
 DR United Kingdom.
 EMBL, AJ410851; CAC44864.1; -.
 FT NON_TER 1
 FT NON_TER 104
 FT NON_TER 104
 SEQUENCE 104 AA; 11046 MW; 74DA86F1PB54D44B CRC64;

Query Match 0.7%; Score 8; DB 12; Length 104;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 FSNLSKTT 86
 DB 48 FSNLSKTT 55

RESULT 40
 O91DU0 PRELIMINARY; PRT; 107 AA.
 AC O91DU0;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GLYCOPROTEIN (FRAGMENT).
 OS respiratory syncytial virus.
 OC viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=12814;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BIRM/12344/96;
 RA Zambon M.C.; Stockton J.D.; Fleming J.P.; Fleming D.M.;
 RT "Influenza and RSV";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BIRM/12344/96;
 RA Stockton J.D.;
 RL Thesis (2000). Department of Life Sciences, Open University, London,
 United Kingdom.
 DR EMBL, AJ410852; CAC44865.1; -.
 FT NON_TER 1
 FT NON_TER 107
 FT NON_TER 107
 SEQUENCE 107 AA; 11537 MW; 252B57C6CCAB5382 CRC64;

Query Match 0.7%; Score 8; DB 12; Length 107;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 FSNLSKTT 86
 DB 42 FSNLSKTT 49

RESULT 41
 O13894 PRELIMINARY; PRT; 124 AA.
 AC O13894;
 DT 01-JAN-1999 (TREMBlrel. 09, Created)
 DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 DE HYPOTHETICAL 14.7 KDA PROTEIN C22A12.02C IN CHROMOSOME I.
 GN SPAC22A12.02C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Pearson D.; Churcher C.M.; Wood V.; Barrell B.G.; Rajandream M.A.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z99295; CAB16572.1; -.
 KW Hypothetical protein.
 SEQUENCE 124 AA; 14736 MW; C93DEAB43D03544A CRC64;

Query Match 0.7%; Score 8; DB 3; Length 124;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 AGLSKNTS 58
 DB 45 AGLSKNTS 52

RESULT 42
 O9BHJ6 PRELIMINARY; PRT; 184 AA.
 AC O9BHJ6;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE 14-3-3-LIKE PROTEIN (FRAGMENT).
 GN TBS1.
 OS Trypanosoma brucei brucei.
 OC Eukaryota; Euzoenzoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-427;
 RA Hara T.; Fukuma T.;
 RT "Trypanosoma brucei 14-3-3 protein homologue";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ306572; CAC35518.1; -.
 DR HSP; P29312; 1A40.
 DR InterPro: IPR000308; 14-3-3.
 DR Pfam: PF00244; 14-3-3; 1.
 DR PRINTS; PR00305; 1433ZETA.
 DR ProDom; PD000600; 14-3-3; 1.
 DR SMART; SM00101; 14-3-3; 1.
 DR PROSITE; PS00796; 1433_1; 1.
 FT NON_TER 1
 FT NON_TER 184
 FT NON_TER 184
 SEQUENCE 184 AA; 21422 MW; 6FC796E64689E07A CRC64;

Query Match 0.7%; Score 8; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 655 KKEKNVTL 662
 DB 34 KKEKNVTL 41

RESULT 43
 P70016 PRELIMINARY; PRT; 217 AA.
 ID P70016
 AC P70016;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE OLFACTORY RECEPTOR (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.

OK NCBI_TaxID=8355;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Freitag J.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96112032; PubMed=8845161;
 RA Freitag J., Krieger J., Strotman J., Breer H.;
 RT "Two classes of olfactory receptors in *Xenopus laevis*.";
 RL Neuron 15:1383-1392(1995).
 DR EMBL: Y08347; CAA69633.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
 KW Receptor.
 FT NON-TER 1 1
 FT SEQUENCE 217 AA: 2498 MW: 633D47D9F2E30D35 CRC64;
 SQ

Query Match 0.7%; Score 8; DB 13; Length 217;
 Best Local Similarity 100.0%; Pred.No.16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524
 DB 35 HSLGSLDS 42

RESULT 44
 ID 097185 PRELIMINARY; PRT; 222 AA.
 AC 097185;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 DE HYPOTHETICAL PROTEIN CAC1767.
 GN CAC1767.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1488;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RA MEDLINE=21359325; PubMed=11466286;
 RA Gibson J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Tatusov R.L., Sabath F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium *Clostridium acetobutylicum*.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007685; AAK79733.1;
 KW Hypothetical protein; Complete proteome.
 KW SEQUENCE 222 AA: 26089 MW: 15DA54912724B246 CRC64;
 SQ

Query Match 0.7%; Score 8; DB 16; Length 222;
 Best Local Similarity 100.0%; Pred.No.16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 KNLFRNYN 156
 DB 4 KNLFRNYN 11

RESULT 45
 ID P95945 PRELIMINARY; PRT; 236 AA.
 AC P95945;

DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 DE ENDONUCLEASE III (DNA ENDONUCLEASE III, PROBABLE) (NTH-1)
 DE (EC 4.2.99.18).
 GN NTH-1.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 OC NCBI_TaxID=2287;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RA MEDLINE=21332296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Aveyar M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Brauso G., Fletcher C., Gordon P.M.K.,
 RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon *Sulfolobus solfataricus* P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL: Y08257; CAA69576.1;
 DR EMBL: AE006650; AAK40470.1;
 DR HSP; P20625; ZABK.
 DR InterPro: IPR004035; Endonuclease_III_FCL.
 DR InterPro: IPR003265; Endo_3c.
 DR InterPro: IPR003651; Fes_bind.
 DR InterPro: IPR003583; HHH_1.
 DR Pfam: PF00730; HHH-GPD; 1.
 DR SMART: SM00478; ENDO3c; 1.
 DR SMART: SM00525; FES; 1.
 DR SMART: SM00278; Hhh1; 1.
 DR PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
 KW Endonuclease; Lyase; Complete proteome.
 KW SEQUENCE 236 AA: 26843 MW: 6F55CADB280ECCD2 CRC64;
 SQ

Query Match 0.7%; Score 8; DB 17; Length 236;
 Best Local Similarity 100.0%; Pred.No.17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1058 DELKLEG 1065
 DB 122 DELKLEG 129

RESULT 46
 ID 0918C4 PRELIMINARY; PRT; 322 AA.
 AC 0918C4;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE OLFACTORY RECEPTOR CLASS I.
 GN XB238.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=OLFACTORY EPITHELIUM;
 RA Mezler M., Breer H.;
 RT "Two classes of olfactory receptors: molecular and functional
 RT studies.";
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ250750; CAC00721.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
 DR

DR PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW RECEPTOR.
 SQ SEQUENCE 322 AA; 36469 MW; F426GA910188F3A3 CRC64;

Query Match 0.7%; Score 8; DB 13; Length 322;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524
 |||||||
 DB 108 HSLGSLDS 115

RESULT 47

OY18C2 PRELIMINARY; PRT; 325 AA.

AC OY18C2: PRELIMINARY; PRT; 325 AA.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE OLFACTORY RECEPTOR CLASS I.
 GN XB242.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OLFACTORY EPITHELIUM;
 RA Meiler M., Breer H.;
 RT "Two classes of olfactory receptors: molecular and functional studies."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ250752; CAC00723.1;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 325 AA; 37075 MW; 94CDE3DC322C97A4 CRC64;

Query Match 0.7%; Score 8; DB 13; Length 325;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524
 |||||||
 DB 108 HSLGSLDS 115

RESULT 48

OY19B2 PRELIMINARY; PRT; 326 AA.

ID OY19B2: PRELIMINARY; PRT; 326 AA.
 AC OY19B2:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE OLFACTORY RECEPTOR CLASS I.
 GN XB107.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OLFACTORY EPITHELIUM;
 RA Meiler M., Breer H.;
 RT "Two classes of olfactory receptors: molecular and functional studies."

RT analyses."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249404; CAB86884.1;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 326 AA; 36971 MW; 9475EBF6E5EAA5C4 CRC64;

Query Match 0.7%; Score 8; DB 13; Length 326;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524
 |||||||
 DB 108 HSLGSLDS 115

RESULT 49

OY18C3 PRELIMINARY; PRT; 326 AA.

AC OY18C3: PRELIMINARY; PRT; 326 AA.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE OLFACTORY RECEPTOR CLASS I.
 GN XB239.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OLFACTORY EPITHELIUM;
 RA Meiler M., Breer H.;
 RT "Two classes of olfactory receptors: molecular and functional studies."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ250751; CAC00722.1;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 326 AA; 36923 MW; D575EBFD82F71878 CRC64;

Query Match 0.7%; Score 8; DB 13; Length 326;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524
 |||||||
 DB 108 HSLGSLDS 115

RESULT 50

OY19B2 PRELIMINARY; PRT; 335 AA.

ID OY19B2: PRELIMINARY; PRT; 335 AA.
 AC OY19B2:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE US8 MEMBRANE GLYCOPROTEIN E (SORF1 C-TERMINUS GE PARTIAL HOMOLOG).
 GN HY1083 OR SORF1.
 OS Meleagrid herpesvirus 1 (herpesvirus of turkeys).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Gammaherpesvirinae.
OX NCBI_TaxID-37108;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FC126;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Rock D.L., Kutish G.K.;
RT "The genome of turkey herpesvirus.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FC126;
RA Kingham B.J., Zelnik V., Kopacek J., Majerclak V., Ney E., Chen Y.,
RA Schmidt C.J.;
RT "Coding potential of herpesvirus of turkey: comparative genetic
RT analysis of Marek's disease serologically related viruses.";
RL Submitted (Jun-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF291866; AAG45808.1; -;
DR EMBL: AF282130; AAG30104.1; -;
DR InterPro: IPR003404; Herpes_glycopE.
DR Pfam: PF02480; Herpes_gE; 1.
SQ SEQUENCE 335 AA; 36810 MW; 619E53C08A1D42AD CRC64;

Query Match 0.7%; Score 8; DB 12; Length 335;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 839 DAGLYVIV 846
| | | | | | | | | |
Db 155 DAGLYVIV 162

Search completed: May 18, 2002, 07:08:02
Job time: 240 sec

AAW24051 ID	AAW24051 standard; Protein; 1165 AA.	ALIGNMENTS				
12	839	72.0	839	18	AAW34502.	Obesity receptor
13	815	70.0	815	20	AAV05701.	Human OB receptor
14	798	68.5	804	18	AAW34501.	Obesity receptor p
15	742	63.7	886	19	AAW26543	Human OB-R receptor
16	681	58.5	893	18	AAW50003	Human OB-R variant
17	681	58.5	904	18	AAW50002	Human OB-R variant
18	681	58.5	958	18	AAW38214	Human OB-R receptor
19	681	58.5	958	18	AAW31911	Human OB-R lepr
20	681	58.5	958	18	AAW19535	Human OB-R lepr
21	681	58.5	958	18	AAW23773	Human OB-R lepr
22	580	49.8	898	17	AAW88912	Human haematopoietic
23	580	49.8	908	17	AAW88911	Haematopoietin rec
24	580	49.8	960	17	AAW88910	Haematopoietin rec
25	568	48.8	1221	19	AAW62544	Human OB-receptor
26	474	40.7	908	18	AAW19536	Human OB-receptor
27	388	33.3	896	18	AAW14841	Variant form of hu
28	213	18.3	213	22	AAW63999	Human haematopoietin
29	213	18.3	235	19	AAW62545	Amino acid sequenc
30	42	3.6	805	18	AAW22106	Soluble leptin biom
31	42	3.6	842	18	AAW22102	Murine leptin rece
32	42	3.6	892	18	AAW34260	Murine leptin rece
33	42	3.6	894	18	AAW37338	Rat ob receptor is
34	42	3.6	894	18	AAW37337	Ob protein receptor
35	42	3.6	894	18	AAW24064	Murine MSX recepto
36	42	3.6	894	18	AAW19114	Murine short form
37	42	3.6	894	22	AAE12608	Murine short form
38	42	3.6	905	18	AAW34258	Rat ob receptor is
39	42	3.6	900	18	AAW22105	Murine leptin rece
40	42	3.6	1015	18	AAW34259	Rat ob receptor is
41	42	3.6	1162	18	AAW23399	Rat wild-type ob r
42	42	3.6	1162	18	AAW23399	Rat ob receptor (f
43	42	3.6	1162	18	AAW23399	Rat ob receptor (w
44	42	3.6	1162	18	AAW19115	Murine long form C
45	42	3.6	1162	20	AAE13473	Peptide Seq ID No:
46	42	3.6	1162	22	AAE12615	Murine long form C
47	42	2.8	783	18	AAW24054	Murine MSX recepto
48	25	2.1	25	22	AAW48723	Human leptin rece
49	23	2.0	23	18	AAW32073	Leptin internalizat
50	23	2.0	23	20	AAW39406	Human leptin rece
51	23	2.0	581	18	AAW22103	Murine leptin rece
52	19	1.6	19	22	AAW73714	Lipid accumulation
53	18	1.5	18	21	AAW57839	Human leptin recep
54	18	1.5	319	18	AAW22104	Murine leptin recep
55	17	1.5	17	21	AAW57840	Human leptin recep
56	17	1.5	17	21	AAW57841	Human leptin recep
57	17	1.5	146	22	AAE00961	Chicken leptin-rec
58	15	1.3	15	21	AAW57842	Human leptin recep
59	15	1.3	15	21	AAW57843	Human leptin recep
60	15	1.3	15	22	AAE10383	Human leptin recep
61	14	1.2	14	22	AAW64509	Gene 25 human secr
62	14	1.2	14	22	AAW48706	Human leptin recep
63	14	1.2	14	22	AAW48707	Mouse leptin recep
64	10	0.9	19	18	AAW22109	Leptin receptor an
65	10	0.9	276	18	AAW37420	Leptin receptor C-
66	9	0.8	9	18	AAW23358	Ligand-specific si
67	9	0.8	9	22	AAE12613	Murine ob receptor
68	8	0.7	8	22	AAE12612	Murine Ob receptor
69	8	0.7	58	22	AAE12614	Murine Ob receptor
70	8	0.7	58	22	AAW9675	Human excretory re
71	8	0.7	58	22	AAW42490	Human kidney relat
72	8	0.7	217	22	AAAG73056	Olfactory receptor
73	7	0.6	17	22	ABB36623	Peptide #7129 enco
74	7	0.6	17	22	AAW60329	Human brain expres
75	7	0.6				

AC AAN24051;
 XX 17-MAR-1998 (first entry)
 XX Human MSX receptor variant 13.2.
 DE
 XX
 KW Human; MSX receptor; variant 13.2; identification; purification;
 KW ligand; activator; antibody; agonist; proliferation; obesity;
 KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
 KW Type II diabetes; polycystic ovarian disease;
 KW cardiovascular disease; osteoarthritis; dermatological disorder;
 KW hypertension; insulin resistance; hypercholesterolaemia;
 KW hypertriglyceridaemia; cancer; cholelithiasis.
 XX
 OS Homo sapiens.
 XX
 PN WO9725425-A1.
 XX
 PD 17-JUL-1997.
 XX
 PF 07-JAN-1997; 97WO-US00325.
 XX
 PR 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 DR WPI: 1997-372864/34.
 DR N-PSDB: AAT85575.
 XX
 PS MSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 XX
 PS Claim 2; Pages 81-85; 219pp; English.
 XX
 CC The present sequence is the human MSX receptor variant 13.2,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-MSX receptor antibody can be used as an agonist to activate
 CC the MSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the MSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. MSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases, Type II diabetes,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 CC
 XX
 SQ Sequence 1165 AA;

Query Match 100.0%; Score 1165; DB 18; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MICGFCVLLHMEFYVTAFNLSPYTPMRFKLSGMPNSGYDFLLPAGISKRTNS 60
 DB 1 micgfcvllhmfeyvtafnlspyptrfklscompnslydflpagskrtns 60
 OY 61 NGHYTAVPEPKNSGTRSNLSKTTFHCCFSPSODRNCSCADNIEGKTFVSTNSLVF 120
 DB 61 nghytavpepknsgrtshnlskttfhccfseqdmslcahniegkltfstnslvf 120

OY 121 QOJDANWNTQCLWKGDLEFICVESLFKNLFENNYKXHLVLPDEVLEDSLPVQKGS 180
 DB 121 qgidanwnntqclwkgdleficveslfnknlfnynykxhllvpdevledslvpqkgs 180
 OY 181 FQWVHNCVHECCCELVPPPTAKLNDTLLMCJKTISGGVTFPQSLMSVOPIMNVHPDP 240
 DB 181 fqwvhncsvhecccelevppptaklndtllmcjktisggvtfpqslmsvopimnvhpdp 240
 OY 241 LGLHMEITDGNLKLKISMSBPPLVPLQYQVKSSENSVTVIRBADIIVSATSLVSDILP 300
 DB 241 lglhmeitdgnlklkismssbpplvpplqyqvksensvtvirbadivsatslvdsilp 300
 OY 301 GSSYEVQVGRKRLDGGTSDMSTPRVFTTODVTVPPRLTSGVSNVSHCIYKKEKNT 360
 DB 301 gssyevqvgkrldggtsgdmsdtpvfttodytvpprltsgvsnvshciykkenk 360
 OY 361 VPSKEITVMMNLAEKIPQSDVDVSDHVSVFTEFNINETPRCKFTYDAVCCNEHECHH 420
 DB 361 vpskelvmmnlakeipqsgydvdsdhvskvtffnlnetkprgkfydayccnehechh 420
 OY 421 RYAEVYIDVNNINISCESTDGVLTKMTCRMSSTFISGLAESTLQLRHRSLSYCSIDIPSH 480
 DB 421 ryaelvyidvnniniscedgyltkmcrwstfsglaestlqlyhrsalsydsidipsh 480
 OY 481 PISEPKDYLQSDGFECFQPIFFILSGYTMIRIHSGISLSDPPTCVLPDSVVRPLRP 540
 DB 481 pisepkdylqsdgyfecfqpiffilsgylmirihsgisldpptcvlpdsvvrplrp 540
 OY 541 SSVKAEITINIGLKLKISWEKVPENNLQFOIRYGLSGKEVQKMEYVDKAKSVSLVP 600
 DB 541 ssvkaeitinigllklkismekvpennlqfoirylsglsgkevqkmyevdaksvslvp 600
 OY 601 PDLCAYAVQVROCKRLDGLGYMSNMSNPAYTVMDIKVPRGPEFRRIINGDTMKKENV 660
 DB 601 pdlcayavvrockrldglgymsnmsnpaytvmdikvprgpefrriingdtmkkenv 660
 OY 661 TLLMKPLKNDLSCSVORVYNHHTSCNGTMSDVGNNHFKFPLMEQAHVTVLAINSI 720
 DB 661 tllmkplkndlscsvorvynhhtscngtmsdvgnnhfkfplmeqahvtvlainsi 720
 OY 721 GASVAFNFTFSPMKNVIVOSLAVPLNSSCVIYSWILSPDYKLMFIIEMKMLNED 780
 DB 721 gasvafnftfspmknvivoslavplnsscviysswilspsydklmfiiemkmlned 780
 OY 781 GEIKWLRISSVKKRYIHDHPIPIEKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
 DB 781 geikwlrissvkkryihdhpipiekyqpslypifmegvgkpkliinsftqddiekhsda 840
 OY 841 GLYIVPYVLISSILLGLLISHSORMKLFMEDVNPKNCSMAOGLNOKPRTFPHLP 900
 DB 841 glyivpyvliissillglilisshormklfmedvnpknscsmaoglnokprtfphlp 900
 OY 901 KHTASVTCPLLEPTEISEDISVDTSMKNKDEMMPTTVVSLSTDLDEKGSVCISDQFN 960
 DB 901 khtasvtcpllepteiasedisvdtssmknkdemmpttvvslstdldekgsvcisdqfn 960
 OY 961 SVNFSEAGTEVYEDESQROPFVKYATLISNKSPEETEGEGLINSVTKCFSSKNSPL 1020
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 DB 1021 kdsfnsswetiraoafilisdqhpniishltfesglidelflkegfpennddksiyvl 1080
 OY 1081 GVTISIKRREGVLLNDKSVSCPPFAPCFTDIRVLODSCSHFVENNIMLGTSKKTAFS 1140
 DB 1081 gvtisikrregvllndksvscppfapcftdirvloedscshfvennimlgtskktfas 1140
 OY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
 DB 1141 ympqfqtcstqthkimenkmdltv 1165


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Db 361 vpskelvwmnlleeklpgsgydvsvdshvskvtfnnlnetkprkfydavyecmehech 420
Qy 421 RYAEIYVIVNINISCEITDGLTKMTCRMSTSTIOSIAESTLQURHRSLSYCSIPSIH 480
Db 421 RYAEIYVIVNINISCEITDGLTKMTCRMSTSTIOSIAESTLQURHRSLSYCSIPSIH 480
Qy 481 PISEPDCTIOSGFECECTFOPIFLISGTYMIRINHSLSGSDSEPTCVLPDSVVKPLP 540
Db 481 PISEPDCTIOSGFECECTFOPIFLISGTYMIRINHSLSGSDSEPTCVLPDSVVKPLP 540
Qy 541 SSVKAETITIGLTKISMEKVPENNLQOIRYGLSGREVKQKVEVDANKSKSLVP 600
Db 541 SSVKAETITIGLTKISMEKVPENNLQOIRYGLSGREVKQKVEVDANKSKSLVP 600
Qy 601 PDICAAVAVQVRCRRLDGLGYSWMSNPATVVMDIRPARGEPFMIINGDMKREKNV 660
Db 601 PDICAAVAVQVRCRRLDGLGYSWMSNPATVVMDIRPARGEPFMIINGDMKREKNV 660
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Db 661 TILMKPLMKNDLSQVQRYVYINHHISGNGTWSDEDVGNHRTFTLMEQAHVLAINST 720
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Db 721 GASVAFNLTFSWPMKSVNIVOSLSAYPLNNSCVIWSMISPSDYKLMYFIEMKNLIND 780
Qy 781 GEIKMLRISSSVKRYVYIHDFIPIEKYOPSLYPIEMEGVQKPKINSPTODIEKHOSDA 840
Db 781 GEIKMLRISSSVKRYVYIHDFIPIEKYOPSLYPIEMEGVQKPKINSPTODIEKHOSDA 840
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Db 841 GLVYIVPVIISSITLGLTLISHQRMKLFMEDVNPKNCSMAOGLNOKPTEFHELF 900
Qy 901 KATASVTCPLLEPEITISEDIVDTSMKNKDEMPVTYSLSTIDLEKSGVCSIDQFN 960
Db 901 KATASVTCPLLEPEITISEDIVDTSMKNKDEMPVTYSLSTIDLEKSGVCSIDQFN 960
Qy 961 SVNFSABETVYEDESOROPFVKYATLISNSKPSGTGEODLINSVTKRCSSKNSP 1020
Db 961 SVNFSABETVYEDESOROPFVKYATLISNSKPSGTGEODLINSVTKRCSSKNSP 1020
Qy 1021 KDSFSSSMEIEAOAFIISDOHNTIISPHLTSEGLDELKEDGFPENNKKSTIYL 1080
Db 1021 KDSFSSSMEIEAOAFIISDOHNTIISPHLTSEGLDELKEDGFPENNKKSTIYL 1080
Qy 1081 GYTSIKKRESGYLLDKSRVSCPPAPCLFTDIRVQDSCHFEVNNINIGTSKRTFAS 1140
Db 1081 GYTSIKKRESGYLLDKSRVSCPPAPCLFTDIRVQDSCHFEVNNINIGTSKRTFAS 1140
Qy 1141 YMPQFOTCSTQHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQHKIMENKMDLTV 1165

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FT /note="encoded by AAT98531"
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FT /label="unknown"
FT /note="encoded by stop codon"
FT Misc-difference 1169
FT /label="unknown"
FT /note="encoded by stop codon"
FT Misc-difference 1187
FT /label="unknown"
FT /note="encoded by stop codon"
FT Misc-difference 1207
FT /label="unknown"
FT /note="encoded by stop codon"
FT Misc-difference 1.1165
FT /note="encoded by stop codon"
FT /note="encoded by AAT98531"
PN W09725424-A1.
PD 17-JUL-1997.
XX
XX 02-JAN-1997; 97WO-US00128.
XX
PR 31-DEC-1996; 96US-0774414.
PR 04-JAN-1996; 96US-0582825.
XX
PA (AMGE-) AMGEN INC.
PI Chang M, Fletcher FA, Welcher AA.
PI WPI: 1997-384981/35.
XX N-PSDB; AAT98531.
XX
XX Obesity protein receptor(s) and related DNA - used to treat weight
XX disorders, e.g. obesity, diabetes and high cholesterol or blood
XX lipid levels
XX
PS Claim 31: Page 76; 15pp; English.
XX
XX This sequence represents the obesity (OB) receptor 2 protein. This
XX sequence has one or more of the biological properties of naturally
XX occurring OB receptor protein. The OB receptor proteins and OB
XX receptor/OB protein complexes are used for the treatment of obesity,
XX diabetes, high blood lipid levels and high cholesterol levels. The
XX proteins may also be used to treat an individual for weight loss or
XX weight maintenance required for purely cosmetic purposes.
XX
SQ Sequence 1220 AA:

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RESULT 3
AAW34500
ID AAW34500 standard; protein: 1220 AA.
XX
XX AAW34500;
XX
XX 18-MAR-1998 (first entry)
XX
XX Obesity receptor D protein.
XX
XX Obesity receptor D protein.
XX
XX Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
XX high blood lipid level; diabetes; diabetes; high cholesterol level;
XX weight loss; therapy; weight maintenance.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 1.1165

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Query Match 100.0%; Score 1165; DB 18; Length 1220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MICOKFCVLLHMEFYVITAFNLASYIPMPKLSCMPNSTYDYFLPAGSKNTSNS 60
Db 1 MICOKFCVLLHMEFYVITAFNLASYIPMPKLSCMPNSTYDYFLPAGSKNTSNS 60
Qy 61 NGHYETAVPEKFNSSGTHPSNLSKTFHCCFRSEODRNSCADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAVPEKFNSSGTHPSNLSKTFHCCFRSEODRNSCADNIEGTFVSTVNSLVF 120
Qy 121 QOQIDAMWNIOCHLKGDLKFLCYVESLFKNLFRNRYKXHLXVLPVELEDSTLVQKRS 180
Db 121 QOQIDAMWNIOCHLKGDLKFLCYVESLFKNLFRNRYKXHLXVLPVELEDSTLVQKRS 180
Qy 181 FQWVHNCSSVHECCLELVVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINMVPDP 240
Db 181 FQWVHNCSSVHECCLELVVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINMVPDP 240
Qy 241 LGLHMEITDGNLKIWSSSPPLVPPLOYQVYXSENSTVIREADKIVATSLSLVDSILP 300
Db 241 LGLHMEITDGNLKIWSSSPPLVPPLOYQVYXSENSTVIREADKIVATSLSLVDSILP 300

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PR 22-JAN-1996; 9605-0599455.
 PR 26-APR-1996; 9605-0638524.
 PR 03-SEP-1996; 9605-0708123.
 PR 28-MAY-1997; 9705-0864564.
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;
 DR WPI; 2001-624489/72.
 XX
 PT Identifying compounds for treating body weight disorder, e.g. obesity,
 PT anorexia or cachexia, comprises contacting cell expressing mammalian Ob
 PT receptor protein, JAK2 protein and mammalian SOCS-1 protein with test
 PT compound -
 PS
 PS Disclosure: Page -: 109pp; English.
 CC The patent discloses obese receptor (OBR) proteins and nucleic acids
 CC encoding them. OBR protein participates in the regulation of mammalian
 CC body weight. The invention also relates to a method of identifying
 CC therapeutic compounds for the treatment of a body weight disorder.
 CC The method involves contacting a cell that expresses a mammalian OBR
 CC protein, a JAK2 protein and a mammalian SOCS-1 protein with a test
 CC compound. The method is useful for identifying compounds which modulate
 CC OBR gene expression and gene product activity, which can be used as
 CC agents to control body weight particularly as therapeutic agents for
 CC treating body weight disorders, including obesity, cachexia and anorexia.
 CC The present sequence is human OBR protein mutant (Y1141F).
 CC Note: This sequence is not shown in the specification but is derived
 CC from the wild-type human OBR protein shown in figure 3 of the
 CC specification (AAE12609).
 CC
 XX
 XX Sequence 1165 AA;
 SQ
 Query Match 97.9%; Score 1140; DB 22; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 micqkfcvllhmfefyvtafnlstypwrfklscompnstydfllpagskntls 60
 QY 61 NGHTEFAVEPKNNSGTHFSNLSTKTHCCFRSEODRNCSLCADNTEGTPVSTNSL 120
 DB 61 nghtefaavepknsghthslnstktfhccfrseodrnscadnlegtfvstnslvf 120
 QY 121 QCIDANMNTOCKLKGDLKLFICYVESLFKNLFNRYKXHLVYLPVLEDSPLVPQKS 180
 DB 121 qcidanmnigcwlkgdlklficyveslfnlfnrykxhllvylpvljedsplvpqks 180
 QY 181 FQMVHNCNSVHECCCECLVEVPTAKLNDTLMLCLKITSQVIFOSPLASQPIKMYKPD 240
 DB 181 fgmvhncnsvehccceclvyptrakindtlmlcklitsqvgifosplmsqpihmkykdpd 240
 QY 241 LCLHMEITDDGNLKITSSWSSPLVPEPQYQVXYSNSTTVIREADKIVSATSLVDSILP 300
 DB 241 lclhmeitddgnlkitsswssplvpepdaqyqvxyssnsttvireadkivatsllvdsilp 300
 QY 301 GSSYEVQVGRKRLDGTGSDMSTRVFTQDVIYFPPRIILSVGSNVSFHCYKKEKNI 360
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 QY 361 VSKSEIVMMNMTAEKIPQSDVDSVSHVSKVTFEFLNTEKPGKFFYDAVYCCNEHECH 420
 DB 361 vpsketivmmnmtaekipsgdgvdsdshvskvtfeflnetkpgkfydadvccnehech 420
 QY 421 RYAEELVIDVNNINISCEITDGLTKMTKRWSTSTIOSLASTQDLRYHRSLSYCSDFPS 480
 DB 421 ryaelvidvnniniscetdgltkmtkrwststioslastqdlryhrslycsdfps 480
 QY 481 RISEEKDCYLGSDGFYECLFQPIFLLSGTYMIRINHSLSGSDSEPTCYLPDSVYKPLP 540

DB 481 piseekdcylgsgdfyecifqpiflfllsgtylmirinhslsgsdseptcylpdsvykpplp 540
 QY 541 SSVKAEITINIGLKTSWEKVPFENNLOFOIYTGSGKEVOKKH EYDPAKSKSYSLPV 600
 DB 541 ssvkaeitiniglktswekvpfennlofoiytgsgkevokkhyeydpsaksksyslpv 600
 QY 601 PDLCAVAYQVRCRRLDGLGWSMNSNPAYTVMDIKVPRGCEIWTIINGDTMKREKNV 660
 DB 601 pdlcaavayvrcrkrlldglgwsnmnsnpaytvmdikvprgceiwtiingdtmkreknv 660
 QY 661 TLIMKRLMKNDLSQVORYINHTSCNGTWSESDVGNHRTFTLTLTECAATVVLAINSI 720
 DB 661 tlmkrlmkndlsqvoryinhntscngtwsestdvgnhrtftlvtltecaatvvlainssi 720
 QY 721 GASVANFNLTFSWPMKSNVIVQSLASVPLNNSCVIYSWILSPDYKLMVFIEKMLNED 780
 DB 721 gasvanfnltfswpmksnvivqslasvplnnsccviyswilspsdyklmvfiekmkned 780
 QY 781 GEIKWLRISSSVKKYIYHDFPIEKEYQFSLVPIFMEGVGKPKTNSFTODDIEKHQSDA 840
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 QY 841 GLVIVIPVLISSSIIILGTLTILSHOBMKLFMEDVDPNPKCSVAGQINQKPTFPHLFI 900
 DB 841 glvivipvli:sssili:gtltilshqtmkrlfmedvdpnprkcsvagg:inqkpetfphlfi 900
 QY 901 KHTASVTCGPLLEPPTISEDISVDPISWKNKDEMPPTVSLSTVYLEGSCVCSIDQFN 960
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 QY 961 SVNFSEAEKTEVYTEDESOROPVKAATLISNKPSETGEODLNSVYTKCSSKN SPL 1020
 DB 961 svnfseaekevtytedesqrptvkayatlisnkspektegey:lnsvytkcfsksnpl 1020
 QY 1021 KDSFNSWIEIEAOFPIISDHPNIIISPHLPSSEGLDELKKEGNEPEENNKKSTIYV 1080
 DB 1021 kdsfnswieieaofpilisdhpniiisphlpsseglde:lkkegnepeennkksiyv 1080
 QY 1081 GYVTSIKKRSQVGLITDKSRVSCFPAPCLFTDIRVLODSCSHFVNININIGTSKKTFFAS 1140
 DB 1081 gyvtsikkrsgvllitdksrsvcfpapclftdirvldscshfvninnigtskktffas 1140
 RESULT 5
 AAY13474
 ID AAY13474 standard; Protein; 1165 AA.
 AC AAY13474;
 XX
 DT 26-JUL-1999 (first entry)
 DE Peptide Seq ID No: 4 of WO9923493.
 DE
 KW Leptin; phosphorylated leptin receptor; tyrosine phosphatase 1D; p17-1D;
 KW modulator; drug; weight loss; adiposity; hypertension; heart disease;
 KW type II diabetes; cancer; AIDS; agriculture.
 OS Homo sapiens.
 XX
 PN WO9923493-A1.
 PD 14-MAY-1999.
 XX
 PF 27-OCT-1998; 98MO-US22797.
 XX
 PR 26-OCT-1998; 98US-0178691.
 PR 31-OCT-1997; 97US-0961809.
 XX
 PA (UYRO) UNIV ROCKEFELLER.
 PI Friedman JM, Li C;

DR WPI: 1999-327025/27.
N-PSDB: AAX35588.

Identifying modulators agents that modulate leptin activity

Disclosure: Page 77-84; 96pp; English.

The invention provides a method for identifying modulators of binding of a phosphorylated leptin receptor with tyrosine phosphatase 1D (PTP-1D). The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin receptor or its phosphorylated fragment with protein PTP-1D or its fragment in the presence and absence of a candidate agent under conditions in which in the absence of the agent the binding of the phosphorylated leptin receptor or fragment with PTP-1D or its fragment can be detected; and (b) detecting the binding of the phosphorylated leptin receptor and PTP 1D, where an increase in binding detected in the presence of the agent, indicates that the agent enhances binding, and a decrease in binding in the presence of the agent indicates that the agent is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin receptor-dependent PTP-1D phosphorylation are useful as drugs in weight loss diet regimens. The drugs identified can regulate adiposity and fat content of animals, particularly in mammals. Disorders that can be treated by PTP-1D modulators include obesity and its associated diseases, e.g. hypertension, heart disease and type II diabetes, and weight loss associated with cancer and AIDS. Additionally the agents identified may be useful in agriculture where body weight of domestic animals can be modulated.

Sequence 1165 AA:

Query Match 91.3%; Score 1064; DB 20; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 NCHYETAVEPKNSGTHSNLSKTTFHCCFRSEDRNCSLADNIEGTFVSTNSLVE 120
DB 61 nghyetavepkfnsqthsnlskttfhccfrseqdrnscsladnlegtfvstnslvf 120
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DB 121 qgidanwnmqcwlkgdflficyveslfnlfrnyykhllvlepvledsplvpqkgs 180
QY 181 FQWVHCNCSVHSGCECTVVPPTAKLNDTLNCLKTRSGGVTFOSPLMSVOPIMVKKDDP 240
DB 181 fqnvhcnscsvhsgcectvvpptaklndtlncclktrsggvtfosplmsvopimvkkddp 240
QY 241 IGLHMEITDDGNLIKISWSSAPLVPEPLQYQVYSENSTVIREADKIVSATSLVDSILP 300
DB 241 lglhmeitddgnlikiswssaplvpeplqyqvysenstvireadkivsatslvdsilp 300
QY 301 GSSYEVQVNGKRLDGGTMSDMSTRVFTQDYVTPPKILTSVGSNVSPHGYKKENKI 360
DB 301 gssyevqvgkrlldggtmsdmstrvftodyvtppekiltsvgsnvspghgykkenk 360
QY 361 VSKKEIVMMNLAERIKPOSOYDVSDHVSQVTFENLNEKPRGKFTYDVAVCCNEHECH 420
DB 361 vskkeivmmnlaerikposoydvshvskvtfenlnekprgkftdydavccnehech 420
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DB 421 ryaelvidvnnisgentgvltakmtcrmwststioslaestlqlrhrsilycsidps 480
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DB 481 pisepdclqsdgfrctcfqfplisgtytmmirinhsglsdspptcylpdsvvkplpp 540
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DB 541 ssvkaeitinigltkiswkpvpennlqfqlrylsgekvqmkwkyevdyaksksvslpv 600
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DB 601 pdlcavayavqckrldglgywnmsnpaytyvmdikypmrghfeffwrlngdtmkkernv 660
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DB 961 svnfseaegetevyedesoropfvkyatlinskpsetgeegdl nssvlykcfssknsp 1020
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DB 1021 kosfnswwiefiaqafiiisdqhpniisphltfselddelkiegfpeendkksiytl 1080
QY 1081 GYTSIKKRESGVLTFRKSNVCEFPAPCFTDIRVLODSCSHFVENNIMLGTSKKRTFAS 1140
DB 1081 gytsikkresgvltfrksnvcefpapcftdirvlo dscshfvennimlgtskkrtfas 1140
QY 1141 YMPQFQTCSTQTHKIMENKRCDLTV 1165
DB 1141 ympqfqtctstqthkimenkrcdltv 1165

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RESULT 6
AAW19116
ID AAW19116 standard; protein; 1165 AA.
XX
AC AAW19116;
DT 26-AUG-1997 (first entry)
XX
DE Human Ob receptor.
KW Ob receptor; OBR; cytokine receptor; signal transduction;
KW eating disorder; obesity; cachexia; anorexia; bulimia; diagnosis;
KW therapy.
OS Homo sapiens.
XX
FH Key
FT Peptide
FT 1..20 location/Qualifiers
FT /label- sig-peptide
FT 21..839
FT /label- ECD
FT /note- "extracellular domain"
FT Domain
FT 840..862
FT /label- TMD
FT /note- "transmembrane domain"
FT Domain
FT 863..1165
FT /label- CD
FT /note- "cytoplasmic domain"
FT 319..323
FT /note- "motif conserved in class I cytokine


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Oy 721 GASVANFNLTFSPMSKVNIVOSLSAYPLNSSCVIWSWILSPSDYKIMFIIEMKNLND
Db 721 gasvanfntfswpmskvnivglsayplnsscvlswilspdykimgfiiemknlned
Oy 781 GEIKWLRILSSSVKYYIHDFPIEKYOSLYPIFMEGVGKPKIINSFTODDIERNQSDA
Db 781 geikwlrilsssvkyyihdfpiiekyslypifmegvgkpkilnsftqddiekhsda
Oy 841 GLYVVPATISSIILGLILSHORMKLEMDVNPKNCSMAGINORFETFEHLFI
Db 841 glyvvpatisiilglilshormklemdvnpknscswaginorfeffehlfi
Oy 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVVSILSTTDEKGSVCISDOFN
Db 901 khtasvtcgpillepetisedivdtsmknkdempptvvsilsttdekgsvcisdofn
Oy 960 901 khtasvtcgpillepetisedivdtswknkdemptlvslstdelekgsvcisdofn
Db 960 901 khtasvtcgpillepetisedivdtswknkdemptlvslstdelekgsvcisdofn
Oy 961 SYNFEABSTETTYEDESOROPFVKYATISNSKPSFTEEGCLNNSVTKCFSSKNSPL
Db 961 synfeabstettyedesoropfvykatinskspsfteeegclnnsvtkcfssknspl
Oy 1020 961 synfeabstettyedesqrpfvykatinskspsfteeegclnnsvtkcfssknspl
Db 1020 961 synfeabstettyedesqrpfvykatinskspsfteeegclnnsvtkcfssknspl
Oy 1021 KSPFENSWEIPAQAFILSDOHPNIIISPHLTFSEGLDELKLEGNFPENNDRKSIYYL
Db 1021 kspfensweipaqafilsdohpniiisphltfsegldekllegnfpenndrksiiyy
Oy 1080 1021 kspfensweipaqafilsdohpniiisphltfsegldekllegnfpenndrksiiyy
Db 1080 1021 kspfensweipaqafilsdohpniiisphltfsegldekllegnfpenndrksiiyy
Oy 1081 GVTSTIKKRESGVLLTDKRSVSCPPAPCLFTDTRVLQDSCHFVENNIMIGTSSKRTFAS
Db 1081 gvtstikkresgvlltdkrsvscppapclftdtrvrlqdschfvennimigtsskrtfas
Oy 1140 1081 gvtstikkresgvlltdkrsvscppapclftdtrvrlqdschfvennimigtsskrtfas
Db 1140 1081 gvtstikkresgvlltdkrsvscppapclftdtrvrlqdschfvennimigtsskrtfas
Oy 1141 YMPQFQCSQCHKIMENKMDLTV 1165
Db 1141 ympqfqcsqchkimenkmcltv 1165

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PT MSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours
XX Claim 2, Pages 86-89; 219pp; English.
CC The present sequence is the human MSX receptor variant 6.4,
CC which can be used to identify and purify ligands and activators.
CC An anti-MSX receptor antibody can be used as an agonist to activate
CC the MSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the MSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. MSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.
SQ Sequence 896 AA:
Query Match 76.5%; Score 891; DB 18; length 896;
Best local similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MTCQKFCVLLHMERIYVITAFNLSTPTTPMRKISCMPPNNTYDYELLPAIGSKTNS
Db 1 mtcqkfcvllhmeriyvitafnlstpttpmrkiscmpnntydyellpaigsktns
Oy 61 NGHYEVAEPKRNSSGTHSNLSKTEFHCCFSEDRNCSLADNIEGTFSTVSNLYF
Db 61 ngyeavepkrnssgthsnlsktefhccfseDRNCSLADNIEGTFSTVSNLYF
Oy 121 QOIDANMNIOCMKGDCLKFCYVESLFKNLFNNYKRVHLYVLPVEVSDPLVPQKS
Db 121 qoidanmnioCMKGDCLKFCYVESLFKNLFNNYKRVHLYVLPVEVSDPLVPQKS
Oy 121 qoidanmnioCMKGDCLKFCYVESLFKNLFNNYKRVHLYVLPVEVSDPLVPQKS
Db 121 qoidanmnioCMKGDCLKFCYVESLFKNLFNNYKRVHLYVLPVEVSDPLVPQKS
Oy 181 FQWYHNCNVHECCBCLVPPPTAKLNDTLMLCKITSGCVTFQSPULNSQPINMVKEPDP
Db 181 fqwYHNCNVHECCBCLVPPPTAKLNDTLMLCKITSGCVTFQSPULNSQPINMVKEPDP
Oy 241 IGLHMETDQGNKITSNNSPPIVPPPIOVYVSESTVIRADKIVATSLVNSIIP
Db 241 iglHMETDQGNKITSNNSPPIVPPPIOVYVSESTVIRADKIVATSLVNSIIP
Oy 301 GGSYEVOVGKRLDGPIMSDMSTPRTVDIYPPKILTSVGSNVEFHCIYKRENTI
Db 301 ggsyeVOVGKRLDGPIMSDMSTPRTVDIYPPKILTSVGSNVEFHCIYKRENTI
Oy 301 ggsyeVOVGKRLDGPIMSDMSTPRTVDIYPPKILTSVGSNVEFHCIYKRENTI
Db 301 ggsyeVOVGKRLDGPIMSDMSTPRTVDIYPPKILTSVGSNVEFHCIYKRENTI
Oy 361 VPSKEIYVMMNIAEKTPSQDYVSDVSKVTFPFINETKPRCKITYDAVYCCNEHECH
Db 361 vpskeIYVMMNIAEKTPSQDYVSDVSKVTFPFINETKPRCKITYDAVYCCNEHECH
Oy 421 RYAEIYVIVDNNISCEGTGYLTKMCGRMSTSTIOSIAESTICLHRHRSIVCSIDPSIH
Db 421 ryaeIYVIVDNNISCEGTGYLTKMCGRMSTSTIOSIAESTICLHRHRSIVCSIDPSIH
Oy 481 PISEPKDYLOSDFECLFOPIFILSGYTMNIRIHSLSJDSIPTCVLPVSVPKPLP
Db 481 pisePKDYLOSDFECLFOPIFILSGYTMNIRIHSLSJDSIPTCVLPVSVPKPLP
Oy 541 SSVKAEITINIGLKTSMKPVPPENNLOPQIRYGLSGKEVQKMYEVDASKSVSLPV
Db 541 ssvKAEITINIGLKTSMKPVPPENNLOPQIRYGLSGKEVQKMYEVDASKSVSLPV
Oy 601 PDLCAVYAVOVCKRDLGIGYMSNNSPFAIYVYVMDIKVPMRGPETWRIINGDTMKKEKRV
Db 601 pdlCAVYAVOVCKRDLGIGYMSNNSPFAIYVYVMDIKVPMRGPETWRIINGDTMKKEKRV

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Db 601 pdicavayavrcrkldgldgyenwsenpaytvmldkvpmpgpefwrllngdtkmekkv 660
 QY 661 TLAMKPLMKNDLSICVQRYVINHTSCNGWSDVGNHRTFTPLMTEOAHVYLAINSI 720
 Db 661 Tllwkpmlkndslcsvqrvynhtscngtwesdvgnhkftllwteqahvtvialnsi 720
 QY 721 GASVANENLTFSPMKSVMNVQSLASVPLNSSCVIWSMISPDIKMYIIEKMLNED 780
 Db 721 gasvanenlftspmksvmlvqslasvplnsscvyswllspdyklymylekmlned 780
 QY 781 GEIKMLRISSSVKRYIHDHFPIEKYQESLYPIFMEGVKPKIINSFQDDIEKHQSDA 840
 Db 781 getkwlriesssvkryihdhfpielkyqfelypifmegvqkplinsftqddiekhsda 840
 QY 841 GLTVIYVPIIISSTILGLTLLISHORMKLFWEDVNPKNCSWAGLNPK 891
 Db 841 gltyivpviissstllgltlisshormklfmedvnpknscswaglnpck 891

RESULT 8

AAW24053
ID AAW24053 standard; Protein; 923 AA.

XX AAW24053;

DT 17-MAR-1998 (first entry)

XX Human MSX receptor variant 12.1.

KW Human; MSX receptor; variant 12.1; Identification; purification;
 KW ligand; activator; antibody; agonist; proliferation; obesity;
 KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
 KW Type II diabetes; polycystic ovarian disease;
 KW cardiovascular disease; osteoarthritis; dermatological disorder;
 KW hypertension; insulin resistance; hypercholesterolaemia;
 KW hypertriglyceridaemia; cancer; cholelithiasis.

XX Homo sapiens.

XX WO9725425-A1.

XX 17-JUL-1997.

XX 07-JAN-1997; 97WO-US00325.

XX 20-JUN-1996; 96US-0667197.

XX 08-JAN-1996; 96US-0585005.

XX (GEMT) GENENTECH INC.

XX Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

XX Rodrigues ML;

XX WPI: 1997-372864/34.

XX N-PSDB; AAT85577.

PS Claim 2; Pages 89-93; 219pp; English.

CC The present sequence is the human MSX receptor variant 12.1,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-MSX receptor antibody can be used as an agonist to activate
 CC the MSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the MSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. MSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,

CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.

XX Sequence 923 AA;

Query Match 76.5%; Score 891; DB 18; Length 923;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTCQKFCVLLHMEFTYVITAEMLSTPIPRMRKISCMPPNKSIVYELPLAGSKRTSNS 60
 Db 1 mtcqkfcvllhweftlyvtalnlstpiipwrkiscmpnstydyellpaglskrtns 60
 QY 61 NGHYETAVERPKFNSGTHFNSLSTTFHCCFSEODRNCSLADTLEGKFTVTSLSVY 120
 Db 61 nghyetavepkfnsqthfnslnsttfhccfseodrnscldadtlegkftvtslnslye 120
 QY 121 QQIDANMNITQWLKGDLEFCYVESLFLNLFNNYKVHLVYLVELEDSPVLPQKGS 180
 Db 121 qqidanwnlqcwllkgdlikficyveslflnlfnnyskvhllyvlevledsplvpqkgs 180
 QY 181 FQWVHNCNSVHECCLELPPPTAKLNDTLIMCKITSGVIRFQSPINSVQIMVVPDPP 240
 Db 181 fgvhncnsvheccelppptaklndtlimckitsgvirfqsplnsvqimvvpdpdp 240
 QY 241 LGHMEITDGNLKIISMSPPLVPPLOQYVKSSENSTVIRADBKIVSATSLVDSILP 300
 Db 241 lghmeitddgnlkiswsppplvpplqyvkysenstviradkivsatllvdsilp 300
 QY 301 GSSYEYQVRGKRLDGFQIMSDMSTPRVFTTQDYITPRPKILISVGSNVSFHCYKKEK 360
 Db 301 gssyevqvrqkrlldgfwlmsdstprvfttqdyitprpkillevgsnvsfhcykkek 360
 QY 361 VPSKEIYVMNNIAEKIPOSQYDVSDHVSVFEPNNIETPRPKIYDAVYCCNEHCCH 420
 Db 361 vpskelvwmniaeklposqydvdsdhvsvfepnnietprpklydavycnehech 420
 QY 421 RYAEIYVIDVNNINISCEIDYLLKMTCRMSTSTIQAIAESTLQRLYHFSLSYDIPSIH 480
 Db 421 ryaeliyvidvnniniscetdyllykmtcrmtststiqiaiaestlqlyhrslycsdipsih 480
 QY 481 PISEPKDCYIQSDGFYECIFQPIFLSLSGYTMIRINHSLSLSLSPICVLPDSVVPPLP 540
 Db 481 pisepkdcylqsdgyfecifqpfllslsgytmwirinhsllsplsplcvlpdsvvpplp 540
 QY 541 SSVKAEITINIGLKTSMKEVPPENNLOFOIRGSLGKEVQKKNHEVDAKRSVLPV 600
 Db 541 ssvkaeitinigllktsmkevppeennlofoirgslgkevkknhevdakrsvlpv 600
 QY 601 PDLCAVAYAVQVRCKRLDGLGYMSNMSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKV 660
 Db 601 pdlcavayavrcrkldgldgymsnmsnpaytvvmdikvpmrgpewriingdtkmekkv 660
 QY 661 TLAMKPLMKNDLSICVQRYVINHTSCNGWSDVGNHRTFTPLMTEOAHVYLAINSI 720
 Db 661 Tllwkpmlkndslcsvqrvynhtscngtwesdvgnhkftllwteqahvtvialnsi 720
 QY 721 GASVANENLTFSPMKSVMNVQSLASVPLNSSCVIWSMISPDIKMYIIEKMLNED 780
 Db 721 gasvanenlftspmksvmlvqslasvplnsscvyswllspdyklymylekmlned 780
 QY 781 GEIKMLRISSSVKRYIHDHFPIEKYQESLYPIFMEGVKPKIINSFQDDIEKHQSDA 840
 Db 781 getkwlriesssvkryihdhfpielkyqfelypifmegvqkplinsftqddiekhsda 840
 QY 841 GLTVIYVPIIISSTILGLTLLISHORMKLFWEDVNPKNCSWAGLNPK 891

Db 841 glyvivpvlisslllgclllshqrmkklfwevdpnpkncswagqlntrkx 891

RESULT 9

AAW34499 standard: protein; 970 AA.

AAW34499;

18-MAR-1998 (first entry)

Obesity receptor C protein.

Obesity receptor; human; OB receptor; OB receptor/OB protein complex; high blood lipid level; obesity; diabetes; high cholesterol level; weight loss; therapy; weight maintenance.

Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 959

FT /label= unknown

FT /note= "encoded by stop codon"

PN MO9725424-A1.

PD 17-JUL-1997.

PF 02-JAN-1997; 97MO-US00128.

PR 31-DEC-1996; 96US-0774414.

PR 04-JAN-1996; 96US-0582825.

PA (AMGE-) AMGEN INC.

PI Chang M, Fletcher FA, Welcher AA;

DR WPI: 1997-384981/35.

DR N-PSDB: AAT98530.

PT Obesity protein receptor(s) and related DNA - used to treat weight disorders, e.g. obesity, diabetes and high cholesterol or blood lipid levels

PS Claim 2; Page 72; 151pp: English.

CC This sequence represents the obesity (OB) receptor C protein. This sequence has one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The CC proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.

XX Sequence 970 AA;

SQ

Query Match 76.5%; Score 891; DB 18; Length 970;

Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;

Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHMEFYVTAFLSYPIPMRFKLSGMPNPNSTYDFLLPAGLSKRTSNS 60

DB 1 micokfcvllhmeffyvtatfnlsyptipwrfklscompnstygyfllpagskrtns 60

QY 61 NGHETFAVPEKNSGTHPSNLSKTTFHCCFNSQDRNCSLCAADNEGKTFVSTVNSLVP 120

DB 61 nghetfavpeknsgthpsnlskttfhccfnsqdrnscslcadnegktfvstvnslvf 120

QY 121 OODDAMWNTOCMLKGDCLKFICVVESELFKNLPFNPNYKXHLVYBEVLEDSLVYOKKS 180

DB 121 qoddamwniocmlkgdclkficyveselfknlpfnpnnykxhllvybevedslvpqkgs 180

QY 181 FQMVHNCNSVHECCCECLVVPPTAKLNDTLMLCKITSGGVIFCPSLMSQPINNAKPDPP 240

DB 181 fgmvhncnsvehceccelvvpptaklndtlmlckitsggvifcpslmsvqpinmvxpdp 240

QY 241 LGHMEITDDGNLKTSNMSPLVPPFLOQYVKSNSSTVINEAOKIVATSLVDSIIP 300

DB 241 lghmeitddgnlktsnmsplvpfploqyvknsstlvineadkivatstllvdsiip 300

QY 301 GSSYEVOVGRKRDGPGISMDSTPVPFTOVIVYPPKILTEVGSNSVFHCILYKRENI 360

DB 301 gssyevovgkrldgpgismdstpvftovivypkillevgnsvfhcilkykreni 360

QY 361 VPSKETVMMNTAEKITPOSQYDVSDVSKVTFENLNTERPKRFTYDAVYCCNEHECH 420

DB 361 vpsketvmmntaekitposqydvdsdvskvtfenlnetkpkrftydavyccnehech 420

QY 421 RYAEIVIVDININISCEPTGTYLTKMCRNSTSTIOSLASTGLRHRSLVCSODIPSIH 480

DB 421 ryaeivivdininiscptgtyltkmcrnststioslastglrhrslvcsodipsih 480

QY 481 PISEPKDCYLQSDGFYECIFOPIFLLSGYTMIRINHSLSLSPPTCVLPDSVVRP 540

DB 481 pisepkdcylqsdgfyecifopifllsgytmirinhslslspptcvlpdsvvvrp 540

QY 541 SSYKAEITINIGLKITSMKEPVPENNLOPQIRYGSKEVOKKKEVYDANKSKSYLV 600

DB 541 ssykaeitiniglkitsmekvpennlopqirysgskvokkkyevydanksksvlyv 600

QY 601 POLCAVAYAOVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGEPFRILINGDMRKEKNV 660

DB 601 pdlcavayavrickrldglgywsnmsnpaytvmdikvpmrgepfrilngdmrkknv 660

QY 661 TLIMKPLMKNDLSQYQRYVINHTSCNGTSEEDVGNHTKFTFLMEQATVTLAINSI 720

DB 661 tlimkplmkndlsqyqryvinhtscngtseedvgnhthkftflmeqatvtlainsi 720

QY 721 GASVANFNLTFSWPMGKVINIVOSLSAYPLNNSCVIYSLISPEQVYLMFTIEMKLNED 780

DB 721 gasvanfnltfswpmgkvinivoslasyplnnsccviyslispesdylmfylewknled 780

QY 781 GEIKMELRISSSVKYYIHHFPIEKYOFSLVPIFMEGAKPPIINSFODOTIEKHQSDA 840

DB 781 geikmelri:sssvkyyihhfpiekoyfslvpiifmegakppiiinsfodotiekhsda 840

QY 841 GLXVIVPVLISSSIIILGTLTLLISHORMKKLFMEDVDPNPKNSAOCGLNFOK 891

DB 841 glyvivpvlisslllgclllshqrmkklfwevdpnpkncswagqlntrkx 891

RESULT 10

AAW34497 standard: protein; 972 AA.

AAW34497;

18-MAR-1998 (first entry)

Obesity receptor A protein.

Obesity receptor; human; OB receptor; OB receptor/OB protein complex; high blood lipid level; obesity; diabetes; high cholesterol level; weight loss; therapy; weight maintenance.

Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 897

FT /label= unknown

FT /note= "encoded by stop codon"

FT /label= unknown

FT /note= "encoded by stop codon"

Query Match	76.5%	Score 891	DB 18	Length 972
Best Local Similarity	100.0%	Pred. NO. 0		
Matches	891	Conservative	0	Mismatches
			0	Indels
			0	Gaps
			0	
QY	1	MICQKFCVLLHMEIYVITAFNLSTPTPMKFKSCMPNPSTYDFLLPAGLSKNTSNS	60	
Db	1	micqkfcvllhweilvltatnlsypltpwrfkiscmpnstydfllpayskntsns	60	
QY	61	NGHETAVEPKFNSSGSTRFNSMLSKTTFHCCFSESDRNCSLCADNIEGTFVSTNSLIV	120	
Db	61	nghetaveprkfnsqgtfnsskttfncfcfsqgdrcmslcaadiegkttfstynsliv	120	
QY	121	QQIDANNMIQCVLKGDLKFLTCYVESLPRKNLFRNRYKRVHLLYDLPEVLEDSPLVPQKOS	180	
Db	121	qqidanwniicwklgdxllficyveslfknlfrorykvhlllylpevleedsplypqkgs	180	
QY	181	FQWVHNCNSVNECCGCLVVPAPAKINDPLMLCKITTSGGVIFQSPFLMSVQPIINWKPDP	240	
Db	181	fqwvhncnsvneccclvvpplakindellmciklitsgvlifqspflmsvqpinmwkppdp	240	
QY	241	LGLHMEITDDGNLKIWSSPPLVPRPDLQYKVSNSNSTTVIREAKIYSATSILVDSILP	300	
Db	241	lgllhmetddgnlkiwsppplvpfpjlyqvykysnssttvireaklvsatsilvdsilp	300	

OY	301	GSSEYVQVRGRRLDQPGTMSWMSNPRTFTODVYIFEPFKILTSVGSWVSFHCITYKKEKNT	360
Db	301	gsseyvqvrgrkrlldqpgtmsdwsnpvrlftdvlyifpkkiltsvgsivsfncllykkeknl	360
OY	361	VPSKEITVMMNLAEIKIPSOQDVSDHKSKEYFNELNETKPRGKFTYDAYCCNEHCCH	420
Db	361	vpskeiivmmnlakeikipsqdvvsdshvskvtfnnelnetkprkftlydayccnehech	420
OY	421	RYAEIYVIDVNVINISCTEDGYLTAKTGRWSTSTQSLAESTLQLRHYRSSLYCSDIPSIH	480
Db	421	ryaeilyvidvnlinscetedgyltkmtcrwststqslaestlclryhrsslycsdipsh	480
OY	481	PISSEPKOCYLOSDFEETIRPPIFLLSGYTMWITINISLCSLSOSPICVLPDSVVRPLRP	540
Db	481	pisepkdcylqsdfeyecifiprllfllsgytmwiriinislsyldseprlcvpipdsvvkrplp	540
OY	541	SSVKAEITINIGLTKISERKEVPFENNLOFOIRYGLSGREKQWMMYEVYDAKSKSYLPIV	600
Db	541	ssvkaeitiniglltkisewkvpfennlqfiryglsgkevqkmyevydaaksyslpv	600
OY	601	PDLCAVYAVOYRCRRLDGLGYSWMSNMPAYTVVNDIKVPMKRGEPWRIINGDTMKREKNV	660
Db	601	pdlcavyavgyrcrkrlldglyswmsnmpaytvyvndikvpmrgpewrilingdtmkkeknv	660
OY	661	TLLMKPLMKNSLCSQVRYYVNHNTSCNGTMSDEVGNHTFTPLTNEQATTVYVLAINSI	720
Db	661	tllmpkmlkndslcsvqryvnhntscngtmsdevgnhtkftlvtqeatvtyvlainsl	720
OY	721	GASVANFNLTFSPMSKKNIVQSLASAYPLNSSCYIVSMILSPSDYKLMYFIEMKNLNEED	780
Db	721	gasvanfnltsfmskknivqslasayplnsscivysmilspsdyklmyfiemknlneed	780
OY	781	GEIKWLRISSSVKKYYIHDHFIPLEKYQFSLYPIFMGVGKPKIYNSEFTODDIEKHQSDA	840
Db	781	geikwlri:sssvkyyihdhfiplekylqfslypifmegvgkpkilnsftgddiekhsda	840
OY	841	GLYIVYPIIISSTILLGTLILSHOBRKKLFMEVYPRPKKCSNAQCINPOK	891
Db	841	glyivypvli:sssilllgtililshqmkliwedvprpkncswaqnintqk	891
RESULT 11			
ID	AAW34498	standard; protein: 999 AA.	
XX	AAW34498;		
XX	18-MAR-1998 (first entry)		
XX	Obesity receptor B protein.		
XX	Obesity receptor: human; OB receptor; OB receptor/OB protein complex;		
KW	high blood lipid level; obesity; diabetes; high cholesterol level;		
KW	weight loss; therapy; weight maintenance.		
XX	Homo sapiens.		
OS			
XX	Key	Location/Qualifiers	
XX	Misc-difference	905	
FT		/label= unknown	
FT		/note= "encoded by stop codon"	
FT		933	
FT		/label= unknown	
FT		/note= "encoded by stop codon"	
FT		971	
FT		/label= unknown	
FT		/note= "encoded by stop codon"	
FT		988	
FT		/label= unknown	
FT		/note= "encoded by stop codon"	
XX			
XX	W09725424-A1.		

PD 17-JUL-1997.
 XX 02-JAN-1997; 97WO-US00128.
 XX 31-DEC-1996; 96US-0774414.
 PR 04-JAN-1996; 96US-0582825.
 XX (AMGE-) AMGEN INC.
 PA Chang M, Fletcher FA, Welcher AA;
 PI MPI: 1997-384981/35.
 DR N-PSDB: AAT98529.
 XX Obesity protein receptor(s) and related DNA - used to treat weight
 PT disorders, e.g. obesity, diabetes and high cholesterol or blood
 PR lipid levels
 XX Claim 2; Page 68; 151pp; English.
 PS This sequence represents the obesity (OB) receptor B protein. This
 CC sequence has one or more of the biological properties of naturally
 CC occurring OB receptor protein. The OB receptor proteins and OB
 CC receptor/OB protein complexes are used for the treatment of obesity,
 CC diabetes, high blood lipid levels and high cholesterol levels. The
 CC proteins may also be used to treat an individual for weight loss or
 CC weight maintenance required for purely cosmetic purposes.
 XX Sequence 999 AA;
 SQ
 Query Match 76.5%; Score 891; DB 18; Length 999;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCGRCFCVLLHMEPTVYTAFLNLSPTIPMRKSLSCMPNSTYDVFLLPACLSKRTS 60
 DB 1 mctgfcvllhmetvltalnlsytlpwrkrlscmpnstydyfllpagskrtsns 60
 QY 61 NCHYEFAVEPKENSSGTHPSNLSTTFHCCPSRSEDNRNCSLCADNTEGKTFVSNLVF 120
 DB 61 nghyefavepkenssgthpsnlssttfhccpsrseodnrncslcadnategkpfvsnlvf 120
 QY 121 QOIDANMNITCKLKGDKLFCYVESLEFKNLFRNRYKVLHLYLPEVLEDSPLVPQKGS 180
 DB 121 qoidanmnitcklkgdklfcyveslefnlfrnrykvhllylpevledsplvpqkgs 180
 QY 181 FQMVHNCNSVHECECTIYVPTAKINDTLMLKITSGSVIRQSPLMSVOPINMVRPDP 240
 DB 181 fqmvhncnsvhecectiyvptakindtlmlckltsqsvirfqsplmsvqplnmvrpdp 240
 QY 241 LGLHMEITDDGNLKITSMSSPLVPFPLOQYKVSSENSTVIREADKIVATSLVDSIIP 300
 DB 241 lglhmeitddgnlkitssmssplvpfploqykvysenstvirleadivatslvsdiip 300
 QY 301 GSSYEYQVNGKRLDGPFGISDMSTPRVFTTODYIFPPKILTSVGSNVSPHCITYKKNKI 360
 DB 301 gssyeqvngkrlldgpfgisdmstprvfttodyifppkiltsvgsnvspfcitykknki 360
 QY 361 VPSKEIVWMNNIAEKIPQSOYDVSVHSAKVPFNNLEKRPGRKFPYDVAVCCNEHCCH 420
 DB 361 vpskeivwmnniaekipqsoydvsvhsakvpfnnlekrpgrkfpdydvavccnehcch 420
 QY 421 RYAEVLVIDVNNISCEITGYLTKMTCRMSTSTIOSLAESTLQLRHRSILVCSDFPSIH 480
 DB 421 ryaelvidvnnisceitgyltkmtcrmtstioslaestlqlrhrsilvcsdfpsih 480
 QY 481 PISEPKDCLQSDGRFECIFQPIFLISGTYTMMIRINHSLSGSDSPRTCVLPDSVAPLPP 540
 DB 481 pisepkdclqsdgrfecifqpiflisgtytmmirinhslsgsdsprtcylvpsvaplpp 540
 QY 541 SSVKAEITINIGLKITSMKPPVPENNLOFOIRYGLSGKEVQMKMEVYDAKSKVSLPV 600
 DB 541 ssvkaeitiniglkitsmkppvpennlofoirylsgkevqmkmevydakskvslpv 600

DB 541 ssvkaeitiniglkitsmkppvpennlofoirylsgkevqmkmevydakskvslpv 600
 QY 601 PDLCAVYAVQVRCRLDGLGYSNMSNPAYTVVMDIKYPMRGPETFWRIINGDTMKKENV 660
 DB 601 pdlcavayavqvrclldglgywsnmsnpaytvvmdikypmrgetfwrilingdtmkkenv 660
 QY 661 TLKKPFLKNDLSQVQKRVINHHSTSCNGTWSEYDGNHTKFFFLTEQAHYTVLAISI 720
 DB 661 tlkwpflkndlsqvgryvinhhtscngtwsevdygnhtkffflteqahvtvlainsi 720
 QY 721 GASVANFNLFSPMSKVIVIOSLSAYPLNNSCVIVSWLSPEDKLMWFIEEMNLND 780
 DB 721 gasvanfnlfsmpskviviolsayplnnsccvsvswlspdyklnmfiwemnlnd 780
 QY 781 GRIKMLRISSSVKRYIHDHFIPIEKYOPSLPPIRMEVGRPKIINSFTODDIENHQSDA 840
 DB 781 grlkwlrissvkkyyihdhfipiekyslplirmegvgrpklnstfgddilekhqda 840
 QY 841 GLIYIVPVITSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQCLNFQK 891
 DB 841 gliyivpvitssillgltllishqrmklfmedvnpknscswaqclnfqk 891

RESULT 12

AAW34502 standard; protein; 839 AA.
 AAW34502;
 18-MAR-1998 (first entry)
 Obesity receptor protein.
 Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
 high blood lipid level; obesity; diabetes; high cholesterol level;
 weight loss; therapy; weight maintenance.
 Homo sapiens.
 WO9725424-A1.
 17-JUL-1997.
 02-JAN-1997; 97WO-US00128.
 31-DEC-1996; 96US-0774414.
 04-JAN-1996; 96US-0582825.
 (AMGE-) AMGEN INC.
 Chang M, Fletcher FA, Welcher AA;
 MPI: 1997-384981/35.
 N-PSDB: AAT98532.
 Obesity protein receptor(s) and related DNA - used to treat weight
 disorders, e.g. obesity, diabetes and high cholesterol or blood
 lipid levels
 Disclosure: Page 82; 151pp; English.
 This sequence represents the obesity (OB) receptor protein. This
 sequence was used to identify the variants shown in AAW34497-W34501. The
 variants have one or more of the biological properties of naturally
 occurring OB receptor protein. The OB receptor proteins and OB
 receptor/OB protein complexes are used for the treatment of obesity,
 diabetes, high blood lipid levels and high cholesterol levels. The
 proteins may also be used to treat an individual for weight loss or
 weight maintenance required for purely cosmetic purposes.
 Sequence 839 AA;

Query Match 72.0%; Score 839; DB 18; Length 839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIOCKFCVLLHMEFIVTAENLSPITPMPFKLSQMPNRYDYLLPAGLSKNSNS 60
 DB 1 mlcgcfcvllhmfivtaenlspitpmpfklsqmpnrydyllpagslksnns 60
 QY 61 NGHYETAVEERKFNSSGTHFSNLSKTFPHCFRSEDORNCSCADNIEGKTFVSNLSVF 120
 DB 61 nghyetaveepkfnsgthfnlskthcfreseqdrncslcadniegkftvsnlsvf 120
 QY 121 QOIDANNIQCWLKGDKLTICYESLFRKULFRYNTKVVHLLYLPVLEDSPLVPQKGS 180
 DB 121 qoidanniqcwlkgdlticyeslfrkulfryntkvvhllylvleedsplvpqkgs 180
 QY 181 FQWVHCNCSYHECCELVPPPTAKLNDTLMLCKITSGVIFQSPILMSVOPINNVKRDPP 240
 DB 181 fgmwhcnscsyheccelvpptaklndtlmlckitsgvifqspilmsvopinmvkrdpp 240
 QY 241 LGLHMEITDDGNLKISWSSPPLVPEPLQOVKYSNSTVIYREADKIVSATSLVDSILP 300
 DB 241 lglhmeitddgnlkiwsspplvpeplqovkysnstviyreadkivsatsllvdsilp 300
 QY 301 GSSYEVQVRKRLDGPCHSDMSPRYFTTQDYIYFPFKILTSVGSNVSFHCITKKKNKI 360
 DB 301 gssyevqvrkrlidgpchsdmstpryfttqdyiyfppkiltsgvsnvsfhcikykenki 360
 QY 361 VPSKEIYVMMNLAEKIPQSOYDVVDVSHVSKYTFEFLNETPRGKFTDAYVCCHEHCH 420
 DB 361 vpskeiyvmmnlakeipqsoydvvdvshvskytfefflnetprgkftdayvccnehech 420
 QY 421 RYAEIYIVDYNINISCTFDGYLTNMCWSTSTIQSLAESTLQURHSSLYCSDIPSIH 480
 DB 421 ryaeiyidvyniniscetfdgyltmcwststiqslaestlqurhsslycsdipsih 480
 QY 481 PISEPKCYLOSDFEYICFOPIFLISGYMMIRINHSISLSDSPRCVLPDSVYKRLPP 540
 DB 481 pisepkcylosdfeyicfopiflisygmwirinhsislsdsprcvlpdsvykrldpp 540
 QY 541 SSVKAEITINIGLTKISWEPVPEPNNLOFOIRGLSGKFEVQWKNVEVYAKSKSVSLPV 600
 DB 541 ssvkaeitinigltkiswepvpepnnlofoirglsgkfevqwnvevyaksksvslpv 600
 QY 601 PDLCAYAVOVRCKRLDGLCYWSNMSNPATVVDIKVPRGPEFWRIINGDPMKKEKNV 660
 DB 601 pdlcayavovrckrlidglcywsnmsnpatvvdikvprgpefwriingdpmkkeknv 660
 QY 661 TLTKMPLMKNDSCSVORVYINHTSCNGTWSEDVGNHTFTPLMTEQATTVYLAINSI 720
 DB 661 tlltkmplmkndslcsvoryinhtscngtwsedvgnhtftplmteqatvtylainsi 720
 QY 721 GASVANENLTFSPMKSQVNIQVSLAAYPLNNSCVIWSLSPSDYKLMYRIIEKKNLND 780
 DB 721 gaavanenlftspmksvniqvslayayplnnsccvswslspdyklmryiiekknlned 780
 QY 781 GEIKWLRISSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSD 839
 DB 781 geikwlriissvkkyyihdhfipiekqfslypifmegvgkpkiiinsftddiekhgsd 839

RESULT 13
 AA05701
 ID AA05701 standard; Protein: 815 AA.
 XX
 AC AA05701;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE Human OB receptor extracellular domain.
 XX
 KW TRU; TNF receptor-like; tumour necrosis factor receptor; human;
 signal transduction; cell differentiation; prostate cancer;

KW Inflammation; arthritis; diabetes; insulin resistance; diagnosis;
 KW therapy; OB receptor; leptin receptor.
 XX
 OS Homo sapiens.
 PN W09915663-A1.
 XX
 PD 01-APR-1999.
 XX
 PF 25-SEP-1998; 98WO-US20219.
 XX
 PR 17-MAR-1998; 98US-0042785.
 PR 26-SEP-1997; 97US-0938996.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 PI Busfield SJ.
 XX
 DR WPI; 1999-254712/21.
 XX
 PS Nucleic acid encoding tumor necrosis factor receptor-like protein
 Example 8; Page 82-83; 170pp; English.

CC The present sequence represents the extracellular domain of the
 CC human OB receptor (leptin receptor). A fusion protein comprising
 CC the mouse OB receptor signal sequence, the human OB receptor
 CC extracellular domain and the human IgG Fc domain has been
 CC constructed. The ability of the OB receptor signal peptide to
 CC direct secretion of the fusion protein in transfected HEK 293 cells
 CC was compared to the ability of the human TRL signal peptide (see
 CC AA05696) to direct secretion of a similar construct. The results
 CC showed that the heterologous TRL signal elevated the amount of
 CC secreted human OB receptor protein in the supernatants of
 CC transfected cells approximately 10-fold. TRL is a novel member of
 CC the tumour necrosis factor receptor superfamily. The invention
 CC provides full-length human and murine TRL proteins (see AA05695-97),
 CC TRL fusion proteins, antigenic peptides and anti-TRL antibodies, as
 CC well as TRL nucleic acids (see AA05320-22), recombinant expression
 CC vectors, host cells and non-human transgenic animals. TRLs are
 CC regulators or modulators of cellular signal transduction, cellular
 CC proliferation or differentiation, cell survival and apoptosis,
 CC immune system cells, and cells involved in insulin resistance or
 CC the diabetic response.

XX
 SQ Sequence 815 AA;

Query Match 70.0%; Score 815; DB 20; Length 815;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 815; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 NLSEYPTPWFKLSQMPNRYDYLLPAGLSKNSNSNGHYETAVEERKFNSSGTHFSNLS 82
 DB 1 nlseypptwfklsqmpnrydyllpagslksnnsnghyetaveepkfnsgthfnsl 82
 QY 83 SKTTFHCFRSEDORNCSCADNIEGKTFVSTVNSLVFOQIDANNIQCWLKGDKLTIC 142
 DB 61 sktthcfreseqdrncslcadniegkftvstvnslvfqoidanniqcwlkgdlticy 120
 QY 143 YVESLFRNRYKVVHLLYLPVLEDSPLVPQKGSFQWVHCNCSYHECCCLVPPPT 202
 DB 121 yveslfrnrykvvhllylvleedsplvpqkgsfgmwhcnscsyheccclvpppt 180
 QY 203 AKLNDTLMLCKITSGVIFQSPILMSVOPINNVKRDPPGLHMEITDDGNLKISWSSPPL 262
 DB 181 akldntlmlckitsgvifqspilmsvopinmvkrdppglhmeitddgnlkiwssppl 240
 QY 263 VPEPLQOVKYSNSTVIYREADKIVSATSLVDSILPSSSYEVQVRKRLDGPCHSDM 322
 DB 241 vpeplqovkysnstviyreadkivsatsllvdsilpsssyevqvrkrlidgpchsdw 300
 QY 323 STPRRYFTTQDYIYFPFKILTSVGSNVSFHCITKKENKIYPSKEIYVMMNLAEKIPQSOYD 382

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|||||
Db 301 scprftctqdvlyfppkllitsvsnvsfnclykknklypskelywmmllaeklpqsgxd 360
OY 383 VYSDVSKVTFENLNETPRGKFTYDAVYCCNEHECHHRAALYIDVYININISCEPDGL 442
Db 361 vvsdvskvtfnnlneetprgkftcydaayccnehehmyaellyidvynlscsedgyl 420
OY 443 TMTCRWSTSTIOSLAESTLQLRYHRSLSYCSIDPSIHPISEPKDCYLOSDFEYCFOP 502
Db 421 tkmtcrwststioslaestlqlryhrrsslycsidpsihpisepkdcylosdfeycfop 480
OY 503 IFLLSGYTMKTRININISLSDSPPTCVLPDSVYKPLPSPSVKAEITINIGLKISMEKV 562
Db 481 ILLISGYTMWIRINISLSDSPPTCVLPDSVYKPLPSPSVKAEITINIGLKISMEKV 540
OY 563 FPENNIOFOIRYGLSGKEVQVMKMEYDYDAKSKSVSLPVPDLCAVAVOYCRKLDGLGYW 622
Db 541 fpenliqqlirylrglsqkeqvmkmeveydaksksvslpvpdlcaavayqrcrldglgyw 600
OY 623 SWSNPATYVVDIVPMRGPEFWRINIGDYNKKKEKNVTLLKPLMKNDSLCSVQRYVIN 682
Db 601 swnsnpaylvvndikvpmrgpefwrilngdtkmkekknvllkplmkndsicsvqryvin 660
OY 683 HHTSCNGTSEVYGNHTRKFTFLMTROAHVTVYLAINSIGASVANFNLTFSSMKSXVNIQ 742
Db 661 hntscngtsevdvgnhtrkftflwteqahlvlylaolsigasyanfnlftswpmkskxnlvq 720
OY 743 SLASAPLNSCVIVSNILSPSDYKILMYFIEMKNINENDEIKWLRISSSVKYYIHDHFI 802
Db 721 slsapylnsscylvswlpspdykilmfyilewknlnedekilwlriasssvkyyihdhti 780
OY 803 PIEKYOFSLYPIFMGCVGKPKIINSEFTQDDIEKHQ 837
Db 781 piekyqfslpylfimegvskpkiinsftqddiekhq 815

RESULT 14
AAW34501
AAW34501 standard; protein: 804 AA.
XX
AC AAW34501;
XX
DT 18-MAR-1998 (first entry)
XX
DE Obesity receptor protein splice variant.
XX
KM Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KM high blood lipid level; obesity; diabetes; high cholesterol level;
KM weight loss; therapy; weight maintenance; splice variant.
XX
OS Homo sapiens.
XX
PN WO9725424-A1.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US00128.
XX
PR 31-DEC-1996; 96US-0774414.
PR 04-JAN-1996; 96US-0582825.
XX
PA (AMGE-) AMGEN INC.
XX
PI Chang M, Fletcher PA, Welcher AA;
XX
DR WPI; 1997-384981/35.
DR N-PSDB; AAT98534.
XX
PT Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol of blood
XX lipid levels
XX
PS Claim 4; Page 89; 151pp; English.

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XX This sequence represents a natural splice variant of the obesity (OB)
CC receptor protein. This sequence has one or more of the biological
CC properties of naturally occurring OB receptor protein. The OB receptor
CC proteins and OB receptor/OB protein complexes are used for the treatment
CC of obesity, diabetes, high blood lipid levels and high cholesterol
CC levels. The proteins may also be used to treat an individual for weight
CC loss or weight maintenance required for purely cosmetic purposes.
SQ Sequence 804 AA:

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Query Match 68.5%; Score 798; DB 18; Length 804:
Best Local Similarity 100.0%; Pred. No. 0:
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

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OY 1 MTCOKFCVLLHMEFYVTAANLSPYTPMFFKSLCMPNSTYDFLLPAGLSKNTNS 60
Db 1 mtcqkfcvvllhmfelyvtainlspylpwrkflscmpnstydfllpagskntns 60
OY 61 NGHYETAVEPKENSSGTHRSNLKTTFHCCFRSEODRNCSLCADNTECKTFVYVNSLVE 120
Db 61 nghyetavepkfnsqthrsnlstfhhccfrseqdnrcslcadnlegkftvsvnslyf 120
OY 121 QOIDANMNIQCMKGDPLKFCYVESLEFKNFRNRYKXHLVLPVLEDESPLPQKS 180
Db 121 qqidamniqcmkldplkfcyveslfnlnrynykxhlylvpeledesplvpqks 180
OY 181 FQMVHNCNSVHSCCECLVVPPTAKLNDTLMLCKTSGVIFCSPLMSQPINMVPDP 240
Db 181 fqmvhncnsvhscceclvvpptaklndtlmlckltsqgvifcsplmsqpinmkvpdp 240
OY 241 LGUHMETDGNMLKISWSSPPLVPEPLQOYVYKSENSITVIREADKIVATSLSLVDSTLP 300
Db 241 lghmetdgnmlkisswsspplvpeplqoyvyksensitvireadkivatslsldstlp 300
OY 301 GSSYEYQVGRKLDGPGTSDMSSTPRVFTTOVYIYPRKILNSVGNVSFHCILYKKNKI 360
Db 301 gssyeyqvgrkldpgtisdmsstprvfttdvlyfprkllcvsygnvsfhclykkkenki 360
OY 361 VPSKEIYVMMNMLAEKIPQSOYDVVSDHVSQVTFENLNETPRGKFTYDAVYCCNEHECHH 420
Db 361 vpskeivwmmnmlaekipqsgdydvshvskvtfennlneetprgkftcydaayccnehech 420
OY 421 RYAEIYVIDVINISCEPDGYLTMTKTCRWSSTIOSLAESTLQLRYHRSLSYCSIDPSIH 480
Db 421 ryaelyvldvnniscedgyltmtcrwststioslaestlqlryhrrsslycsidpsih 480
OY 481 PISEPKDCYLOSDFEYCFIOPFIILSGYTMWIRINISLSDSPPTCVLPDSVYKPLP 540
Db 481 pisepkdcylosdfeycfiopfllsgytmwlrlnhslycsidpslpsdvkplp 540
OY 541 SSYKAEITINIGLKISMEKPVPENNILOFOIRYGLSGKEVQVMKMEYDYDAKSKSVSLPV 600
Db 541 ssykaeitnigllkismekpvpeennlfooiryglsgkevqvmkmeveydaksksvslpv 600
OY 601 PDLCAVAVOYCRKLDGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRINIGDYNKKKEKNV 660
Db 601 pdlcaavayqrcrldglgywsnmsnpaytvvmdikvpmrgpefwrilngdtkmkekknv 660
OY 661 TILMKPLMKNDSLCSVQRYVINHHTSCNGTSEVDVGNHTRKFTFLTEQAHVTVYLAINSI 720
Db 661 tilmkplmkndslcsvqryvinhhtscngtsevdvgnhtrkftflteqahlvtylainsi 720
OY 721 GASVANFNLTFSMPMSKVNIQSLASYPANSSCVIYVSNILSPSDYKILMYFIEMKNLNED 780
Db 721 gasvanfnlftswpmkskvniqslasypansscvlyvsnilspdykilmfyilewknlned 780
OY 781 GEIKWLRISSSVKYYIYH 798
Db 781 geikwlriasssvkyyih 798

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RESULT 15
ID AAM62543 standard; protein; 883 AA.
XX
AC AAM62543;
XX
DT 12-OCT-1998 (first entry).
XX
DE Human ob-receptor deletion mutant D(41-322).
XX
KM ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;
XX anorexia; cachexia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Msc-difference 41..42
FT /note="Deletion of 281 amino acids"
XX
PN WO9824881-A1.
XX
PD 11-JUN-1998.
XX
PF 26-NOV-1997; 97WO-US22165.
XX
PR 02-DEC-1996; 96US-0032367.
XX
PA (MER1) MERCK & CO INC.
XX
PI Fong TM, Huang RC, Van Der Ploeg L;
XX
DR MPI; 1998-33304/29.
XX
XX
XX New mutant ob receptor(s) - used to develop products for drug
XX screening and for gene therapy for weight control, e.g. obesity or
XX anorexia
XX
XX Claim 4; Fig 1; 27pp; English.
XX
XX The ob-receptor (OB-R), a member of the cytokine receptor family is
XX transcribed in the hypothalamus and is involved in obesity. The
XX deletion mutant D(41-322) has had the first CK-P3 module; present
XX in the OB-R, removed. The D(41-322) mutant together with mutants lacking
XX a functional second CK-P3 module or a functional intracellular domain can
XX be used in assays for the detection of ligands, agonists, antagonists and
XX ligand mimetics. The leptin agonists identified can be used in
XX situations where leptin insufficiency causes obesity, diabetes or
XX infertility. The leptin antagonists identified can be used in the
XX treatment of anorexia and cachexia. The mutant receptor nucleic acids
XX can also be used in gene therapy for weight control, e.g. for treating
XX obesity or anorexia.
XX
SQ Sequence 883 AA:

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Query Match 63.7%; Score 742; DB 19; Length 883;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 842; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 221 tflisgytmirlnhsldspptcylpdsvvkplppssvkaejlinlglklswekpv 280
OY 563 FPENNLQFQIRYGLSGKEVOMKMYEYDAKSKSVSLPVPDLCAVAVOYVCKRLDGLGYW 622
DB 281 fpenmlqfqlryglsgkevwmkyevdaksksvslpvpdlcavavqvcrlldglgyw 340
OY 623 SNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLMKPLKNDSLCSVQRYVIN 662
DB 341 snwnspaytyvmldikvpmrgpewrilingdtmkkekvncllwplmkndslcsvgryvin 400
OY 683 HHTSCNGTSEDEDGNHTRKFFLTBOAHVTVLAINSIGSVANFNLTSPWPMKXNIYQ 742
DB 401 hhtscngtsedevgnhtkffltwceqahvclvalinsigasvanfnltspwpmkxniyq 460
OY 743 SLSAYPLNSSCVIYVSWILSPSDYKLMWFIEWMNLNDEGEIKWLRISSSVKRYIHDFHI 802
DB 461 slsayingnsscvlyswilspdyklymflewmnlndegeklwlrlsssvkryihdfhi 520
OY 803 PIEKYQPSLYPIFMEGVGKPKIINSFTODDIENHSDAGLYVIVYIISSSIIILGLTLLI 862
DB 521 piekyqfslypifmegvgrpklinsftgddlekhgsdaqlyvivylisslilgltlil 580
OY 863 SHORAKKLEWEDVPMKNCMAOGLNPOKRETEHNFIRHTASVTCGPIILPEETSEDI 922
DB 581 shgrmkklwedyvpmkncwagglntqpetehnfikhtasvrcgpiilpeetisedi 640
OY 923 SVDTSMKNKDEMPPTVVSLLSTTDEKGSVCISDQFNSVNFSEAEATVEYTEDESOROP 982
DB 641 svdtswnkndempptlvvsllsttlekgsvcisdqfnsvnfseaeatveyteytedesqrq 760
OY 983 FVKYATLISNSKPSFTEGEOGLINSVYKCFSSKNSPLKDSFNSMWEIQAQFFLLSDQ 1042
DB 701 fvkyaatlinskpsefgeoglinssvykcfssknsplkdsfnsmeleaqaffllsdq 760
OY 1043 HPNIISPHLTFSGDLDELKLEGNFPENNDDKSIYVLTGTSIKKRESGVLLTRDKSRVSG 1102
DB 761 hpnlisphltfsegldellklegnfpennddksiyvltgstikkrresgvlltrdksvsg 820
OY 1103 PFPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFAVYPOFOTCSTOTHKIMENKMD 1162
DB 821 pfpapclftdirvlgdscshfvennlnlgtsskktfasvmpofotcstcthkimenkmd 880
OY 1163 LTV 1165
DB 881 ltv 883

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RESULT 16
ID AAM50003 standard; Protein; 896 AA.
XX
AC AAM50003;
XX
DT 11-JUN-1998 (first entry)
XX
DE Human OB-R variant Form 3.
XX
KM Detection: defective obese protein receptor; defective OB-R; human;
XX defective leptin receptor; variant Form 3; infertility.
XX
OS Homo sapiens.
XX
PN WO9741263-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-US07676.
XX
PR 29-APR-1996; 96US-0640389.
XX
PA (PROG-) PROGENITOR INC.
XX
PI Cioffi J, Shafer AW, Snodgrass RH, Zupancic TJ;

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XX WPI: 1997-549757/50.
DR N-PSDB: AAT95781.
XX
XX Detecting defective obese protein or leptin receptor in reproductive
PT cells - using variant receptor gene specific probes
XX
PS Disclosure: Fig 3; 40pp: English.
XX
XX The present sequence was used in the development of a novel method
CC for detecting a defective obese protein or leptin receptor (OB-R)
CC in cells. Them method comprises contacting RNA extracted from a
CC cell population (preferably an ovary, prostate, testis, sperm, ova,
CC ovarian follicular or blood cell population) with an
CC oligonucleotide derived from a portion of the human OB-R variant
CC Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
CC associated with infertility, as they are unable to correctly
CC transduce signals from leptin binding. The detection method can be
CC used to diagnose infertility, or predisposition to infertility,
CC while treatments that inhibit or down regulate the variants, gene
CC therapy to replace them in homozygotes or direct activation of
CC downstream signal transduction can be used to improve fertility.
CC Also described is the use of labelled DNA probes based on the OB-R
CC sequence to screen for other variants.
XX
XX Sequence 896 AA:
SQ

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Query Match          58.5%; Score 681; DB 18; Length 896;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Db 710 hctvtalainsigavsnfltsmpmskvnivgsisayplnscvlspsdyklny 769
OY 770 FTIEMKLNDEDEIKMLRISSSVKKYIHDHPIPIKYGFSLYPIIMEGKPKIINSPT 829
Db 770 filewknlnedeikwrlissvkkryindhfpilekyqfslpimegykpklnstft 829
OY 830 ODDIEKHQSDAGLYVIVPIIISSTIILGTLISHQRMKRLWEIYPNKNCMAOGLNF 889
Db 830 qddiekhgadaglyvlypvlisslllgtllshqrmkrlfexedvnpknswaglnf 889
OY 890 OK 891
Db 890 qk 891

```

RESULT 17
AAM50002
ID AAM50002 standard; Protein; 904 AA.
XX
XX AAM50002;
AC
XX
XX 11-JUN-1998 (first entry)
DT
XX
XX Human OB-R variant Form 2.
DE
XX
XX Detection; defective obese protein receptor; defective OB-R; human;
KW defective leptin receptor; variant Form 2; infertility.
XX
XX Homo. sapiens.
OS
XX
XX WO9741263-A1.
PN
XX
XX 06-NOV-1997.
PD
XX
XX 28-APR-1997; 97WO-US07676.
PF
XX
XX 29-APR-1996; 96US-0640389.
PR
XX
XX (PROG-) PROGENITOR INC.
PA
XX
XX Cioffi J, Shafer AW, Snodgrass RH, Zupancic JJ;
PI
XX
XX WPI: 1997-549757/50.
DR
XX
XX N-PSDB: AAT95780.
DR
XX
XX Detecting defective obese protein or leptin receptor in reproductive
PT cells - using variant receptor gene specific probes
XX
XX
XX Disclosure: Fig 3; 40pp: English.
PS
XX
XX The present sequence was used in the development of a novel method
CC for detecting a defective obese protein or leptin receptor (OB-R)
CC in cells. Them method comprises contacting RNA extracted from a
CC cell population (preferably an ovary, prostate, testis, sperm, ova,
CC ovarian follicular or blood cell population) with an
CC oligonucleotide derived from a portion of the human OB-R variant
CC Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
CC associated with infertility, as they are unable to correctly
CC transduce signals from leptin binding. The detection method can be
CC used to diagnose infertility, or predisposition to infertility,
CC while treatments that inhibit or down regulate the variants, gene
CC therapy to replace them in homozygotes or direct activation of
CC downstream signal transduction can be used to improve fertility.
CC Also described is the use of labelled DNA probes based on the OB-R
CC sequence to screen for other variants.
XX
XX Sequence 904 AA:
SQ

```

Query Match          58.5%; Score 681; DB 18; Length 904;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 110 TFSVTSNLSVFOQIDANMNITQCMKGDGLFICVESLFRNLFRRNRYKXHLVYVEVL 169
DB 110 TFSVTSNLSVFOQIDANMNITQCMKGDGLFICVESLFRNLFRRNRYKXHLVYVEVL 169
QY 170 EDSPLVPQKSGFQWVNCNCVHECCCECLVVPRAKINDTLMLCKITSGVIFQSPIMSV 229
DB 170 EDSPLVPQKSGFQWVNCNCVHECCCECLVVPRAKINDTLMLCKITSGVIFQSPIMSV 229
QY 230 QPINMVKPDPPLGLHMEITDDGNLKITSSWSPPLVPPLOYOVYSENSTTVIREADKIVS 269
DB 230 QPINMVKPDPPLGLHMEITDDGNLKITSSWSPPLVPPLOYOVYSENSTTVIREADKIVS 269
QY 290 ATSLVDSILPGSSSYEQVGRKLDGPGIWSMDSTPRVFTTODVYFPPKILTSVGSNVS 349
DB 290 ATSLVDSILPGSSSYEQVGRKLDGPGIWSMDSTPRVFTTODVYFPPKILTSVGSNVS 349
QY 350 FHCITKKENKIVPSKEIVMMNLAERIPQSOYOVVSDHVKVFFNLETRKPGKRTYDA 409
DB 350 FHCITKKENKIVPSKEIVMMNLAERIPQSOYOVVSDHVKVFFNLETRKPGKRTYDA 409
QY 410 VYCNEHECHHRYAELVIDVININISCEITDGYLTMTKTCRMSTSTIOSLAESTLQRLYHRS 469
DB 410 VYCNEHECHHRYAELVIDVININISCEITDGYLTMTKTCRMSTSTIOSLAESTLQRLYHRS 469
QY 470 SLVCSDIPISTHPISEPKDCYLOSDGFEYECIFQPIFLLSGTMMIRINHSIGSLDSPPTCV 529
DB 470 SLVCSDIPISTHPISEPKDCYLOSDGFEYECIFQPIFLLSGTMMIRINHSIGSLDSPPTCV 529
QY 530 LPPSVVKEPPESSVKAETITINIGLTKISMEKPYFPENNLOFOIRYGLSGKEVQMKMEYV 589
DB 530 LPPSVVKEPPESSVKAETITINIGLTKISMEKPYFPENNLOFOIRYGLSGKEVQMKMEYV 589
QY 590 DAKSKSVSLPVDLCAYAVQVGRKLDGLGYWSMNSNPATYVMDIKVBRGPPEFWRII 649
DB 590 DAKSKSVSLPVDLCAYAVQVGRKLDGLGYWSMNSNPATYVMDIKVBRGPPEFWRII 649
QY 650 NGDPTMKKEKVVTLTKMKPLMNDSLCSQORVYVNHHTSCNCTWSEDDVGNHRTFPLMEQA 709
DB 650 NGDPTMKKEKVVTLTKMKPLMNDSLCSQORVYVNHHTSCNCTWSEDDVGNHRTFPLMEQA 709
QY 710 HTVTVALINSIGASVANFNLTFSMPMSKVINIYOSLSAVPNSCIVYTWILSPSDYLMY 769
DB 710 HTVTVALINSIGASVANFNLTFSMPMSKVINIYOSLSAVPNSCIVYTWILSPSDYLMY 769
QY 770 FITEKKNLNEDEGELKMLRISSSVKXYIHDFIPIEKYOFSLYPTMEGVGKPKIINSFT 829
DB 770 FITEKKNLNEDEGELKMLRISSSVKXYIHDFIPIEKYOFSLYPTMEGVGKPKIINSFT 829
QY 830 ODDIEKHOSAGLYVIVPVISSIIILGTLISHQRMKLFMEDVDPNPKNCMAGCINR 889
DB 830 ODDIEKHOSAGLYVIVPVISSIIILGTLISHQRMKLFMEDVDPNPKNCMAGCINR 889
QY 890 QK 891
DB 890 QK 891

```

RESULT 18

AAW38214 standard; Protein; 958 AA.

ID AAW38214

AC AAW38214

XX 11-JUN-1998 (first entry)

XX Human OB-R variant Form 1.

XX Detection; defective obese protein receptor; defective OB-R; human;

XX defective leptin receptor; variant Form 1; infertility.

XX Homo sapiens.

```

PN MO9741263-A1.
XX 06-NOV-1997.
PD 28-APR-1997; 97MO-US07676.
XX 29-APR-1996; 96US-0640389.
XX (PROG-) PROGENITOR INC.
PA Cioffi J, Shafer AM, Snodgrass RH, Zupancic TJ;
PI WPI; 1997-549757/50.
XX N-PSDB; AAT95779.
PT Detecting defective obese protein or leptin receptor in reproductive
DB cells - using variant receptor gene specific probes
XX disclosure; Fig 3; 40pp; English.
PS The present sequence was used in the development of a novel method
XX for detecting a defective obese protein or leptin receptor (OB-R)
CC in cells. Them method comprises contacting RNA extracted from a
CC cell population (preferably an ovary, prostate, testis, sperm, ova,
CC ovarian follicular or blood cell population) with an
CC oligonucleotide derived from a portion of the human OB-R variant
CC Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
CC associated with infertility, as they are unable to correctly
CC transduce signals from leptin binding. The detection method can be
CC used to diagnose infertility, or predisposition to infertility,
CC while treatments that inhibit or down regulate the variants, gene
CC therapy to replace them in homozygotes or direct activation of
CC downstream signal transduction can be used to improve fertility.
CC Also described is the use of labelled DNA probes based on the OB-R
CC sequence to screen for other variants.
XX SO Sequence 958 AA:

```

Query Match 58.5%; Score 681; DB 18; Length 958;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 110 TFSVTSNLSVFOQIDANMNITQCMKGDGLFICVESLFRNLFRRNRYKXHLVYVEVL 169
DB 110 TFSVTSNLSVFOQIDANMNITQCMKGDGLFICVESLFRNLFRRNRYKXHLVYVEVL 169
QY 170 EDSPLVPQKSGFQWVNCNCVHECCCECLVVPRAKINDTLMLCKITSGVIFQSPIMSV 229
DB 170 EDSPLVPQKSGFQWVNCNCVHECCCECLVVPRAKINDTLMLCKITSGVIFQSPIMSV 229
QY 230 QPINMVKPDPPLGLHMEITDDGNLKITSSWSPPLVPPLOYOVYSENSTTVIREADKIVS 269
DB 230 QPINMVKPDPPLGLHMEITDDGNLKITSSWSPPLVPPLOYOVYSENSTTVIREADKIVS 269
QY 290 ATSLVDSILPGSSSYEQVGRKLDGPGIWSMDSTPRVFTTODVYFPPKILTSVGSNVS 349
DB 290 ATSLVDSILPGSSSYEQVGRKLDGPGIWSMDSTPRVFTTODVYFPPKILTSVGSNVS 349
QY 350 FHCITKKENKIVPSKEIVMMNLAERIPQSOYOVVSDHVKVFFNLETRKPGKRTYDA 409
DB 350 FHCITKKENKIVPSKEIVMMNLAERIPQSOYOVVSDHVKVFFNLETRKPGKRTYDA 409
QY 410 VYCNEHECHHRYAELVIDVININISCEITDGYLTMTKTCRMSTSTIOSLAESTLQRLYHRS 469
DB 410 VYCNEHECHHRYAELVIDVININISCEITDGYLTMTKTCRMSTSTIOSLAESTLQRLYHRS 469
QY 470 SLVCSDIPISTHPISEPKDCYLOSDGFEYECIFQPIFLLSGTMMIRINHSIGSLDSPPTCV 529
DB 470 SLVCSDIPISTHPISEPKDCYLOSDGFEYECIFQPIFLLSGTMMIRINHSIGSLDSPPTCV 529
QY 530 LPPSVVKEPPESSVKAETITINIGLTKISMEKPYFPENNLOFOIRYGLSGKEVQMKMEYV 589

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Db 530 lpdsvvklpssvkaeltiniglkliswekpvfpeemlqfityglsgkevqkmyevy 589
 QY 590 DANKSVSLPVPDLCAYAYAVQVRCKRLDGLGYSNMSNPATVYMDIKVPRGPEFMRIT 649
 Db 590 daksksvslpvpdlcayavqvrckridgylgysnmsnpayltvymdlkvpmtgpefwlil 649
 QY 650 NGDTMKKEKNTVLLMKRLMKNDSCSQRYRYINHTSCNGWSESDYGNHTFTFTMTQA 709
 Db 650 ngdtmkkekntvllmkrlmkndscsqryryinhtscngwsewdygnhtftftmtqea 709
 QY 710 HTVTLAINSGASVANPNTFSPMSKVNIVOSLSAFLPMSCCYIWMISPSDYKLMY 769
 Db 710 htvtlainsgasvanpntfswpmakvniyvglsayplmsccyiswslpsdykilmY 769
 QY 770 FTIEWKMLNEDGELKWLRISSSVKRYIHDHPIEIKYQFSLYPDMGCGKPKIINSFT 829
 Db 770 ftiewkmlnedgelkwlriSSsvkryihdhpiiekYqfslylpmegvqpkilnsft 829
 QY 830 ODDIEKHQSDAGLYVYVPIYIISSTILLGLTLLISHQRMKRIFWEDVYPRKCSMAQGLNF 889
 Db 830 qddiekhqsdaglyvypviyIiSStillglTllshqrmkrlfwevprpkncswaglnf 889
 QY 890 QK 891
 Db 890 qk 891
 RESULT 19
 AAM31911
 ID AAM31911 standard; Protein: 958 AA.
 AC AAM31911:
 XX 02-FEB-1998 (first entry)
 DE Human OB-R leptin receptor variant.
 KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
 KM diagnosis; human.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 85 /note= "variation from published sequence"
 FT Misc-difference 109 /note= "variation from published sequence"
 FT Misc-difference 223 /note= "variation from published sequence"
 FT Domain 845..862 /label= "Transmembrane-domain"
 FT Misc-difference 892..958 /note= "divergence from published sequence"
 FT
 XX
 PN MO9726370-A1.
 XX 24-JUL-1997.
 PD
 XX 17-JAN-1997: 97MO-US00570.
 PF
 XX 18-JAN-1996: 96US-0588190.
 PR
 PA (PROC-) PROGENITOR INC.
 PI Clotfi J, Shafer AM, Snodgrass HR, Zupancic TJ;
 XX WPI: 1997-385353/35.
 DR N-PSDB; AAT89193.
 XX
 PT Detecting defective leptin receptor by hybridisation assay - and
 PT treatment of obesity with agent that inhibits the defective
 PT receptor, also screening for compounds that supplement leptin
 PT activity

XX
 XX Claim 12: Fig 1A-E: 26pp: English.
 PS
 XX This polypeptide comprises a variant of the human leptin receptor
 CC (OB-R). Its sequence was deduced from a continuous cDNA (AAT89193)
 CC derived from overlapping clones isolated from a human foetal liver
 CC library. The sequence shows near identity to a published OB-R
 CC sequence in the extracellular domain, with the exception of 3 amino
 CC acids, but there is extensive diversity in the intracellular
 CC cytoplasmic domain at the C-terminal end. A claimed method for
 CC detection of OB-R in cells comprises extraction of RNA and testing
 CC this for hybridisation to an oligonucleotide (i) derived from the
 CC OB-R variant gene, especially from the region beyond nucleotide
 CC 2770. Also claimed are methods of: (1) treating obesity by
 CC administration of an agent that inhibits expression of the OB-R
 CC variant gene; and (2) identification of a compound that can
 CC supplement activity of leptin by: (1) incubating cells expressing
 CC OB-R variant first with leptin and then with a test compound, and
 CC (11) comparing activation signals between cells treated and not
 CC treated with the test compound. Inhibition/down-regulation of the
 CC variant OB-R (found in obese people) improves response of cells to
 CC weight regulation by leptin. Replacing variant OB-R by gene therapy
 CC (in homozygous individuals) can be used to treat obesity. Labelled
 CC probes based on the gene can be used to isolate other variant forms
 CC of the receptor gene or to detect the variant gene (e.g. for
 CC determining predisposition to obesity), while the OB-R gene can be
 CC used to express recombinant OB-R (optionally as fusion protein) and
 CC in standard hybridisation assays. The OB-R gene can also be used
 CC therapeutically in cases of overexpression of functional OB-R
 CC (causing loss of appetite and hypermetabolic activity). Cells
 CC engineered to express variant receptor are used in method (2) to
 CC screen for (ant)agonists of leptin/OB-R interaction, also to generate
 CC antibodies that competitively inhibit, neutralise or enhance activity
 CC of the variant receptor.
 CC
 SO Sequence 958 AA:
 Query Match 58.5%; Score 681; DB 18; length 958;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 110 TRVSVVNSLVFPQIDANNITQGWKGLKLFICYVESLFKNLFRRNTNYVHLIYVPEVL 169
 Db 110 tlvsvvnslvfpqidannitqgwklficyveslfknlfrrntyvhllyvpevl 169
 QY 170 EDSPIVPOKGFOMVHCNCSVEHCECELVPPYAKINDLLKCLKTSQGVJFOSPLMSY 229
 Db 170 edspivpokgfomvhcncsvehcecelvppyakindllmclksqgvjfrsplmsv 229
 QY 230 QPINNVKPPDPLGLHMETDDGNLKSWSPPVLPFPLQYQKYSNSTTVIREADKIVS 289
 Db 230 qpinnvkkppdplglhmetddgnlkswspplvplpfplqykyesnsttvireadkivs 289
 QY 290 ATSLVDSTLPSSSYEVQYRGRUDGPGIWSWSTPRVTTQVYVFPFKILTSSVSNVS 349
 Db 290 atslivdstlpsssyevqyrgkrudgpgiwsdwstprvttdqvayfppkiltssvsnvs 349
 QY 350 FHCITKKEKNIYPSKEIYMMNMIAEKIPOSQYDVVSDHAKYLFNNINTEKRGKRTTYDA 409
 Db 350 fhciykkkenkiypskeiywmnmiaekiposqydvvsdhsakylfnnintekrgkrttyda 409
 QY 410 VYCCNEHECHHRYAEIYVDVININISCEITDGYLTNWTGWSSTSTIOSIAESTLOLRHRS 469
 Db 410 vyccnehechhyaeiyvdivniniscedgyltkmtcrwststqsiaestlqlrhys 469
 QY 470 SLXCSDFISIHISRPKOCYLOSDFYECIRPPIFLISYTMWIRHNLSGSDSPPTCV 529
 Db 470 slxcsdfisihisrpkocylosdfyeciRppiflisytmwirhnlsgsdspptcv 529
 QY 530 LPDSVVKPLPSSVAAETITINIGLKLISWEKVPFPENNILOFOIFGLSCKEYOMKMYEY 589
 Db 530 lpdsvvklpssvkaeltiniglkliswekvpfpeemlqfityglsgkevqkmyevy 589

QY 550 DAKSKSVSLPYVDLCAYVAVQVRCRKLDDGYSWNSMNPATYVMDIKYMGKPEFWRII 649
 DB 550 daksksvslpyvdlcayvavqvrckrlldgyswmsnpayevmdikymgkpefwrii 649
 QY 650 NCDYMKKKKNTVLLMKPLMKNDLSCVQRYVINHTSCNGTWSEVDGNHTKFTFLMTEQA 709
 DB 650 ngdymkknkntvllwplmkndslscvqryvinhtscngtwsevdgnhtkftflwteqa 709
 QY 710 HVTVLATINSGASVANFLTFSWPMKRNIVOSLSAYPLNSSCVVSLTSPDVKLMY 769
 DB 710 hvtvlatinsgasvanfltfswpmkvnlvqslsayplnsscvvslvslpsdvlkmy 769
 QY 770 FLEKKNLNEDEIKWLRISSSVKRYIHDHPPIEKYQSLPYLFMEGVGPKIINSET 829
 DB 770 flekknlnedeklwlrlsssvkryihdhpriekeyqslpylfmegvgpkiiinset 829
 QY 830 QDDIRKHOSDAGLYIVPTIISSTILLGTLISHQKMKLWEDVPNPKNSMAOGLNF 889
 DB 830 qddirkhosdaglyivptiisssillgtilishqmkllwedvpnpknscwaqglnf 889
 QY 890 OK 891
 DB 890 qk 891

RESULT 20

AA019535
 ID AAM19535 standard; Protein: 958 AA.

AC AAM19535;

DT 02-FEB-1998 (first entry)

DE Human OB-R leptin receptor variant.

KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;

KM diagnosis; human.

OS Homo sapiens.

FX Key location/Qualifiers

FT Misc-difference 85 /note= "variation from published sequence"

FT Misc-difference 109 /note= "variation from published sequence"

FT Misc-difference 223 /note= "variation from published sequence"

FT Domain 845..862 /note= "variation from published sequence"

FT Misc-difference 892..958 /note= "divergence from published sequence"

PN W09726272-A1.

PD 24-JUL-1997.

PE 17-JAN-1997; 97WO-US00080.

PR 18-JAN-1996; 96US-0588189.

PA (PROG-) PROGENITOR INC.

PI Cloffert J, Shafer AW, Snodgrass HR, Zupancic TJ;

DR WPI: 1997-385291/35.

DR P-PSDB: AAT72649.

PT Detecting defective form of leptin receptor by probing cellular RNA
 PT - with oligonucleotide derived from DNA of receptor variant, also
 PT treatment of obesity by inhibiting expression of variant receptor
 PT and screening for agents that increase leptin activity

PS Claim 12; Fig 1A-E; 26pp; English.

CC This polypeptide comprises a variant of the human leptin receptor
 CC (OB-R). Its sequence was deduced from a contiguous cDNA (AAT72649)
 CC derived from overlapping clones isolated from a human foetal liver
 CC library. The sequence shows near identity to a published OB-R
 CC sequence in the extracellular domain, with the exception of 3 amino
 CC acids, but there is extensive diversity in the intracellular
 CC cytoplasmic domain at the C-terminal end, suggesting alternative
 CC splicing of a common precursor mRNA. A claimed method for
 CC detection of OB-R in cells comprises extraction of RNA and testing
 CC this for hybridisation to an oligonucleotide (1) derived from the
 CC OB-R variant gene, especially from the region beyond nucleotide
 CC 2770. Also claimed are methods of: (1) treating obesity by
 CC administration of an agent that inhibits expression of the OB-R
 CC variant gene; and (2) identification of a compound that can
 CC supplement activity of leptin by: (1) incubating cells expressing
 CC OB-R variant first with leptin and then with a test compound, and
 CC (11) comparing activation signals between cells treated and not
 CC treated with the test compound. Inhibition/down-regulation of the
 CC variant OB-R (found in obese people) improves response of cells to
 CC weight regulation by leptin. Replacing variant OB-R by gene therapy
 CC (in homozygous individuals) can be used to treat obesity. Labelled
 CC probes based on the gene can be used to isolate other variant forms
 CC of the receptor gene or to detect the variant gene (e.g. for
 CC determining predisposition to obesity), while the OB-R gene can be
 CC used to express recombinant OB-R (optionally as fusion protein) and
 CC in standard hybridisation assays. The OB-R gene can also be used
 CC therapeutically in cases of overexpression of functional OB-R
 CC (causing loss of appetite and hypermetabolic activity). Cells
 CC engineered to express variant receptor are used in method (2) to
 CC screen for (ant)agonists of leptin/OB-R interaction, also to generate
 CC antibodies that competitively inhibit, neutralise or enhance activity
 CC of the variant receptor.

SO Sequence 958 AA:

Query Match 58.5%; Score 681; DB 18; length 958;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TVSTVSNLSLVFOOIDANMNIQCKLKDGLFTCYVSLKRNLFRRNRYKVLHYLYPEVL 169
 DB 110 tfstvsnlslvfqoidanwniqcklkdglftcyveslkrnlfrnrykvlhylypevl 169
 QY 170 EDSPLVPOKGFOMVHNCNSVHECCCLVVPYPAKNDTLMLKLTSGVIFOSPLMSY 229
 DB 170 edsplvpqkgsfqmwhncnsvehccclvvpriakndtlmlc:ltsgvgvifrsplmsy 229
 QY 230 QPINWKKPDPPLGLHMETDNDGNLKSWSPPPLVPEPQYQVKNYSNSTTVIREADKIVS 289
 DB 230 qpimwkkpdpplglhmetdndgnlkswsppplvpepdyqvknysnsttvireadkivs 289
 QY 290 ATSLVDSILPSSSYEVQVGRKLDGPTWSDMSTRVTTQVYCTFPPKILTVSASNS 349
 DB 290 atslvdsilpsssyevqvrkldgptwsdmsrvtvtqov:ctfppkiltvsasns 349
 QY 350 FHCITKKNKIYPSKEIYVMWMLAEKIPSOYDVADSHSKYTFEFLNTEKTPRGKTYDA 409
 DB 350 fhciytkknkiypskeiyvmwmlaekipsoydvadshskvtfeflnetektprgktyda 409
 QY 410 VYCCNEHECHHRYAELIYVIDVINISCEEDGYLTAKTCRMSTSTIOSLAESTLQRLYHRS 469
 DB 410 vycnehechhryaeliyvidviniscceedgyltakmtcrwststioslaestlqlrlyhrs 469
 QY 470 SLVCSDDIPSIPISSEPKDCYLOSDFYECIFOPIFLLSGYTWKIRINHSGLSDSPPCY 529
 DB 470 slvcsddipsipisepkdcylsdfyecifopifllsgytwmirinhsldspspcy 529
 QY 530 LBDSSVKKPLPSSSVKAEITINIGLKISWEKVPFPNNIOFOIRGLSCKEYQMKWEY 589
 DB 530 lpdssvkkplpsssvkaeltiniglkwskvfpenniofoirglsgkevqmkwey 589

QY 590 DAKSKSVSLPVPDLCAYAVAVOYRCKRLDGLGYMSNMPATVYMDIKVPMRGEFMRIT 649
 D 590 daksksvslpvpdlcayavavoyrcrldglgymswnmpatvymdikvpmrgpelfwrl 649
 QY 650 NGDPMKKKKNTLLMKPLMKNDLSQVORYVINHTSCNGTSGVSDVGNHKKFTFLMTEDA 709
 D 650 ngdpmkkknvcllwkplmkndlsqsvoryvinhtscngtsgvsdvgnhckftflwteda 709
 QY 710 HTVTVLAINSIGASVANFNLTFSWPMKSVNIQVSLASAYPLNLSGVYISWILSPDYKLMY 769
 D 710 htvtvlainSIGASVANFNLTFSWPMKSVNIQVSLASAYPLNLSGVYISWILSPDYKLMY 769
 QY 770 FIIEKKNLNDEGEIKWLRISSSVKRYIYHDFIPIEKYQFSLPIFMEGVGKPKIINSET 829
 D 770 fliewklnedgeikwlrissvkkryihdfipiekqfslpifmegvgkpklinst 829
 QY 830 ODDIEKHOSDAGLYVIVPVIISSIIILGTLIIISHORMKKLFMDVNPKNKCSMAOGLNF 889
 D 830 qddlekhsdaglyvivpvilssiiilgtliishqrmkklfmedvnpknkcswaqglnt 889
 QY 890 QK 891
 D 890 qk 891

RESULT 21

AAW22773
 ID AAW22773 standard; Protein; 958 AA.

AAW22773:

11-FEB-1998 (first entry)

Human haematopoietin receptor variant Hu-B1.219 form 1.

Haematopoietin receptor; Hu-B1.219; obese gene; leptin; obesity;
 human; cancer; leukaemia; immunodeficiency; myeloid deficiency;
 anaemia; therapy.

Homo sapiens.

Key Location/Qualifiers
 Domain 845..862
 /label=Transmembrane_domain

MO9727286-A1.

31-JUL-1997.

21-JAN-1997; 97MO-US00767.

13-SEP-1996; 96US-0713296.

23-JAN-1996; 96US-0589915.

20-MAR-1996; 96US-0618957.

(PROG-) PROGENITOR INC.

Bart BA, Cioffi J, Mikhail AA, Shafer AW, Snodgrass HR.

Supernatant T₀.

WPI; 1997-393674/36.

N-PSDB; AAT75172.

Using leptin to activate haematopoietic cells - to treat

immunodeficiency, anaemia or myeloid deficiency

Claim 32; Fig 1A-E; 82pp; English.

This protein comprises a novel human haematopoietin receptor,
 designated Hu-B1.219 form 1, that has been detected in brain cells
 and shown to bind to the obese gene product, leptin. Its sequence
 was deduced from cDNA clones (see AAT75172) isolated from a human

CC foetal liver library. Hu-B1.219 has been isolated in 3 isoforms
 CC that are nearly identical to the published leptin receptor (OB-R)
 CC sequence in the extracellular domain (only 3 amino acid variations)
 CC but differ extensively in the intracellular domain (downstream from
 CC nucleotide 2771). Hu-B1.219 is a marker for haematopoietic and
 CC endothelial progenitor cells, especially those cells capable of
 CC long-term repopulation. Hu-B1.219 nucleic acid sequences or
 CC binding agents for Hu-B1.219 protein can be used in claimed methods
 CC for identifying haematopoietic progenitor cells in a cell mixture
 CC or tissue, and for detecting cancer. A claimed method for treating
 CC cancer comprises the administration of leptin to a patient
 CC suffering from a cancer which expresses Hu-B1.219; to result in
 CC suppression of cancer growth. Leukaemia is a typical Hu-B1.219
 CC expressing cancer.
 CC
 SQ Sequence 958 AA;
 Query Match 58.5%; Score 681; DB 18; length 958;
 Best Local Similarity 99.9%; Pred. NO. 0;
 Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 110 TFEVTVNSLVEFOQIDANNIQCWLKGLKFLCYVESLFRKNEFRHYNKVHLLVYLPVL 169
 D 110 tfevtnslvfeqoidannniqcwlgkflfcyveslfrknefrhyknkvhllylpevl 169
 QY 170 EDSPLVPQKSFQWVHCNCSVHECECELPVPTAKLNTLLMCLRTSGVIFQSPMSV 229
 D 170 edsplvpqksgfwmvncnscsvhececelvpptaklntllmclrtsgvifrsplmsv 229
 QY 230 QPINNVKPDPLGLHMETTDGNTKISNSPPLVFPLOYQVYKSENSTTVREDAKIVS 289
 D 230 qpinnvkpdpplglhmettdgntkisspplvpfployqvysensttvreadakivs 289
 QY 290 APTSLVDSILPQSSSEYQVGRKRLDGPGLMSDWSRPVFTQDDVYFEPKILTSVSNVS 349
 D 290 aptslvdsilpqssseyqvgrkrldgpplmsdwsrpvftqddvyfepkiltsvsnvs 349
 QY 350 FHCIIYKKNKIYPSKEIYWMNIAEKIPQSQDYVSDHYSKVFPLNETKRGKRTYDA 409
 D 350 fhciiykknkiypskeiywmniaekipqsqdyvshyskvfplnetkrgkrtйда 409
 QY 410 VYCCNEHCCHRYAEVYVIDVININISCTDGYLTMTKRWSTSTIQSLAESLQIRHRS 469
 D 410 vyccnehcchryaevyvidvininiscetdgyltmtkrwststiqslaeslqirhrs 469
 QY 470 SLVCSDISHPISRPKCYIOSDGEFYECIPQIFLLSGYTMKIKINSLGLSDSPCTV 529
 D 470 slvcsdishpisrpkcyiosdgefyecipqifllsgytmkikinslglsdspctv 529
 QY 530 LPDSVYKPLPPSSVKAETITINIGLKISMEKFPFENNLOEQIRYGLSGKEVQMKYEVY 589
 D 530 lpdsvykpplppssvkaetitiniglkismekfpfennloeqiryglsgkevqmkyyevy 589
 QY 590 DAKSKSVSLPVPDLCAYAVOYRCKRLDGLGYMSNMPATVYMDIKVPMRGEFMRIT 649
 D 590 daksksvslpvpdlcayavoyrcrldglgymswnmpatvymdikvpmrgpelfwrl 649
 QY 650 NGDPMKKKKNTLLMKPLMKNDLSQVORYVINHTSCNGTSGVSDVGNHKKFTFLMTEDA 709
 D 650 ngdpmkkknvcllwkplmkndlsqsvoryvinhtscngtsgvsdvgnhckftflwteda 709
 QY 710 HTVTVLAINSIGASVANFNLTFSWPMKSVNIQVSLASAYPLNLSGVYISWILSPDYKLMY 769
 D 710 htvtvlainSIGASVANFNLTFSWPMKSVNIQVSLASAYPLNLSGVYISWILSPDYKLMY 769
 QY 770 FIIEKKNLNDEGEIKWLRISSSVKRYIYHDFIPIEKYQFSLPIFMEGVGKPKIINSET 829
 D 770 fliewklnedgeikwlrissvkkryihdfipiekqfslpifmegvgkpklinst 829
 QY 830 ODDIEKHOSDAGLYVIVPVIISSIIILGTLIIISHORMKKLFMDVNPKNKCSMAOGLNF 889
 D 830 qddlekhsdaglyvivpvilssiiilgtliishqrmkklfmedvnpknkcswaqglnt 889

```

OY      890 QK 891
DB      890 QK 891

RESULT 22
AAR88912
ID      AAR88912 standard; Protein: 898 AA.
AC      AAR88912;
DE      07-JUN-1996 (first entry)
KW      Haematopoietin receptor Hu-BI.219 Form 3 protein.
KW      Haematopoietin receptor; Hu-BI.129; probe; prenatal testing; cancer;
KW      leukaemia; diagnosis; therapy.
OS      Homo sapiens.
FH      Key
FT      Location/Qualifiers
FT      Domain
FT      /label= Transmembrane_domain
XX      MO9608510-A1.
XX      21-MAR-1996.
XX      30-AUG-1995; 95WO-US10965.
XX      14-DEC-1994; 94US-0355888.
XX      14-SEP-1994; 94US-0306231.
XX      (PROG-) PROGENITOR INC.
XX      PA
XX      PI
XX      PI
XX      Cloff J, Shafer AM, Snodgrass RH, Zupancic TJ;
XX      WPI: 1996-179901/18.
XX      DR
XX      N-PSDB; AAT12913.
XX      PT
XX      Human haematopoietin receptor Hu-BI.219 - useful in design of
XX      molecular probes for prenatal testing and cancer diagnosis
XX      PS
XX      Claim 26; Fig 3B; 67pp; English.
XX      CC
XX      A novel haematopoietin receptor (AAR88912), HuBI.219 Form 3 protein,
XX      CC is the product of a cDNA clone (AAT12913) isolated from a human
XX      CC foetal liver library. 2 Other forms of HuBI.219 (see AAR88910 and
XX      CC AAR88911) have also been identified. The Hu-BI.219 protein, or a
XX      CC portion of it, is pref. prepd. by culturing a host cell engineered
XX      CC to express HuBI.219 cDNA. The Hu-BI.219 protein (whether in sol.
XX      CC form or expressed on the cell surface and opt. as part of a fusion
XX      CC protein) is used to screen peptide libraries to identify ligands
XX      CC of Hu-BI.219.
XX      SQ
XX      Sequence 898 AA;

Query Match      49.8%; Score 580; DB 17; Length 898;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      110 TFSVTSNLSVQOQIDANNNIQCMKLGDKLFTCYESLFKNLFRNANKVHLVLPVYL 169
DB      112 tfvetnsnlvlgqldannnlgcwkkgdtklftcyeslfknlfrynkvhlvlpvyl 171
OY      170 EDSPLVPOKGSFQWYHCNCSVHECCCLVPPYPAKLANDFLMCKITSGVIFQSPLSMV 229
DB      172 edsplvpokgsfwmhcnscvheccclvppypaklandflmckitsgvifrsplmsv 231
OY      230 QPIMVWKPDPPLGLHMETTDGNIKISSSPPLVFPFIOYQVKSSENTTYVIREADKIVS 289
DB      111

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DB      232 qpimwkpdpplglhmetddgnlkiswsspplvfpplgyvkvysenstvtvireadkivs 291
OY      290 ATSLVDSILIPGSSYEVOYGRKRLDPCGIMSDMSTPRVETPDVYFPPKILTSVGNVS 349
DB      292 atslvdsilipgssyevgyrgrldpgjmgdmsprvtctdv-yfppkiltsvgnvs 351
OY      350 FHCITRKKNKIVPSKEIYWMNLAEKIPQSDYDVSDHVSKEYTFINLNTKRGKFTYA 409
DB      352 fhciykrknkivpskeiymnmlaekipqsydvsvdhvskvtfihnlntkprgkftya 411
OY      410 VYCCNEHECHHRYAELVYVDVNIINISCEPDGYLTWKTCRMSSTIOSIAESTLOJLRHNS 469
DB      412 vycnehechhryaelvldvnlinscedgylltkmctcrmsstiosiaestlqirlyhs 471
OY      470 SLVCSDIPIHPIPSPKDCYLOSDFYECIFQPIFLLSGYTWKIRINHSGLSDSPPTCV 529
DB      472 slvcsdipihpipspkdcylsgdfyecifqpfifllsgytwmriinhslgsldspptcv 531
OY      530 LPDSVYVKKPLPSSVKAETITINIGLAKISWEKRVFPENNIOPIQIRYGLSCKEYQWKMEYV 589
DB      532 lpdsvvkkplpssvkaeltinlgllklswekvpfpennioqirylglsckevqwkmyev 591
OY      590 DAKSKSVSLPVPDLCAVYAVQYRCRKLDDLGYSWNSMNPAYTVVHDIKVPMRGPEFMRIT 649
DB      592 daksksvslpvpdlcaavyavqyrcrklldlgyswnsnmpaylvndikvpmrgpelfrit 651
OY      650 NGDTMKKKNKNTLLMKPMLKNDLSCVORYVINHHTSCNGTSESDVGNHTKFTPLWTEQA 709
DB      652 ngdtmkkeknvllwkpmlkndslcsvqryvinhhtscngtsevdgnhtkftflwteqa 711
OY      710 HRTVYLAINSIGASVANFRLTSPWPSKKNIVQSLASAYPLNNSCVIVSILSPSOYKLMY 769
DB      712 hrtvylainsigasvanflltspwpskknivqslasayplnnsccvsvslspsoyklmy 771
OY      770 FTIEWKNLNDEDEIRKMLRISSSVKKRYIHDRFPIEKYQFSLYPIFMEGVGPKIINSEPT 829
DB      772 ftiewknlndedekmlrissvkkryihdrfpielkyqfslypifmegvgpklinsept 831
OY      830 QDDIERHOSDAGLYVIVPIYISSILLGTLTISHQRMKLFWEVNPKNKCSMAQGLNF 889
DB      832 qddierhogsdaglyvlpvliissilllgcllshqrmklfwevnpknkcsmaqglnf 891
OY      890 QK 891
DB      892 QK 893

RESULT 23
AAR88911
ID      AAR88911 standard; Protein: 908 AA.
AC      AAR88911;
DE      07-JUN-1996 (first entry)
KW      Haematopoietin receptor Hu-BI.219 Form 2 protein.
KW      Haematopoietin receptor; Hu-BI.129; probe; prenatal testing; cancer;
KW      leukaemia; diagnosis; therapy.
OS      Homo sapiens.
FH      Key
FT      Location/Qualifiers
FT      Domain
FT      /label= Transmembrane_domain
XX      MO9608510-A1.
XX      21-MAR-1996.
XX      30-AUG-1995; 95WO-US10965.
XX      14-DEC-1994; 94US-0355888.

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PR 14-SEP-1994; 94US-0306231.
 XX (PROG-) PROGENITOR INC.
 XX Cioffli J, Shafer AM, Snodgrass RH, Zupancic TJ;
 XX WPI; 1996-179901/18.
 DR N-PSDB; AAT12912.
 XX Human haematopoietin receptor Hu-B1.219 - useful in design of
 PT molecular probes for prenatal testing and cancer diagnosis
 XX
 PS Claim 25; Fig 3B; 67pp; English.
 CC A novel haematopoietin receptor (AAR88911), HuB1.219 Form 2 protein,
 CC is the product of a cDNA clone (AAT12912) isolated from a human
 CC foetal liver library. 2 Other forms of HuB1.219 (see AAR88910 and
 CC AAR88912) have also been identified. The Hu-B1.219 protein, or a
 CC portion of it, is pref. prepd. by culturing a host cell engineered
 CC to express HuB1.219 cDNA. The Hu-B1.219 protein (whether in sol.
 CC form or expressed on the cell surface and opt. as part of a fusion
 CC protein) is used to screen peptide libraries to identify ligands
 CC of Hu-B1.219.

XX Sequence 908 AA;

Query Match 49.8%; Score 580; DB 17; Length 908;

Best Local Similarity 99.7%; Pred. No. 0;
 Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 110 TFVSTVNSLVFQOQIDANNITCWLKGLDKLFICYVESLFKNLFRRNRYKVALLYLPEVL 169
 DB 112 lfvtstnslyfvgqldanwnlqclwklgdlklfcyveslfknlfrrnykvallylpevl 171
 OY 170 EDSPLVPOKSGFQWVHCNCSVHECCCECLVPVPTAKLNDTLMCLKITSGVIFPOSPLMSV 229
 DB 172 edsplyvpkgsfgmwhcnscvheccceclvpvtaklnlmlclkitsgvifposplmsv 231
 OY 230 QPIMKVRDPPLGLHMETTDGDLKISWSPPLVPLQYOVKTSNSTVYREADKTIVS 289
 DB 232 qpimvvpdpplglhmetiddgnlkiswspplvplfqyovktsnstvylreadkivs 291
 OY 290 ATSLVNSILPGSSYEVQVRKRLDGRISDSTPRFTODVYFPPKILTSVGSNVS 349
 DB 292 atslvnsilpgssyevqvrkrlidgrisdstprfttdvlyfppkiltsvgsnvs 351
 OY 350 FHCITYKKENKIVPSKETIWMNNLAEKIPQSOQDYVSDHVSVTFPNNLNETPRGFTEDA 409
 DB 352 fhcitykknkivpsketiwmnnlaekipsgdydvshvsvtfpnnlnetprgfteda 411
 OY 410 VYCCNEHECHHRAELVYIDVNNINISCTEDGYLTRKTCRMSTSTIOSLAESTLQRYHRS 469
 DB 412 vycnehechhryaelvyidvnniniscetdgyltrktrcmststioslaestlqryhrs 471
 OY 470 SLVCSOIPSHIRIEPRDCIQSDGFYFCIFQPIFLSLGTYMWTIKINSLSGLSDSPICY 529
 DB 472 slvcsdipshiriesprdciqsdgfyfcifqpiflslgtymwtkinslsdpspcy 531
 OY 530 LPDSVNPPLPSSVKAETINIGLKISMEKPPENNLQOIRGLSGKEVOMKMYEV 589
 DB 532 lpdsvnpplpssvkaetlniglkiswekppennlqoirglsgkevomyev 591
 OY 590 DAKRSVSLPVPDLCAYAVOVROCKRLDGLGYWSNWSNPATVVDIKVPMRGPFRRII 649
 DB 592 daksvslpvpdlcayavovrockrlidglgywsnwnspatvvdikvpmrgpfrrii 651
 OY 650 NGDTMKKEKNYTLMLKPLMKNDSCSVORYIYNHHTSCNGWSEDPVGNHTFTFLMTEQA 709
 DB 652 ngdtmkkeknytlmlkplmkndscsvoryiynhhtscngwsedepvgnhtftflmtega 711
 OY 710 HTVTVLAINSIGASVANENLFEFSPMKSQVNTVQSLAAYPLNLSGCVTVMILSPSDYKLMY 769
 HTVTVLAINSIGASVANENLFEFSPMKSQVNTVQSLAAYPLNLSGCVTVMILSPSDYKLMY

DB 712 htvtvlainsigasvanenlfefspmksqvnlyvqslsayplnlsccvlsvslpsdyklm 771
 OY 770 FILEKKNLNEDGELKWLRISSSVKRYIYHDHPIPEKYOFSLYPTFMGKPKITINSFT 829
 DB 772 filekknlnedgelkwlri:sssvkryy:indhpi:pekyofsl:yp:tfmgv:gp:k:instf 831
 OY 830 QDDIEKHOSDAGLYTVIVYITSSSTILLIGTLLISHQRMKKLEWEDVYPMKNCSSMAQGLNF 889
 DB 832 qddiekhsdaglyvlyvpyitssstlllgtllishqrmkklfwevdpmpkncswaglnf 891
 OY 890 QK 891
 DB 892 qk 893

RESULT 24

AAR88910
 ID AAR88910 standard; Protein; 960 AA.

XX AAR88910;

XX 07-JUN-1996 (first entry)

XX Haematopoietin receptor Hu-B1.219 Form 1 protein.

XX Haematopoietin receptor; Hu-B1.219; probe; prenatal testing; cancer;
 XX leukaemia; diagnosis; therapy.

XX Homo sapiens.

XX Key location/qualifiers
 FT Domain 871..898
 FT /label= Transmembrane_domain

PN W09608510-A1.

PD 21-MAR-1996.

XX 30-AUG-1995; 95WO-US10965.

XX 14-DEC-1994; 94US-035888.

XX 14-SEP-1994; 94US-0306231.

XX (PROG-) PROGENITOR INC.

XX Cioffli J, Shafer AM, Snodgrass RH, Zupancic TJ;

XX WPI; 1996-179901/18.
 DR N-PSDB; AAT12911.

XX Human haematopoietin receptor Hu-B1.219 - useful in design of
 PT molecular probes for prenatal testing and cancer diagnosis

XX Claim 24; Page 35-38; 67pp; English.

XX A novel haematopoietin receptor (AAR88910), HuB1.219 Form 1 protein,
 CC is the product of a cDNA clone (AAT12911) isolated from a human
 CC foetal liver library. 2 Other forms of HuB1.219 (see AAR88911 and
 CC AAR88912) have also been identified. The Hu-B1.219 protein, or a
 CC portion of it, is pref. prepd. by culturing a host cell engineered
 CC to express HuB1.219 cDNA. The Hu-B1.219 protein (whether in sol.
 CC form or expressed on the cell surface and opt. as part of a fusion
 CC protein) is used to screen peptide libraries to identify ligands
 CC of Hu-B1.219.

XX Sequence 960 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 49.8%; Score 580; DB 17; Length 960;

Best Local Similarity 99.7%; Pred. No. 0;
 Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 110 TFVSTVNSLVFQOQIDANNITCWLKGLDKLFICYVESLFKNLFRRNRYKVALLYLPEVL 169

```

Db      112  lftsvtnslvltqldanmnlqclkgldklficyveslfnkllfrnykvhllylpevl 171
Qy      170  EDSPLVPQGSFQWVHNCNSVEHCECELPVPYTAKNLNTLMLCKLITSGVIFQSPLSNV 229
Db      172  edsplvpqkgsfqmwhncsvhececlvypylaklndllmclktsgvlfirplmsv 231
Qy      220  QPINNVKDPPLGLMEITDDGNLKTSSSPLVPEPLQYQVYKSENSTVITREADKIVS 289
Db      222  qplnmvxpdpplglmeitddgnlktsswspplvpfpdygykysensctivreadkiv 291
Qy      290  ATSLVDSILRPSSEVQYRGKRLDGPQKMSDMSTPRVFTTDDVLYFPFKLITSGSNVS 349
Db      292  atslvdsilrpsseyvqyrgkrltgpqkmsdmstprvfttddvlyfppkltsgsnvs 351
Qy      350  FHCITKKNKIVPSKEIYVMMNLAEKIPQSDYVSDHVSKTYPFNLTNPKRGKFTYDA 409
Db      352  fhcltkkknkivpskeiyvmmnlakelpsgydvsvdhvskvtfhlnetkprgkftcyda 411
Qy      410  VYCCNEHECHHRYAEIYVIVNINISCEITDGYLITKMTCSMTSTTQSLAESTLQLRHRS 469
Db      412  vycnehechhryaeliyvdivniniscetdgyltkmtcwtsttqslaeestqlrlrhrs 471
Qy      470  SLXCDISFISHPISPKCYLQSDGFECIFQPIFLSLGYTWMTININSLGSLDPPCTCV 529
Db      472  slxcdisfshpispkcylysdgfyecifqpiflslgytwmtirlnslsgslsdppctcv 531
Qy      530  LPDSVVKPLPSSVKAETITINIGLKTISWEKVPFENNLOFOIRYGLSGKEVQWKNYEY 589
Db      532  lpdsvvkplpsssvkaetitinigllktiswekvpfpennlofoirylsgkevqwkmyey 591
Qy      590  DAKSKSVSLPVPDLCAVYAVOYRCRLDGLGYSMNSMNPAYTVVMDIKVPMRGPEFWRII 649
Db      592  daksksvslpvpdlcavyavoyrcrldglysmnswnpaytvvmdikvpmrgpewfwril 651
Qy      650  NQDPTKKEKNVTLMLKPLKNDKSLCSQYRYVYNHHTSCNGTSEDEVGNHTKFTFLMTBEA 709
Db      652  ngdptkkeknavtlmkplmkndslcsqyryvynhhtscngtsedevgnhtkftflwbeqa 711
Qy      710  HTVTVLAINISGASVANFNLFESWPMKVNIVQSLAAYPLNNSCVIVSIIISPSDYKLMAY 769
Db      712  htvtvlnslsgasvanfnlftswpmkvnivqslaysplnnsctivswiispsdykilmay 771
Qy      770  FIIEKNKLNDEGEIKWLRISSSVKRYIYHDFPIEKTQFSLYPIFMEGVGKPKIINSEFT 829
Db      772  flieknlnedgelnkwlrlsssvkryiindhfpiekyqfslypifmegvgkpkilnseft 831
Qy      830  ODDIEKHQSDAGLYVTVVITSSSILGLTLLISHQRMKLFMEVDPNPKNSMAQGLNF 889
Db      832  qddlekhqsdaglyvtpvllsssilgltilishqrmklfmedvpnpknscwaglnf 891
Qy      890  QK 891
Db      892  qk 893

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RESULT 25
AAM62544
ID AAM62544 standard; protein: 1221 AA.
XX
AC AAM62544;
XX
XX 12-OCT-1998 (first entry)
XX
DE Human ob-receptor replacement mutant.
KW
KW ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;
KW anorexia; cachexia.
XX
OS Homo sapiens.
XX
XX MO9824881-A1.
XX

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PD      11 -JUN-1998.
XX
XX 26-NOV-1997; 97WO-US22165.
XX
XX 02-DEC-1996; 96US-0032367.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Fong TM, Huang RC, Van Der Ploeg LJ.
XX
XX WPI: 1998-333304/29.
XX
XX
XX Claim 6; Fig 2; 27pp; English.
XX
XX The ob-receptor (OB-R), a member of the cytokine receptor family is
XX transcribed in the hypothalamus and is involved in obesity. The
XX replacement mutant has had amino acids 420-496 the second CK-F3
XX module in OB-R deleted and replaced by amino acids 500-632. The
XX replacement mutant together with mutants lacking a functional first CK-F3
XX module or a functional intracellular domain can be used in assays for the
XX detection of ligands, agonists, antagonists and ligand mimetics. The
XX leptin agonists identified can be used in situations where leptin
XX insufficiency causes obesity, diabetes or infertility. The leptin
XX antagonists identified can be used in the treatment of anorexia and
XX cachexia. The mutant receptor nucleic acids can also be used in gene
XX therapy for weight control, e.g. for treating obesity or anorexia.
XX
XX Sequence 1221 AA:

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Query Match      48.8%; Score 568; DB 19; Length 1221.
Best Local Similarity 99.9%; Pred. No. 0;
Matches 668; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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XX		Human haemopoietin receptor NR2.
DE		
KW		Haemopoietin receptor; new receptor 2; NR2; leptin; human;
KX		autoimmune disease; nervous system; cerebral palsy;
KV		trauma induced paralysis; vascular ischemia; stroke;
KW		neuronal tumour; motor neurone disease; Parkinson's disease;
KW		Huntington's disease; Alzheimer's disease; multiple sclerosis;
KW		peripheral neuropathy; heavy metal; alcohol; toxicity;
KW		kidney failure; infectious disease; herpes; rubella; measles;
KX		chicken pox; HIV; HTLV-1; therapy.
OS		
XX		Homo sapiens.
FH		
FT	Key	Location/Qualifiers
FT	Misc-difference 223	/note= "encoded by CNG"
FT	Misc-difference 687	/note= "encoded by TSC"
FT		
XX		WO9712037-A1.
PN		
XX		03-APR-1997.
PD		
XX		26-SEP-1996; 96WO-AU000607.
PF		
XX		26-SEP-1995; 95AU-0005641.
PR		
XX		(AMRA-) AMRAD OPERATIONS PTY LTD.
PA		
XX		Alexander WS, Gainsford T, Hilton DJ, Metcalf D,
PI		Ng A, Nicola NA, Willsonc;
PL		WP1; 1997-212896/19.
DR		N-PSDB; AAT64442.
XX		
PT		Human haemopoietin receptor NR2, and corresponding DNA - used e.g.
PP		for treatment of autoimmune diseases
PS		
XX		Claim 11; Page 50-54; 96pp; English.
XX		
CC		Human haemopoietin receptor NR2 (AAW14841) interacts with leptin,
CC		and can be used to develop (ant)agonists, therapeutics and
CC		diagnostic reagents based on ligand interaction. Its amino acid
CC		sequence was deduced from an isolated DNA molecule (AAT64442).
CC		Recombinant NR2 can also be used in a claimed method to identify
CC		ligands capable of interacting with a haemopoietin receptor, and
CC		in a method for therapy of autoimmune diseases. Recombinant
CC		soluble NR2 polypeptides can be used in the treatment of disease,
CC		injury or abnormality in the nervous system, cerebral palsy, trauma
CC		induced paralysis, vascular ischemia associated with stroke,
CC		neuronal tumours, motor neurone disease, Parkinson's disease,
CC		Huntington's disease, Alzheimer's disease, multiple sclerosis,
CC		peripheral neuropathies associated with diabetes, heavy metal or
CC		alcohol toxicity, renal failure and infectious diseases such as
CC		herpes, rubella, measles, chicken pox, HIV or HTLV-1.
SQ		
Sequence	896 AA:	
Query Match	33.3%; Score 388; DB 18; Length 896;	
Best Local Similarity	99.7%; Pred. No. 0;	
Matches	588; Conservative 0; Mismatches 2; Indels 0; Gaps	0;
OY	1	MICQAFCYVLHWERTIYTANLSYPITPMWFKISCSAPPNSTYDFLLPAGISKNTNS
Dd	1	mIQGFvCVllhwetiyyItafnlslpyltipwxfkIscompnstydfllpAglsKntns
OY	61	NCGHTAEPEKRNSSGTHESNLSTKTTPHCCESEDDRNCSLCADNTECKTFYSTNSLVE
Dd	61	nghytAEepkrnssgthfnslnsktltfnccrtisegqdnscldahlegtllystvnslvf
OY	121	QQIDANNMIQCWLAKDGLFLFCYVESLEFRNFRRNYKRVLHYLVLPVELDESPVPORKS
Dd	121	QQIDANNMIQCWLAKDGLFLFCYVESLEFRNFRRNYKRVLHYLVLPVELDESPVPORKS

Accession	Protein	Species	Length (aa)	Source			
Db	121	cgidennwaglcwlgdtkllfcyveslfknlftrnykvhlllylpevlcdsrlvpqkgs	180				
Qy	161	FOVWHNCSEVHCEBCLVVPFPAKLNDTLLMCLKITSGGVEFGYLMSVOPINNVKDDP	240				
Db	161	fgmvcnscsvhceccclvypvtaklndtllmclkitsgvlfksplmsvgplimvxpdp	240				
Qy	241	LGILHEITDDDCNLKISMSPPLYVFPFLQYKYSSENSPTVIRENDKIVSATSLIVDSILP	300				
Db	241	lgllmeitddgnlkiswsspplyvpflqykvysensltvirendkivsatstllvdsllp	300				
Qy	301	GSSYEVQYRGKRLDGPGLMSDMSTPRVFTTDVITYFPFKILTSVGSVSHFHCILYKKNKI	360				
Db	301	gssyevqyrgkrlldgpqglmsdmsprvfttdvityfpfkiltsvgsnshfchlykknkl	360				
Qy	361	VPSKRTVMMMLAKRTIPDSQVDVSDHNSKVTFFNLNETPRGFTVDAYCCNEHECHH	420				
Db	361	vpskrtvmmmlaekltpdsqdvdsdhnskvtflnlnektprgftvdayccnehechh	420				
Qy	421	RYAEELYVDVNIINISCEFDGYLFRMTCKMSTSTQSLAESTLQLRYHRRSSLYCSDIPSIH	480				
Db	421	ryaeelyvdvnlinscetdgylltmtctwststqlsaestllqlyrhrrsslycsdipsih	480				
Qy	461	PISPKDCYLOSDFEYECIFOPFLLSGTYWIRLNHSLGSLDSPRCVLPDSVYKRLRP	540				
Db	461	pisepkdcylsdsdgyecifipflisgtywmirlnhslgslsdprcvcvlpdsvvkrlrp	540				
Qy	541	SSVKAEITINIGLKLISWEKVPFPENNLOFQIRGLSGKEVQWAKMEVYD	590				
Db	541	ssvkaeitinigllkliswekvpfpennlofqirgylsgkevqwmkmyevd	590				
RESULT 28							
AA663999	AAG63999 standard; protein: 213 AA.						
XX	AA663999;						
XX	NC						
XX	26-NOV-2001 (first entry)						
XX	DE						
XX	Amino acid sequence of human CRH.						
KW	Leptin; CRH-Leptin receptor; weight loss; CRH;						
KW	protein co-ordinate data.						
OS	Homo sapiens.						
XX	WO200166593-A1.						
XX	13-SEP-2001.						
XX	05-MAR-2001; 2001WO-JP01666.						
XX	07-MAR-2000; 2000JP-0062404.						
PA	(BIOM-) BIOMOLECULAR ENG RES INST.						
XX	Toh H, Hiroike T, Aritomi M, Kunishima N, Morikawa K;						
XX	WPI; 2001-565574/63.						
CC	The specification describes a three-dimensional (3D) structural coordinate of a complex formed from leptin and a binding domain of its receptor (CRH-leptin receptor). The 3D structural coordinate is applicable in identifying, searching, evaluating or designing leptin mutants with superior biological activity or its agonists and antagonists.						
CC	Example 6: Page 676-677; 683pp; Japanese.						

CC antagonists after mutation or modification, particularly for providing
 CC effect on accurate nuclei, and in inhibiting intake or reducing weight
 CC loss. The present sequence represents a human protein, designated CRH.
 CC The protein is used in the course of the invention.

XX Sequence 213 AA;

Query Match 18.3%; Score 213; DB 22; Length 213;
 Best Local Similarity 100.0%; Pred. No. 2.3e-214;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 ELAYIDVAININISCTEDGYLTMTCTCRWSTSTQSLAEFTLQLRHNSSLYCSPISPIHS 483
 DB 1 elayidvaininiscetdgyltkmtcrwststqslaestlqlyrhnslycsdpslpsl 60
 QY 484 EPKCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDPPTCVLPDSVYKPPSPSSV 543
 DB 61 epkcyldsdfyecifqpfllsgytmirinhslgsldspptcvlpdsvykppspssv 120
 QY 544 KAEITINIGLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLPVDL 603
 DB 121 kaeltiniglkliswekvpfennlqfiryglsgkevqwkmyevdaksksvslpvd 180
 QY 604 CAYAVQYRCRRLDGLGYSMNSNPAYTVMDI 636
 DB 181 cayavqyrcrklldgldgymsnnpaytvm 213

RESULT 29

AAW62545
 ID AAW62545 standard; protein: 235 AA.

XX AAW62545;
 AC AAW62545;
 XX 12-OCT-1998 (first entry)
 DE Soluble leptin binding domain.
 XX ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;
 KW anorexia; cachexia.
 XX Homo sapiens.
 OS
 XX MO9824881-A1.
 PN 11-JUN-1998.
 PD 26-NOV-1997; 97WO-US22165.
 XX 02-DEC-1996; 96US-0032367.
 PR (MERI) MERCK & CO INC.
 XX
 PA Fong TM, Huang RC, Van Der Ploeg L;
 PI WPI; 1998-333304/29.
 DR WPI; 1998-333304/29.
 XX New mutant ob receptor(s) - used to develop products for drug
 PT screening and for gene therapy for weight control, e.g. obesity or
 PT anorexia
 PS Disclosure; Fig 5; 27pp; English.
 XX The ob-receptor (OB-R), a member of the cytokine receptor family is
 CC transcribed in the hypothalamus and is involved in obesity. The
 CC soluble secreted form of leptin binding domain is used in the screening
 CC of OB-R ligands. The leptin agonists identified can be used in
 CC situations where leptin insufficiency causes obesity, diabetes or
 CC infertility. The leptin antagonists identified can be used in the
 CC treatment of anorexia and cachexia. The OB-R mutant receptor nucleic
 CC acids can also be used in gene therapy for weight control, e.g. for
 CC treating obesity or anorexia.

XX Sequence 235 AA;

Query Match 18.3%; Score 213; DB 19; Length 235;
 Best Local Similarity 100.0%; Pred. No. 2.6e-214;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 HRYAEYIDVAININISCTEDGYLTMTCTCRWSTSTQSLAEFTLQLRHNSSLYCSDIPSI 479
 DB 23 hryaelyidvaininiscetdgyltkmtcrwststqslaestlqlyrhnslycsdpsl 82
 QY 480 HPISEPKCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDPPTCVLPDSVYKPPSP 539
 DB 83 hpisepkyldsdfyecifqpfllsgytmirinhslgsldspptcvlpdsvykppsp 142
 QY 540 PSSVAEITINIGLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLP 599
 DB 143 pssvkaeltiniglkliswekvpfennlqfiryglsgkevqwkmyevdaksksvslp 202
 QY 600 VPDLCAYAVQYRCRRLDGLGYSMNSNPAYTV 632
 DB 203 vpdlcayavqyrcrklldgldgymsnnpayt 235

RESULT 30

AAW22106
 ID AAW22106 standard; protein: 805 AA.

XX AAW22106;
 AC AAW22106;
 XX 16-MAR-1998 (first entry)
 DE Murine leptin receptor splice variant OB-Re.
 XX Murine; leptin receptor; OB-R; obesity; diabetes; high blood pressure;
 KW high cholesterol; body weight.
 XX Mus musculus.
 OS
 XX MO9726335-A1.
 PN 24-JUL-1997.
 PD 16-JAN-1997; 97WO-US01010.
 XX 14-FEB-1996; 96US-0599974.
 PR 16-JAN-1996; 96US-0586594.
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 XX
 PI Friedmann JM, Ioffe E, Lee G, Proenca R;
 DR WPI; 1997-38538/35.
 DR N-PSDB; AAT75707.
 XX
 PT Leptin receptor, OB-R, polypeptide - useful to treat obesity,
 PT optionally in conjunction with treatment for diabetes, high blood
 PT pressure and high cholesterol
 PS Claim 16; Page 111-113; 171pp; English.
 XX The present sequence represents a leptin receptor (OB-R) protein, OB-Re.
 CC The OB-R can be used to treat obesity, optionally in conjunction with
 CC a treatment for diabetes, high blood pressure and high cholesterol,
 CC or in cosmetic compositions for reducing body weight. It may also be
 CC used in agriculture to produce leaner food animals, e.g. beef cattle,
 CC swine, poultry, sheep. An antibody specific for OB-R can be used to
 CC measure the presence of OB-R in a sample, optionally in vivo, while the
 CC nucleic acid molecule encoding OB-R can be used to detect defects in the
 CC OB-R polypeptide associated with obese phenotypes, or diagnostically to
 CC measure its encoded RNA and protein in nutritional disorders. The
 CC nucleic acid molecule can be used in gene therapy, or the antisense

CC nucleic acid molecule can be used to antagonise leptin activity. The
 CC nucleic acid molecule, or the antisense nucleic acid molecule, can be
 CC used to treat weight loss e.g. associated with AIDS, cancer or anorexia
 CC nervosa.

CC Sequence 805 AA;

Query Match 3.6%; Score 42; DB 18; Length 805;
 Best Local Similarity 100.0%; Pred. No. 1.5e-34;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 498 fqpifllsgytmwlrlnhslnsglsdspptcvlpdsvvkplpps 539

RESULT 31

AAW22102
 ID AAW22102 standard; Protein; 842 AA.

AC AAW22102;

DT 16-MAR-1998 (first entry)

DE Murine leptin receptor splice variant OB-Ra.

XX Murine leptin receptor; OB-R; obesity; diabetes; high blood pressure;
 XX high cholesterol; body weight.

OS Mus musculus.

XX Key Location/Qualifiers

FT Misc-difference 29 /label= Stop-codon
 FT /note= "encoded by TAG"

XX W09726335-A1.

XX 24-JUL-1997.

XX 16-JAN-1997; 97WO-US01010.

XX 14-FEB-1996; 96US-0509974.
 XX 16-JAN-1996; 96US-0586594.

XX (UYRQ) UNIV ROCKEFELLER.

XX Friedman JM, Ioffe E, Lee G, Proenca R;

XX WPI; 1997-385338/35.

XX N-PSDB; AAT75703.

XX Leptin receptor, OB-R, polypeptide - useful to treat obesity,
 XX optionally in conjunction with treatment for diabetes, high blood
 XX pressure and high cholesterol

XX Disclosure; Page 95-97; 17pp; English.

CC The present sequence represents a leptin receptor (OB-R) protein, OB-Ra.
 CC The OB-R can be used to treat obesity, optionally in conjunction with
 CC a treatment for diabetes, high blood pressure and high cholesterol,
 CC or in cosmetic compositions for reducing body weight. It may also be
 CC used in agriculture to produce leaner food animals, e.g. beef cattle,
 CC swine poultry, sheep. An antibody specific for OB-R can be used to
 CC measure the presence of OB-R in a sample, optionally in vivo, while the
 CC nucleic acid molecule encoding OB-R can be used to detect defects in the
 CC OB-R polypeptide associated with obese phenotypes, or diagnostically to
 CC measure its encoded RNA and protein in nutritional disorders. The
 CC nucleic acid molecule can be used in gene therapy, or the antisense
 CC nucleic acid molecule can be used to antagonise leptin activity. The
 CC nucleic acid molecule, or the antisense nucleic acid molecule, can be
 CC used to treat weight loss e.g. associated with AIDS, cancer or anorexia

CC nervosa.
 XX Sequence 842 AA;

Query Match 3.6%; Score 42; DB 18; Length 842;
 Best Local Similarity 100.0%; Pred. No. 1.6e-34;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 446 fqpifllsgytmwlrlnhslnsglsdspptcvlpdsvvkplpps 487

RESULT 32

AAW34260
 ID AAW34260 standard; Protein; 892 AA.

AC AAW34260;

DT 11-MAY-1998 (first entry)

DE Rat ob receptor isoform c'.

XX Ob receptor isoform c'; obesity; leptin; ligand; rat.

XX Rattus sp.

XX W09742340-A1.

XX 13-NOV-1997.

XX 02-MAY-1997; 97WO-US07521.

XX 24-MAY-1996; 96GB-0010995.

XX 06-MAY-1996; 96US-0016899.

XX (MERI) MERCK & CO INC.

XX Caskey CT, Hess JW, Hey P, Phillips MS;

XX WPI; 1997-558993/51.

XX New isoform(s) of the Ob (leptin) receptor - used for identifying
 XX specific binding ligands, potentially useful for study, prevention
 XX and treatment of obesity

XX Disclosure; Page -: 34pp; English.

CC This protein comprises isoform c' of the rat ob receptor. The ob
 CC receptor has numerous isoforms resulting from alternative splicing;
 CC 3 novel isoforms, designated f, g and c' are disclosed (see
 CC AAW34258-60). Isoform c' differs from the 1162-residue wild-type
 CC protein (see AAW34257) in that after lys-889 there are only 3 amino
 CC acids. The c' isoform can be expressed in host cells, particularly
 CC E. coli, yeast or mammalian cells. It is used to identify specific
 CC binding ligands. Agonists, antagonists and ligand mimetics can be
 CC identified that are potentially useful in the study, prevention and
 CC treatment of obesity.
 CC (NB, the amino acid sequence of isoform c' was produced by
 CC adaptation of the wild-type ob receptor sequence provided in Fig 1
 CC of the specification).

XX Sequence 892 AA;

Query Match 3.6%; Score 42; DB 18; Length 892;
 Best Local Similarity 100.0%; Pred. No. 1.7e-34;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 498 fqpifllsgytmwlrlnhslnsglsdspptcvlpdsvvkplpps 539

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RESULT 33
AAW37338
ID AAW37338 standard; Protein; 894 AA.
XX
AC AAW37338;
XX
DT 07-MAY-1998 (first entry)
XX
DE Ob protein receptor.
XX
KM Ob protein receptor; obese phenotype detection; rat.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 805 /note="encoded by TGT"
FT
XX
PN WO9741217-A1.
XX
PD 06-NOV-1997.
XX
PF 24-APR-1997; 97WO-JP01470.
XX
PR 30-APR-1996; 96JP-0134422.
XX
PA (SAKA ) OTSUKA PHARM CO LTD.
XX
PI Iida M, Kodaira T, Murakami T, Shima K;
XX
DR WPI: 1997-549722/50.
DR N-PSDB: AAT97156.
XX
PT Ob protein receptor gene and variant having cytosine at base 806 -
PT for diagnosis of mutation(s) leading to development of obesity in
PT animals
XX
PS Disclosure; Page 57-62; 71pp; Japanese.
XX
CC This sequence represents the obesity protein receptor of the
CC invention. The gene sequence may be used for screening of warm blooded
CC animals (such as rats) for spontaneous mutations resulting in the variant
CC Ob protein receptor gene which leads to animals having an obese
CC phenotype. These are useful in the study of mechanisms of obesity and the
CC development of anti-obesity drugs.
XX
SQ Sequence 894 AA;

Query Match 3.6%; Score 42; DB 18; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX
FH Key Location/Qualifiers
FT Misc-difference 805 /note="encoded by TGT"
FT
XX
PN WO9741217-A1.
XX
PD 06-NOV-1997.
XX
PF 24-APR-1997; 97WO-JP01470.
XX
PR 30-APR-1996; 96JP-0134422.
XX
PA (SAKA ) OTSUKA PHARM CO LTD.
XX
PI Iida M, Kodaira T, Murakami T, Shima K;
XX
DR WPI: 1997-549722/50.
DR N-PSDB: AAT97149.
XX
PT Ob protein receptor gene and variant having cytosine at base 806 -
PT for diagnosis of mutation(s) leading to development of obesity in
PT animals
XX
PS Claim 1; Page 49-54; 71pp; Japanese.
XX
CC This sequence represents the obesity protein receptor of the
CC invention. The gene sequence may be used for screening of warm blooded
CC animals (such as rats) for spontaneous mutations resulting in the variant
CC Ob protein receptor gene which leads to animals having an obese
CC phenotype. These are useful in the study of mechanisms of obesity and the
CC development of anti-obesity drugs.
XX
SQ Sequence 894 AA;

Query Match 3.6%; Score 42; DB 18; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 38
AAW34258
ID AAW34258 standard: Protein; 895 AA.
XX
XX AAW34258;
AC
XX
XX 11-MAY-1998 (first entry)
DT
XX
XX Rat ob receptor isoform f.
DE
XX Ob receptor isoform f; obesity; leptin; ligand; rat.
XX
XX Rattus sp.
OS
XX
XX W09742340-A1.
XX
XX 13-NOV-1997.
PD
XX
XX 02-MAY-1997; 97WO-US07521.
PF
XX
XX 24-MAY-1996; 96GB-0010995.
PR
XX 06-MAY-1996; 96US-0016899.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Caskey CT, Hess JW, Hey P, Phillips MS;
XX
XX WPI: 1997-558993/51.
DR
XX N-PSDB; AAT93104.
XX
XX New isoform(s) of the Ob (leptin) receptor - used for identifying
PT specific binding ligands, potentially useful for study, prevention
PR and treatment of obesity
XX
XX
XX Disclosure: Page -: 34pp: English.
PS
XX
XX This protein comprises isoform f of the rat ob receptor. The ob
CC receptor has numerous isoforms resulting from alternative splicing;
CC 3 novel isoforms, designated f, g and c' are disclosed (see
CC AAW34258-60). Isoform f differs from the 1162-residue wild-type
CC protein (see AAW34257) in that after Lys-889 there are only 6 amino
CC acids. In the cDNA (see AAT93104), these codons are then followed by
CC a stop codon. The f isoform can be expressed in host cells,
CC particularly E. coli, yeast or mammalian cells. It is used to
CC identify specific binding ligands. Agonists, antagonists and
CC ligand mimetics can be identified that are potentially useful in
CC the study, prevention and treatment of obesity.
CC (NB, the amino acid sequence of isoform f was produced by
CC adaptation of the wild-type ob receptor sequence provided in Fig 1
CC of the specification).
XX
XX
XX Sequence 895 AA:
SQ

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```

Query Match 3.6%; Score 42; DB 18; Length 895;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541
DB 498 fqpiflisytmwlrinhslgsldspptcvlpdsvvkplpps 539

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RESULT 39
AAW22105
ID AAW22105 standard: Protein; 900 AA.
XX
XX AAW22105;
AC
XX
XX 16-MAR-1998 (first entry)
DT
XX

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```

DE Murine leptin receptor splice variant OB-Rd.
XX
XX Murine; leptin receptor; OB-R; obesity; diabetes; high blood pressure;
XX high cholesterol; body weight.
XX
XX Mus musculus.
OS
XX
XX W09726335-A1.
XX
XX 24-JUL-1997.
PD
XX
XX 16-JAN-1997; 97WO-US01010.
PF
XX
XX 14-FEB-1996; 96US-0599974.
PR
XX 16-JAN-1996; 96US-0586594.
XX
XX (UYRQ ) UNITV ROCKEFELLER.
XX
XX Friedman JM, Ioffe E, Lee G, Proenca R;
XX
XX WPI: 1997-38538/35.
DR
XX N-PSDB; AAT75706.
XX
XX Leptin receptor, OB-R, polypeptide - useful to treat obesity,
PT optionally in conjunction with treatment for diabetes, high blood
PR pressure and high cholesterol
XX
XX
XX Disclosure: Page 105-109; 171pp: English.
PS
XX
XX The present sequence represents a leptin receptor (OB-R) protein, OB-Rd.
CC The OB-R can be used to treat obesity, optionally in conjunction with
CC a treatment for diabetes, high blood pressure and high cholesterol,
CC or in cosmetic compositions for reducing body weight. It may also be
CC used in agriculture to produce leaner food animals, e.g. beef cattle,
CC swine poultry, sheep. An antibody specific for OB-R can be used to
CC measure the presence of OB-R in a sample, optionally in vivo, while the
CC nucleic acid molecule encoding OB-R can be used to detect defects in the
CC OB-R polypeptide associated with obese phenotypes, or diagnostically to
CC measure its encoded RNA and protein in nutritional disorders. The
CC nucleic acid molecule can be used in gene therapy, or the antisense
CC nucleic acid molecule can be used to antagonise leptin activity. The
CC nucleic acid molecule, or the antisense nucleic acid molecule, can be
CC used to treat weight loss e.g. associated with AIDS, cancer or anorexia
CC nervosa.
XX
XX
XX Sequence 900 AA:
SQ

```

```

Query Match 3.6%; Score 42; DB 18; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541
DB 498 fqpiflisytmwlrinhslgsldspptcvlpdsvvkplpps 539

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RESULT 40
AAW34259
ID AAW34259 standard: Protein; 1015 AA.
XX
XX AAW34259;
AC
XX
XX 11-MAY-1998 (first entry)
DT
XX
XX Rat ob receptor isoform g.
DE
XX
XX Ob receptor isoform g; obesity; leptin; ligand; rat.
XX
XX Rattus sp.
OS
XX
XX W09742340-A1.
XX

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XX PA (MERI ) MERCK & CO INC.
XX PI Caskey CT, Hess JW, Liu Q, Phillips MS;
XX DR WPI: 1997-435085/40.
XX DR N-PSDB: AAT64962.
XX PT Rat wild-type and mutant ob receptor protein - useful in
XX PT identification of new ligands for prevention and treatment of
XX PT obesity
XX PS Claim 4; Page -: 35pp; English.
XX CC This protein comprises the rat fatty (fa) mutant ob receptor
XX CC (OB-R). Its amino acid sequence was deduced from a cDNA sequence
XX CC (see AAT64962) obtained by PCR amplifications. The sequence differs
XX CC at only 1 position from the wild-type (i.e. lean) OB-R sequence;
XX CC the fa OB-R mutant receptor has proline at amino acid 269 rather
XX CC than glutamine (see AAW23398). This is a result of an A to C
XX CC transversion in the fa OB-R gene (see AAT64962). Every tissue
XX CC examined in an fa/fa Zucker rat was homozygous for this mutation.
XX CC The wild-type and mutant OB-R can be expressed in prokaryotic or
XX CC eukaryotic host cells. They are useful in assays to identify or
XX CC putative ligands, which may be receptor agonists or antagonists or
XX CC bind with little effect, and which may be useful in understanding
XX CC obesity and for its prevention and treatment.
XX CC (NB. the sequence for the fa OB-R was obtained by adapting the
XX CC sequence of wild-type OB-R provided in Fig 1 of the specification).
XX SQ Sequence 1162 AA:

Query Match 3.6%; Score 42; DB 18; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMIRINHSLSGSDSPPTCVLPDVSVKPLPPS 541
DB 498 fgpfiflsgytmirinhslsgsdspptcvlpdsvkplpps 539

RESULT 43
AAW23398
ID AAW23398 standard; Protein; 1162 AA.
AC AAW23398;
XX
XX 23-FEB-1998 (first entry)
DT
XX
XX Rat ob receptor (wild-type).
DE
XX
XX Ob receptor; obesity; leptin; rat; rodent; animal model; ligand;
KW fatty; fa mutation; therapy.
XX
XX Rattus sp.
OS
XX
XX
XX Key Location/Qualifiers
XX FH 1..28
XX FT /label= Sig_peptide
XX FT 29..1162
XX FT Protein
XX FT /label= Mat_protein
XX FT 29..830
XX FT Domain
XX FT /label= Extracellular_domain
XX FT 839..860
XX FT /label= Transmembrane_domain
XX FT /note= "6"
XX FT 860..1162
XX FT Domain
XX FT /label= Cytoplasmic_domain
XX FT 269
XX FT /note= "site of mutation in fa OB-R"
XX
XX W09731015-A1.

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XX PD 28-AUG-1997.
XX PF 18-FEB-1997; 97MO-US02397.
XX PR 25-APR-1996; 96GB-0008473.
XX PR 22-FEB-1996; 96US-0090405.
XX PR 22-MAR-1996; 96US-0013969.
XX PA (MERI ) MERCK & CO INC.
XX PI Caskey CT, Hess JW, Liu Q, Phillips MS;
XX DR WPI: 1997-435085/40.
XX DR N-PSDB: AAT64961.
XX PT Rat wild-type and mutant ob receptor protein - useful in
XX PT identification of new ligands for prevention and treatment of
XX PT obesity
XX PS Claim 5; Fig 1A-1B; 35pp; English.
XX CC This protein comprises rat wild-type (i.e. lean) ob receptor
XX CC (OB-R). Its amino acid sequence was deduced from a cDNA sequence
XX CC (see AAT64961) obtained by PCR amplifications. The sequence differs
XX CC at only 1 position from the OB-R sequence from rats with a fatty
XX CC (fa) mutation; the fa OB-R mutant receptor has proline at amino
XX CC acid 269 rather than glutamine (see AAW23398). This is a result of
XX CC an A to C transversion in the fa OB-R gene (see AAT64962). Every
XX CC tissue examined in an fa/fa Zucker rat was homozygous for this
XX CC mutation. The wild-type and mutant OB-R can be expressed in
XX CC prokaryotic or eukaryotic host cells. They are useful in assays to
XX CC identify putative ligands, which may be receptor agonists or
XX CC antagonists or bind with little effect, and which may be useful in
XX CC understanding obesity and for its prevention and treatment.
XX SQ Sequence 1162 AA:

Query Match 3.6%; Score 42; DB 18; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMIRINHSLSGSDSPPTCVLPDVSVKPLPPS 541
DB 498 fgpfiflsgytmirinhslsgsdspptcvlpdsvkplpps 539

RESULT 44
AAW19115
ID AAW19115 standard; Protein; 1162 AA.
AC AAW19115;
XX
XX 26-AUG-1997 (first entry)
DT
XX
XX Murine long form Ob receptor.
DE
XX
XX Ob receptor; OBR; cytokine receptor; signal transduction;
KW eating disorder; obesity; cachexia; anorexia; bulimia; diagnosis;
XX therapy.
XX
XX Mus musculus.
OS
XX
XX
XX Key Location/Qualifiers
XX FH 1..22
XX FT /label= Sig_peptide
XX FT 23..837
XX FT Domain
XX FT /label= ECD
XX FT /note= "extracellular domain"
XX FT 838..860
XX FT Domain
XX FT /label= TMD
XX FT /note= "transmembrane domain"
XX
XX

```


XX	The invention provides a method for identifying modulators of binding of
CC	a phosphorylated leptin receptor with tyrosine phosphatase 1D PTP-1D).
CC	The method comprises: (a) contacting a tyrosine-985 phosphorylated Leptin
CC	receptor or its phosphorylated fragment with protein PTP-1D or its
CC	fragment in the presence and absence of a candidate agent under
CC	conditions in which the absence of the agent the binding of the
CC	phosphorylated leptin receptor or fragment with PTP-1D or its fragment
CC	can be detected; and (b) detecting the binding of the phosphorylated
CC	leptin receptor and PTP 1D; where an increase in binding detected in the
CC	presence of the agent, indicates that the agent enhances binding, and a
CC	decrease in binding in the presence of the agent indicates that the agent
CC	is a binding inhibitor. Modulators of tyrosine-985-phosphorylated Leptin
CC	receptor-dependent PTP-1D phosphorylation are useful as drugs in weight
CC	loss diet regimens. The drugs identified can regulate adiposity and fat
CC	content of animals, particularly in mammals. Disorders that can be
CC	treated by PTP-1D modulators include obesity and its associated diseases,
CC	e.g. hypertension, heart disease and type II diabetes, and weight loss
CC	associated with cancer and AIDS. Additionally the agents identified may
CC	be useful in agriculture where body weight of domestic animals can be
CC	modulated.
SQ	Sequence 1162 AA:
OY	Query Match 3.6%; Score 42; DB 20; Length 1162;
Db	Best Local Similarity 100.0%; Pred. No. 2,2e-34;
	Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	500 FQPIFLSGYTWMIRINHSGLSDSPPCVDPDYVKPLPPS 541
	fqpiflslsgytcwfrimhsigsldspcvcvdpdyvvkplpps 539
RESULT 46	
ID AAE12615	
AAE12615 standard; Protein: 1162 AA.	
AC AAE12615;	
XX	
DT 03-JAN-2002 (first entry)	
XX	
DE Murine long form Ob receptor (OBR) protein.	
XX	
KW Murine; obese receptor; Ob; anorectic; anabolic; body weight disorder;	
KM therapy; obesity; cachexia; anorexia.	
XX	
OS Mus sp.	
XX	
FH Key	Location/Qualifiers
FT Peptide	1..22
FT Protein	/label-Signal_peptide
FT Domain	23..1162
FT Domain	/label-Murine_mature_short_form_OBR_protein
FT Domain	23..837
FT Domain	/label-Extracellular_domain
FT Domain	838..860
FT Domain	/label-Transmembrane_domain
FT Domain	861..1162
FT Domain	/label-Cytoplasmic_domain
XX	
US6287782-B1.	
XX	
PD 11-SEP-2001.	
XX	
PF 29-APR-1998;	980S-0069781.
XX	
PR 27-NOV-1995;	950S-0562663.
PR 04-DEC-1995;	950S-0566622.
PR 08-DEC-1995;	950S-0569485.
PR 11-DEC-1995;	950S-0570142.
PR 28-DEC-1995;	950S-0583153.
PR 22-JAN-1996;	960S-0599455.

PR	26-APR-1996;	96US-0638524.	
PR	03-SEP-1996;	96US-0708123.	
PR	28-MAY-1997;	97US-0864564.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Tartaglia LA, Tepper RI, Cuipepper JA, White DW;		
XX			
DR	WPI: 2001-624489/72.		
XX	N-PSTDB; AAD20541.		
PT			
PT	Identifying compounds for treating body weight disorder, e.g. obesity,		
PT	anorexia or cachexia, comprising contacting cell expressing mammalian Ob		
XX	receptor protein, JAK2 protein and mammalian SOCS-1 protein with test		
XX	compound		
PS			
PS	Disclosure: Fig 6; 109pp; English;		
XX			
CC	The patent discloses obese receptor (Obr) proteins and nucleic acids		
CC	encoding them. Obr protein participates in the regulation of mammalian		
CC	body weight. The invention also relates to a method of identifying		
CC	therapeutic compounds for the treatment of a body weight disorder.		
CC	The method involves contacting a cell that expresses a mammalian Obr		
CC	protein, a JAK2 protein and a mammalian SOCS-1 protein with a test		
CC	compound. The method is useful for identifying compounds which modulate		
CC	Obr gene expression and gene product activity, which can be used as		
CC	agents to control body weight particularly as therapeutic agents for		
CC	treating body weight disorders, including obesity, cachexia and anorexia.		
CC	The present sequence is murine long form Obr protein.		
XX			
SO	Sequence 1162 AA;		
XX			
Query Match	3.6%; Score 42; DB 22; Length 1162;		
Best Local Similarity	100.0%; Pred. No. 2.2e-34;		
Matches 42:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	500 RQPIFLSLGYTMWIRINHSLSGLSDSPPTCYLPDSVYKPLPPS 541		
Db	498 IqPIfILSLGYTMWIRINHSLSGLSDSPPTCYLPDSVYKPLPPS 539		
XX			
RESULT 47			
AAW24054			
XX	AAW24054 standard; Protein: 783 AA.		
AC	AAW24054;		
XX			
DT	17-MAR-1998 (first entry)		
XX			
DE	Murine MSX receptor extracellular domain.		
XX			
KW	Murine; MSX receptor; mouse; identification; purification;		
KW	ligand; activator; antibody; agonist; proliferation; obesity;		
KW	differentiation; anemia; treatment; neoplasia; arteriosclerosis;		
KW	Type II diabetes; polycystic ovarian disease;		
KW	cardiovascular disease; osteoarthritis; dermatological disorder;		
KW	hypertension; insulin resistance; hypercholesterolaemia;		
KW	hypertiglyceridaemia; cancer; cholesterolstasis.		
XX			
OS	Mus sp.		
XX			
PN	WO9725425-A1.		
XX			
PD	17-JUL-1997.		
XX			
XX	07-JAN-1997; 97WO-US00325.		
XX			
XX	20-JUN-1996; 96US-0667197.		
PR	08-JAN-1996; 96US-0585005.		
XX			
PA	(GETH) GENENTECH INC.		
XX			

PT Peptide(s) derived from a cell surface receptor extracellular domain
 PT - correspond to the internalisation sequence, modulate
 PT internalisation of cell surface receptors, for treating disease with
 PT reduced hormone sensitivity
 XX
 PS Claim 12: Page 23: 37pp; English.
 XX
 CC The present leptin internalisation sequence receptor fragment, was
 CC used in the preparation of a novel oligopeptide. The oligopeptide
 CC comprises an internalisation domain of 8-40 amino acids having a
 CC sequence corresponding to the extracellular domain of a cell
 CC surface receptor, where the oligopeptide enhances the effect of
 CC ligand binding to the receptor expressed by a cell. The
 CC oligopeptide and cell can be used to screen for bioactive agents
 CC capable of modulating the internalisation of a cell surface
 CC receptor. Internalisation sequences of the extracellular domains of
 CC receptor inhibit internalisation of the receptor, but do not affect
 CC binding of the ligand. Inhibition of receptor internalisation
 CC results in more receptors at the cell surface to bind the ligand,
 CC i.e. an increase in ligand binding effectiveness. The increase in
 CC ligand signalling is useful for treating diseases where hormone
 CC sensitivity is reduced, e.g. non-insulin dependent diabetes
 CC mellitus (NIDDM).
 XX
 SQ Sequence 23 AA;
 XX

Query Match 2.0%; Score 23; DB 18; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.9e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 KKENKIYPSKEIYWMNMLAEKIP 377
 DB 1 kkenkiypskeiywmmlaekip 23

RESULT 50
 AAY39406
 ID AAY39406 standard; peptide: 23 AA.
 XX
 AC AAY39406;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human leptin receptor-derived activation peptide.
 XX
 KM Leptin; receptor; activation; internalisation; obesity.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO942127-A2.
 XX
 PD 26-AUG-1999.
 XX
 PF 23-FEB-1999; 99MO-US03910.
 XX
 PR 24-FEB-1998; 98US-0028938.
 XX
 PA (RECE-) RECEPTRON INC.
 XX
 PI Olsson L, Naranda T;
 XX
 DR WPI; 1999-527422/44.
 XX
 PT Modulating activity of type-2 cell surface receptors used in treatment
 PT of, e.g. obesity -
 XX
 PS Claim 8: Page 17: 92pp; English.
 XX
 CC This sequence represents a peptide derived from the extracellular
 CC activation sequence of the human leptin receptor.
 CC Activation sequences are involved in modulation of receptor

CC responses and are separate from the ligand binding site. Activation
 CC sequences are important in two distinct ways: in the modulation of
 CC receptor internalisation; and/or in the modulation of activation of the
 CC receptor. Use of peptides corresponding to the activation sequence of a
 CC receptor can retard or inhibit receptor internalisation, thereby
 CC increasing or stabilising the steady-state number of active receptors on
 CC the cell surface. This has the effect of increasing signalling per unit
 CC of ligand. In addition, the receptor is classed as a type 2 cell surface
 CC receptor, meaning that such peptides can actually replace the requirement
 CC for the ligand, causing ligand-independent activation. This activation is
 CC probably brought about by a dimerisation mechanism in which one peptide
 CC molecule is bound by two receptors, mimicking the dimerisation and
 CC subsequent activation that occurs when two receptors bind one ligand.
 CC This peptide could be used to treat disorders involving an inadequate
 CC or inappropriate response from its corresponding receptor e.g., obesity.
 XX

SQ Sequence 23 AA;
 XX

Query Match 2.0%; Score 23; DB 20; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.9e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 KKENKIYPSKEIYWMNMLAEKIP 377
 DB 1 kkenkiypskeiywmmlaekip 23

Search completed: May 18, 2002, 07:03:58
 Job time: 532 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 07:02:01 ; Search time 124.34 Seconds

(without alignments)
3297,872 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 1165

Sequence: 1 MICOQFCVVLHMEFIYIT.....QTCSTQFKIMKNKMDLTV 1165

Scoring table: OLIGO

Searched: 3502263 seqs, 351980561 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database: Pending Patents_AA.Main:*

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2: /cgn2_6/ptodata/1/paa/US06.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1165	100.0	US-08-570-142D-4	Sequence 4, Appli
2	1165	100.0	US-08-583-153A-4	Sequence 4, Appli
3	1165	100.0	US-08-585-005-2	Sequence 2, Appli
4	1165	100.0	US-08-638-524B-4	Sequence 4, Appli
5	1165	100.0	US-08-667-197-2	Sequence 2, Appli
6	1165	100.0	US-08-708-123D-4	Sequence 4, Appli
7	1165	100.0	US-08-779-457-2	Sequence 2, Appli

8	1165	100.0	US-08-780-562-2	Sequence 2, Appli
9	1165	100.0	US-09-094-410-4	Sequence 4, Appli
10	1165	100.0	US-09-137-132-4	Sequence 4, Appli
11	1165	100.0	US-09-950-149-4	Sequence 4, Appli
12	1165	100.0	US-08-774-414-7	Sequence 7, Appli
13	1165	100.0	US-09-671-049-7	Sequence 7, Appli
14	1165	91.3	US-08-599-974C-56	Sequence 56, Appli
15	1165	91.3	US-08-713-296-11	Sequence 11, Appli
16	1165	91.3	US-08-961-809-4	Sequence 4, Appli
17	1165	91.3	US-09-178-691-4	Sequence 4, Appli
18	1165	91.3	US-09-700-113-10	Sequence 10, Appli
19	1165	91.3	US-09-948-933-256	Sequence 256, App
20	1165	91.3	US-09-948-947-73	Sequence 73, Appli
21	1165	91.3	US-10-095-929-11	Sequence 11, Appli
22	1165	91.3	US-08-583-153-4	Sequence 4, Appli
23	1165	91.3	US-08-599-455A-4	Sequence 4, Appli
24	1165	91.3	US-08-638-524A-4	Sequence 4, Appli
25	1165	91.3	US-08-708-123C-4	Sequence 4, Appli
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27	1165	91.3	US-10-079-625-4	Sequence 4, Appli
28	1165	91.3	US-09-948-933-284	Sequence 284, App
29	1165	91.3	US-08-570-142B-4	Sequence 4, Appli
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32	1165	91.3	US-08-582-825A-1	Sequence 1, Appli
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34	1165	91.3	US-08-667-197-3	Sequence 3, Appli
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36	1165	91.3	US-08-780-562-3	Sequence 3, Appli
37	1165	91.3	US-08-582-825-5	Sequence 5, Appli
38	1165	91.3	US-08-667-197-4	Sequence 4, Appli
39	1165	91.3	US-08-779-457-4	Sequence 4, Appli
40	1165	91.3	US-08-780-562-4	Sequence 4, Appli
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44	1165	91.3	US-08-582-825-5	Sequence 5, Appli
45	1165	91.3	US-08-582-825A-5	Sequence 5, Appli
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49	1165	91.3	US-08-671-049-6	Sequence 6, Appli
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53	1165	91.3	US-08-671-049-3	Sequence 3, Appli
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56	1165	91.3	US-08-569-485-4	Sequence 4, Appli
57	1165	91.3	US-08-774-414-13	Sequence 13, Appli
58	1165	91.3	US-09-116-676-10	Sequence 10, Appli
59	1165	91.3	US-08-671-049-13	Sequence 13, Appli
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61	1165	91.3	US-08-595-405-2	Sequence 2, Appli
62	1165	91.3	US-08-713-296-10	Sequence 10, Appli
63	1165	91.3	US-09-357-914-33	Sequence 33, Appli
64	1165	91.3	US-10-095-929-10	Sequence 9, Appli
65	1165	91.3	US-08-713-296-9	Sequence 9, Appli
66	1165	91.3	US-09-357-914-32	Sequence 32, Appli
67	1165	91.3	US-10-095-929-9	Sequence 9, Appli
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70	1165	91.3	US-08-589-915A-3	Sequence 3, Appli
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74	1165	91.3	US-08-982-430-2	Sequence 2, Appli
75	1165	91.3	US-08-588-189-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-08-570-142D-4
: Sequence 4, Application US/08570142D
: GENERAL INFORMATION:
: APPLICANT: Tartaglia, Louis A.
: APPLICANT: Tepper, Robert I.
: APPLICANT: Culpepper, Janice A.
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
: TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: US
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/570,142D
: FILING DATE: 11-DEC-1995
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/569,485
: FILING DATE: 08-DEC-1995
: APPLICATION NUMBER: 08/566,622
: FILING DATE: 04-DEC-1995
: APPLICATION NUMBER: 08/562,663
: FILING DATE: 27-NOV-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Melkielejohn, Ph.D., Anita L.
: REGISTRATION NUMBER: 35,283
: REFERENCE/DOCKET NUMBER: 07334/014001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-542-5070
: TELEFAX: 617-542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: FRAGMENT TYPE: Internal
: US-08-570-142D-4

Query Match      100.0%: Score 1165; DB 9; Length 1165;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 RYAEIYDIVNINISCEGTGYLTKMCRWSTSTIGSLASTTOLKXHRASLCSDPISIH 480
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Db 661 TLIMKPLMKNDLSQVQRYVINHHSTSCNGTSEEDGNHTKFTPLATEQAHVYVLAINSI 720
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Db 781 GEIKMLRISSVKKYIHDHFIPIEKYQSLPIFMEGYCKPKIINSFTODDIEKHQSDA 840
Qy 841 GLYIVIPYIISILLGLTLLISHQMKLEEDVDPNPKCSAQAOLNOKRETEHLEFI 900
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RESULT 2
US-08-583-153A-4
: Sequence 4, Application US/08583153A
: GENERAL INFORMATION:
: APPLICANT: Tartaglia, Louis A.
: APPLICANT: Tepper, Robert I.
: APPLICANT: Culpepper, Janice A.
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
: TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING

```

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NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583.153A
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/570.142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569.485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566.622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562.663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melk1eJohn, Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/016001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-583-153A-4

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Query Match 100.0%; Score 1165; DB 9; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 VPSKRIYMMNLAEKIPSOVDYSDHYSKYTFENLNKPKRGKTTYDAVYCCNHECH 420
DB 361 VPSKRIYMMNLAEKIPSOVDYSDHYSKYTFENLNKPKRGKTTYDAVYCCNHECH 420

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DB 421 RYAEIYVIDVINISCEFDGYLTAKTCRWSTSTIOSLAESTQLRYHRSLSYCDIPSI 480
QY 481 PISEPKDCYOSDGFYECIFPFIILSGTMMIRINHSLSGLSPPTCYLPDSVYKPL 540
DB 481 PISEPKDCYOSDGFYECIFPFIILSGTMMIRINHSLSGLSPPTCYLPDSVYKPL 540
QY 541 SVKAEITINIGLKIISMEKRPVPENNILOFQIRYGLSGREVQMKRYEYDASKSVSL 600
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QY 841 GLYIVPVIYISSILLGLILSHQRMKLFMEDVNPKNCSMAOGLNOKPETHFLTI 900
DB 841 GLYIVPVIYISSILLGLILSHQRMKLFMEDVNPKNCSMAOGLNOKPETHFLTI 900
QY 901 KKTASVTCGPLLPEPTISEDIVSTSMKNKDEMMPTVYVSLSTTDLKSGVCSIDQPN 960
DB 901 KKTASVTCGPLLPEPTISEDIVSTSMKNKDEMMPTVYVSLSTTDLKSGVCSIDQPN 960
QY 961 SVNFSAEGETEYVDESGQRPVYATLISNSKPSSETGEEOGLINSSVYKCFSSKNSPL 1020
DB 961 SVNFSAEGETEYVDESGQRPVYATLISNSKPSSETGEEOGLINSSVYKCFSSKNSPL 1020
QY 1021 KDSFNSSWELIAQAFILISDQHPNIIISPHLTFSELDLLEGFPEENNDRKSIYYL 1080
DB 1021 KDSFNSSWELIAQAFILISDQHPNIIISPHLTFSELDLLEGFPEENNDRKSIYYL 1080
QY 1081 GYTSIKKRESGYLLDPKSVSCPPFAPCLFTDIRVLQDSCHFVENNIMLGTSKRTFAS 1140
DB 1081 GYTSIKKRESGYLLDPKSVSCPPFAPCLFTDIRVLQDSCHFVENNIMLGTSKRTFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

```

RESULT 3
 US-08-585-005-2
 : Sequence 2, Application US/08585005
 : GENERAL INFORMATION:
 : APPLICANT: Matthews, William
 : APPLICANT: Bennett, Brian
 : TITLE OF INVENTION: WSX RECEPTOR
 : NUMBER OF SEQUENCES: 45
 : CORRESPONDENCE ADDRESS:
 : ADDRESSSEE: Genentech, Inc.
 : STREET: 460 point San Bruno Blvd
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
 : COMPUTER: IBM PC compatible

```

: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/585.005
: FILING DATE: 08-Jan-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0986
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELETYPE: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
: US-08-585-005-2

```

```

Query Match      100.0%; Score 1165; DB 9; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MICQFCVLLHMEFIYTAFAFLSYPTTPMRFKLSMPNSTYDFLLPAGLSKNTS 60
DB 1 MICQFCVLLHMEFIYTAFAFLSYPTTPMRFKLSMPNSTYDFLLPAGLSKNTS 60
QY 61 NGHYFAVEPRKNSGTHFSNLSKTFHCCFSEODRNSLCADNIEGTFVSTNSLYF 120
DB 61 NGHYFAVEPRKNSGTHFSNLSKTFHCCFSEODRNSLCADNIEGTFVSTNSLYF 120
QY 121 QCIDANMNIOQWLKAGDLKFLICYVESLEFNLEFRNRYKAYHLLYVPEVLEDSPLYPOKGS 180
DB 121 QCIDANMNIOQWLKAGDLKFLICYVESLEFNLEFRNRYKAYHLLYVPEVLEDSPLYPOKGS 180
QY 181 FOMVHNCNSVHECCCLVLPVPTAKINDTLMLCKITSGGVIFQSPILMSVOPINMVKPDP 240
DB 181 FOMVHNCNSVHECCCLVLPVPTAKINDTLMLCKITSGGVIFQSPILMSVOPINMVKPDP 240
QY 241 LGHMEITDDGGLKISWSSPPLVPPLOYQVYSNSTVIREAKIVSATSLVDSILP 300
DB 241 LGHMEITDDGGLKISWSSPPLVPPLOYQVYSNSTVIREAKIVSATSLVDSILP 300
QY 301 GSSYEVOVRGKRDLPGIWSMDSTPRVFTQDVIYFPRKILTSVGSNVSFHC1YKKENKI 360
DB 301 GSSYEVOVRGKRDLPGIWSMDSTPRVFTQDVIYFPRKILTSVGSNVSFHC1YKKENKI 360
QY 361 VPSKEIVMMNIAEKIPOSQYVSDHVSQVTFENLNETKPRGKFTYDAVTCNEHECHH 420
DB 361 VPSKEIVMMNIAEKIPOSQYVSDHVSQVTFENLNETKPRGKFTYDAVTCNEHECHH 420
QY 421 RAEELYVIDVININISCETDGYLTKMTCRMSTSTIOSLAESTIQLRYHNSLSYCSIPSH 480
DB 421 RAEELYVIDVININISCETDGYLTKMTCRMSTSTIOSLAESTIQLRYHNSLSYCSIPSH 480
QY 481 PISEPKDCYLOSDFYECIFQPIFLLSGYTMIRINHSIGSLDSPPTCVLPDVSVPKPLPP 540
DB 481 PISEPKDCYLOSDFYECIFQPIFLLSGYTMIRINHSIGSLDSPPTCVLPDVSVPKPLPP 540
QY 541 SSVKAEITINIGLKLISMEKPYFPENNLOFOIRGLSGKEVQWKMYEYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLKLISMEKPYFPENNLOFOIRGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVOVRCKRLDGLGYSNMSNPAYTVVMDIKVPMRGPEEVRRIINGDTMKKENV 660
DB 601 PDLCAVYAVOVRCKRLDGLGYSNMSNPAYTVVMDIKVPMRGPEEVRRIINGDTMKKENV 660
QY 661 TLLMKPRLKNDLSGVQRYVINHHTSCNGTSESDGNTKFTFLTEQAHNTVYLAINSI 720
DB 661 TLLMKPRLKNDLSGVQRYVINHHTSCNGTSESDGNTKFTFLTEQAHNTVYLAINSI 720

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```

QY 721 GASVANFNLTESWPMKSVNIYOSLAYSAPLNSSCVIVSWILSPSDYKLMYFIEMKNLMD 780
DB 721 GASVANFNLTESWPMKSVNIYOSLAYSAPLNSSCVIVSWILSPSDYKLMYFIEMKNLMD 780
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQSLYPIRMEGVGAKRIINSTFODDIEKHQSDA 840
DB 781 GEIKWLRISSSVKRYIHDHFIPIEKYQSLYPIRMEGVGAKRIINSTFODDIEKHQSDA 840
QY 841 GLYIVIPVYISSILLGLTLLISHORMKLFEDVDPNPNKCSMAOGLNFORPETFENLPT 900
DB 841 GLYIVIPVYISSILLGLTLLISHORMKLFEDVDPNPNKCSMAOGLNFORPETFENLPT 900
QY 901 KHTASVTCGPLLEPETISEDIVDTSMKKNKDEMPPTVYSLSTTDEKSGVCISDQFN 960
DB 901 KHTASVTCGPLLEPETISEDIVDTSMKKNKDEMPPTVYSLSTTDEKSGVCISDQFN 960
QY 961 SYNFEAEGETEYTYDESGROPFVYKATLISKRSCEGEEOGLINSSVTKCFSSKNSPL 1020
DB 961 SYNFEAEGETEYTYDESGROPFVYKATLISKRSCEGEEOGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIQAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIYVL 1080
DB 1021 KDSFNSNSWEIQAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIYVL 1080
QY 1081 GVTSIKRRREGVLLTDKRSVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
DB 1081 GVTSIKRRREGVLLTDKRSVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
QY 1141 YMPOFOTCSTOTHKIMENKMDLTV 1165
DB 1141 YMPOFOTCSTOTHKIMENKMDLTV 1165

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RESULT 4
US-08-638-524B-4
: Sequence 4, Application US/08638524B
:
: GENERAL INFORMATION:
: APPLICANT: Tartaglia, Louis A.
: APPLICANT: Tepper, Robert I.
: APPLICANT: Culpepper, Janice A.
: APPLICANT: White, David W.
: TITLE OF INVENTION: THE OR RECEPTOR AND METHODS FOR THE
: TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: US
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/638,524B
: FILING DATE: 26-APR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/599,455
: FILING DATE: 22-JAN-1996
: APPLICATION NUMBER: 08/583,153
: FILING DATE: 28-DEC-1995
: APPLICATION NUMBER: 08/570,142
: FILING DATE: 11-DEC-1995
: APPLICATION NUMBER: 08/569,485
: FILING DATE: 08-DEC-1995
: APPLICATION NUMBER: 08/566,622
: FILING DATE: 04-DEC-1995
: APPLICATION NUMBER: 08/562,663

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: FILING DATE: 27-NOV-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Melkjohn, Pn.D., Anita L.
: REGISTRATION NUMBER: 35,283
: REFERENCE/DOCKET NUMBER: 07334/018001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-542-5070
: TELEFAX: 617-542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: FRAGMENT TYPE: Internal
: US-08-638-524B-4

Query Match      100.08; Score 1165; DB 10; Length 1165;
Best Local Similarity 100.08; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MICOECVALLHMERIVYITAFNLSTYPTMPERKLSGMPNSTYDYLPAKLSKNTS 60
Db 1 MICOECVALLHMERIVYITAFNLSTYPTMPERKLSGMPNSTYDYLPAKLSKNTS 60
Oy 61 NGHYETAPEPKFNSGTFNSLSTKTFHCFCSEODRNCSLCADNIEGTFSTNSLVE 120
Db 61 NGHYETAPEPKFNSGTFNSLSTKTFHCFCSEODRNCSLCADNIEGTFSTNSLVE 120
Oy 121 QOIDANNNIQCWLKGDGLKFLICYVESLEFKNLFRNTNKKVHLVLEVEDSPLVPQKS 180
Db 121 QOIDANNNIQCWLKGDGLKFLICYVESLEFKNLFRNTNKKVHLVLEVEDSPLVPQKS 180
Oy 181 FOMVHCNCSVEHCCGCLVPVPTAKINDTLMLGKLTSGSVTFOSPMSQPIINMKPDP 240
Db 181 FOMVHCNCSVEHCCGCLVPVPTAKINDTLMLGKLTSGSVTFOSPMSQPIINMKPDP 240
Oy 241 LGLHMEITDDGKLTSMSSPPLVPEPLOYOVKSENSSTTVIREADKIVATSLLVDSILP 300
Db 241 LGLHMEITDDGKLTSMSSPPLVPEPLOYOVKSENSSTTVIREADKIVATSLLVDSILP 300
Oy 301 GSSYEVQVGRKRLDGPGLMSDMSSTPRVFTQDVIYFPKILTSVGSNSFHCIYKKENKI 360
Db 301 GSSYEVQVGRKRLDGPGLMSDMSSTPRVFTQDVIYFPKILTSVGSNSFHCIYKKENKI 360
Oy 361 VPSKEIYVMMNLAEKIPQSOYDVSDHYSKVFENLNETKPRGKFTYDAVVCNEHECHH 420
Db 361 VPSKEIYVMMNLAEKIPQSOYDVSDHYSKVFENLNETKPRGKFTYDAVVCNEHECHH 420
Oy 421 RYAEIYVIDVNNINISGCTDGYLTMTCKMSTSTIOSLAESTLQLRHRSLSXCSIDPSIH 480
Db 421 RYAEIYVIDVNNINISGCTDGYLTMTCKMSTSTIOSLAESTLQLRHRSLSXCSIDPSIH 480
Oy 481 PISEPKDCYLOSDFYECIFQPIFLISGYTMMIRINHSLGSLDSDPPTCVLPDSVVKPLDP 540
Db 481 PISEPKDCYLOSDFYECIFQPIFLISGYTMMIRINHSLGSLDSDPPTCVLPDSVVKPLDP 540
Oy 541 SSVKAEITINIGLTKISWKEPVEPENNLOFOIRYGLSGKEVQMKWEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLTKISWKEPVEPENNLOFOIRYGLSGKEVQMKWEYVDAKSKSVSLPV 600
Oy 601 PDLCAVYAVQVCKRLDGLGYWNSMNSPAYVMDIKYMRGPEFWRILNGDTMKKEKNV 660
Db 601 PDLCAVYAVQVCKRLDGLGYWNSMNSPAYVMDIKYMRGPEFWRILNGDTMKKEKNV 660
Oy 661 TLAKPPLKNDKSLCQVQYVYVNHHTSCNCTWSEEDVGNHTKFTFLTEQAHYTVVLAINSI 720
Db 661 TLAKPPLKNDKSLCQVQYVYVNHHTSCNCTWSEEDVGNHTKFTFLTEQAHYTVVLAINSI 720
Oy 721 GASVANFNLTFSWPMKSVIYQSLAYPLNSSCVIYSWILSSDYKLMVFIEEMKRLNED 780
Db 721 GASVANFNLTFSWPMKSVIYQSLAYPLNSSCVIYSWILSSDYKLMVFIEEMKRLNED 780

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Db 721 GASVANFNLTFSWPMKSVIYQSLAYPLNSSCVIYSWILSSDYKLMVFIEEMKRLNED 780
Oy 781 GEIKMLRISSSVKYYIHDHFIPIEKYQSLVPIMVEGYGPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRISSSVKYYIHDHFIPIEKYQSLVPIMVEGYGPKIINSFTQDDIEKHQSDA 840
Oy 841 GLYIVPVYISSLILGLLISHQBMKLFMEDVNPKNCSWAGCLNQKRETEPHLFI 900
Db 841 GLYIVPVYISSLILGLLISHQBMKLFMEDVNPKNCSWAGCLNQKRETEPHLFI 900
Oy 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVYSLSTDLKSGVCSIDQPN 960
Db 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVYSLSTDLKSGVCSIDQPN 960
Oy 961 SVNFSEAECTEYTYEDESQROPFVRYATLISNSKPSGTEEGQGLNLSVTCKFSSKNSP 1020
Db 961 SVNFSEAECTEYTYEDESQROPFVRYATLISNSKPSGTEEGQGLNLSVTCKFSSKNSP 1020
Oy 1021 KDSFNSSSWEIQAQAFILSDHPNISPILTFSEGLDELKLEGNFPEENNDKSIYVL 1080
Db 1021 KDSFNSSSWEIQAQAFILSDHPNISPILTFSEGLDELKLEGNFPEENNDKSIYVL 1080
Oy 1081 GVTSTIKKRESGVLTDKRSVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSTIKKRESGVLTDKRSVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Oy 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 5
US-08-667-197-2
: Sequence 2, Application US/08667197
: GENERAL INFORMATION:
: APPLICANT: Matthews, William
: TITLE OF INVENTION: USES FOR WSX LIGANDS
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/667,197
: FILING DATE: 20-Jun-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/585005
: FILING DATE: 01/08/96
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: P-40,378
: REFERENCE/DOCKET NUMBER: P0986P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-08-667-197-2

```

Query Match 100.0%; Score 1165; DB 10; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCQRCVLLMEFIYTTAENLSPTPRKLSCHMPNSTYDFLLPAGLSKMTNS 60
 DB 1 MLCQRCVLLMEFIYTTAENLSPTPRKLSCHMPNSTYDFLLPAGLSKMTNS 60

QY 61 NGHYEAVPEKNSSGTSHSNLSKTFHCFCFSEQDRNCSLADNTEGTFSTVSLVF 120
 DB 61 NGHYEAVPEKNSSGTSHSNLSKTFHCFCFSEQDRNCSLADNTEGTFSTVSLVF 120

QY 121 QOIDANNIQCMLKGLDKLFICYVESLEKMLEFRNRYKXHLLYLREVLDSLPQOKS 180
 DB 121 QOIDANNIQCMLKGLDKLFICYVESLEKMLEFRNRYKXHLLYLREVLDSLPQOKS 180

QY 181 FQWVHNCVHCCCECLVVPATKNDTLMCLKITSGGVIQSPMSVQPIVMVAPDP 240
 DB 181 FQWVHNCVHCCCECLVVPATKNDTLMCLKITSGGVIQSPMSVQPIVMVAPDP 240

QY 241 LGLHMETDGNLKLISWSSPLVPEPLQYQVXSENSSTVIREADKIVATSILVDSILP 300
 DB 241 LGLHMETDGNLKLISWSSPLVPEPLQYQVXSENSSTVIREADKIVATSILVDSILP 300

QY 301 GSSYEYQVGRKRLDGPGLSDMSTPRVFTTQDYIYFPKILTSVGSVNSFHCYKKEKNI 360
 DB 301 GSSYEYQVGRKRLDGPGLSDMSTPRVFTTQDYIYFPKILTSVGSVNSFHCYKKEKNI 360

QY 361 VPSKETVMMNLAERIPQSOYDVSDHVSQVTFPNLNETKPRKFTYDAVCCNEHECH 420
 DB 361 VPSKETVMMNLAERIPQSOYDVSDHVSQVTFPNLNETKPRKFTYDAVCCNEHECH 420

QY 421 RYAEIYVIDVININISCEITDGYLTMTKMWSTSTIOSLAESTIOLRYHRSLSYCSIDIPSIH 480
 DB 421 RYAEIYVIDVININISCEITDGYLTMTKMWSTSTIOSLAESTIOLRYHRSLSYCSIDIPSIH 480

QY 481 PISEPRDCYLOSDGFECEIFOPRFLISGYTMMRINHSGISDSPCTVCLPDSVAPRDP 540
 DB 481 PISEPRDCYLOSDGFECEIFOPRFLISGYTMMRINHSGISDSPCTVCLPDSVAPRDP 540

QY 541 SSVKAEITINIGLKLISWEPVFPENNLOFOIRYGLSGKEVQMKMEVDAKSKSVSLPV 600
 DB 541 SSVKAEITINIGLKLISWEPVFPENNLOFOIRYGLSGKEVQMKMEVDAKSKSVSLPV 600

QY 601 PDLCAVYAVQVGRKRLDGLGYWSNMSNPAYTYVMDIKVPMRGPPEFRINIGDTMKKEKNV 660
 DB 601 PDLCAVYAVQVGRKRLDGLGYWSNMSNPAYTYVMDIKVPMRGPPEFRINIGDTMKKEKNV 660

QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTSEDVGNHTKFTFLMTEQAHYTVLAINSI 720
 DB 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTSEDVGNHTKFTFLMTEQAHYTVLAINSI 720

QY 721 GASVANFNLTFSMPMSKVIYOSLSAYPLNSSCVIYSWILSPSDXYLMFIEMKNLND 780
 DB 721 GASVANFNLTFSMPMSKVIYOSLSAYPLNSSCVIYSWILSPSDXYLMFIEMKNLND 780

QY 781 GEIKMLRISSSVKYYIHDFPIEKYQSLYPIFMEGVKPKIINSFQODIEKHQSDA 840
 DB 781 GEIKMLRISSSVKYYIHDFPIEKYQSLYPIFMEGVKPKIINSFQODIEKHQSDA 840

QY 841 GLYIVPYVYISSILLGLTLLISHQBMKLEMDVPNPKNCSMAOGLNQKETEHEHFT 900
 DB 841 GLYIVPYVYISSILLGLTLLISHQBMKLEMDVPNPKNCSMAOGLNQKETEHEHFT 900

QY 901 KHTASVTCGPLLEPPTISEDISVDTSMKNKDEMPPTYVSLSTTDLEKGSVCISDQFN 960
 DB 901 KHTASVTCGPLLEPPTISEDISVDTSMKNKDEMPPTYVSLSTTDLEKGSVCISDQFN 960

QY 961 SVNFSEAEGETEYTYDESGROPFVAYATLISNSKPESETGEEOGLINSVATKCFSSKN SPL 1020
 DB 961 SVNFSEAEGETEYTYDESGROPFVAYATLISNSKPESETGEEOGLINSVATKCFSSKN SPL 1020

QY 1021 KDSFNSNSWEIEAOAFILSDQHPNII SPHLTFSGLDELKLEGNFPEENNDKKSIIYL 1080

DB 1021 KDSFNSNSWEIEAOAFILSDQHPNII SPHLTFSGLDELKLEGNFPEENNDKKSIIYL 1080

QY 1081 GYTSIKKRRESGVLLDNDKSVSCPEPAPCLFTDIRVLQDSCSHFVENNILGTSKKTFFAS 1140
 DB 1081 GYTSIKKRRESGVLLDNDKSVSCPEPAPCLFTDIRVLQDSCSHFVENNILGTSKKTFFAS 1140

QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
 DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 6
 US-08-708-123D-4
 ; Sequence 4, Application US/08708123D
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; APPLICANT: Tepper, Robert I.
 ; APPLICANT: Culpepper, Janice A.
 ; APPLICANT: White, David W.
 ; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 ; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
 ; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/708,123D
 ; FILING DATE: 03-SEP-1996
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/638,524
 ; FILING DATE: 26-APR-1996
 ; APPLICATION NUMBER: 08/599,455
 ; FILING DATE: 22-JAN-1996
 ; APPLICATION NUMBER: 08/583,153
 ; FILING DATE: 28-DEC-1995
 ; APPLICATION NUMBER: 08/570,142
 ; FILING DATE: 11-DEC-1995
 ; APPLICATION NUMBER: 08/569,485
 ; FILING DATE: 08-DEC-1995
 ; APPLICATION NUMBER: 08/566,622
 ; FILING DATE: 04-DEC-1995
 ; APPLICATION NUMBER: 08/562,663
 ; FILING DATE: 27-NOV-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Melkijohn, Ph.D., Anita L.
 ; REGISTRATION NUMBER: 35,283
 ; REFERENCE/DOCKET NUMBER: 07334/019001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1165 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-708-123D-4

Query Match 100.0%; Score 1165; DB 11; Length 1165;


```

Db 121 QOIDANMNIOCKLKGDLKFLICYVESLFRNFRNTNYKHLLYLPEVLDSPLVPQGS 180
Qy 181 FOMVANCNSVHECCBCLVLPVPTAKLNDTLMLCKITSGVIFOSPLMSVOPINMYKPPPP 240
Db 181 FOMVANCNSVHECCBCLVLPVPTAKLNDTLMLCKITSGVIFOSPLMSVOPINMYKPPPP 240
Qy 241 LGLHMETDDGGLKITSMSSPPLVPPLOYOVKYSNSTTIVREADKIVSATSLLVDSILP 300
Db 241 LGLHMETDDGGLKITSMSSPPLVPPLOYOVKYSNSTTIVREADKIVSATSLLVDSILP 300
Qy 301 GSSYEVQVGRKLDGPGIMSDMSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKEKNI 360
Db 301 GSSYEVQVGRKLDGPGIMSDMSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKEKNI 360
Qy 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSKEYTFENLNETKPRGKFTYAVVACNEHECHH 420
Db 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSKEYTFENLNETKPRGKFTYAVVACNEHECHH 420
Qy 421 RYAEIYVIDVNIINISCEFDGYLTAKTCWSTSTIOSLAESTLQLRHNSLYCSDIPSIH 480
Db 421 RYAEIYVIDVNIINISCEFDGYLTAKTCWSTSTIOSLAESTLQLRHNSLYCSDIPSIH 480
Qy 481 PISEKDCYLOSDFECLFQPIFLLSGVTWIRINHSIGLSDSPCTCVLPDSVYKPLRP 540
Db 481 PISEKDCYLOSDFECLFQPIFLLSGVTWIRINHSIGLSDSPCTCVLPDSVYKPLRP 540
Qy 541 SSVKAEITINIGLKITSEKPEVPENNLOFOIRYGLSGKEVOMKMYEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKITSEKPEVPENNLOFOIRYGLSGKEVOMKMYEYVDAKSKSVSLPV 600
Qy 601 PDLCAVYAVOVRCKRLDGLGKTSWNSNPAIYVMDIKVPMRGPFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVOVRCKRLDGLGKTSWNSNPAIYVMDIKVPMRGPFWRIINGDTMKKEKNV 660
Qy 661 TLKMPKLNKNSLGVQRYVINHHTSCNGTSEVDGNHTKFFELTBOAHVTVLAINSI 720
Db 661 TLKMPKLNKNSLGVQRYVINHHTSCNGTSEVDGNHTKFFELTBOAHVTVLAINSI 720
Qy 721 GASVANFNILTFESWPMKSNIVOSLAYSAPLNSSCVIVSILSPSDYKLMFIIEMKNLND 780
Db 721 GASVANFNILTFESWPMKSNIVOSLAYSAPLNSSCVIVSILSPSDYKLMFIIEMKNLND 780
Qy 781 GEIKMLRISSSVKKYIHDHFIPIEKYOPSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSSVKKYIHDHFIPIEKYOPSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Qy 841 GLYVYVPIISSLITGLTLLISHQRMKLEWEDVPNPKNCNMACGLNPOKRETEHLEFI 900
Db 841 GLYVYVPIISSLITGLTLLISHQRMKLEWEDVPNPKNCNMACGLNPOKRETEHLEFI 900
Qy 901 KHTASVTCGPLLEPETISEDI SVDTSMKNKDEMAPTTVVSLSTTDELEKGSVCISDOFN 960
Db 901 KHTASVTCGPLLEPETISEDI SVDTSMKNKDEMAPTTVVSLSTTDELEKGSVCISDOFN 960
Qy 961 SVNFEAGTEVYEDESOROPFYKATLISNSKPSSETGEBGLINSVATCKFSSKNSPL 1020
Db 961 SVNFEAGTEVYEDESOROPFYKATLISNSKPSSETGEBGLINSVATCKFSSKNSPL 1020
Qy 1021 KDSFNSNMEI EAOAFILSDOHPNII SPHLTFSEGIDELKLEBNFENNDDKSIYLL 1080
Db 1021 KDSFNSNMEI EAOAFILSDOHPNII SPHLTFSEGIDELKLEBNFENNDDKSIYLL 1080
Qy 1081 GVTISIKKRESGVLLDKSRVSCPPAPCLFTDIRVLDQSCSHFVANNINLGTSSKKTAS 1140
Db 1081 GVTISIKKRESGVLLDKSRVSCPPAPCLFTDIRVLDQSCSHFVANNINLGTSSKKTAS 1140
Qy 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

```

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US-08-780-562-2
; Sequence 2, Application US/08780562
; General Information:
; Applicant: Matthews, William
; Applicant: Bennett, Brian
; Title of Invention: MSX RECEPTOR
; Number of Sequences: 45
; Correspondence Address:
; Addressee: Genentech, Inc.
; Street: 460 Point San Bruno Blvd
; City: South San Francisco
; State: California
; Country: USA
; Zip: 94080
; Computer Readable Form:
; Medium Type: 3.5 inch, 1.44 Mb floppy disk
; Computer: IBM PC compatible
; Operating System: PC-DOS/MS-DOS
; Software: WinPatlin (Genentech)
; Current Application Data:
; Application Number: US/08/780,562
; Filing Date:
; Classification: 435
; Prior Application Data:
; Application Number: 08/585005
; Filing Date: 01/08/97
; Prior Application Data:
; Application Number: 60/
; Filing Date: 01/08/97
; Attorney/Agent Information:
; Name: Lee, Wendy M.
; Registration Number: 40,378
; Reference/Document Number: P0986RL
; Telecommunication Information:
; Telephone: 415/225-1994
; Telefax: 415/952-9881
; Telex: 910/371-7168
; Information for SEQ ID NO: 2:
; Sequence Characteristics:
; Length: 1165 amino acids
; Type: Amino Acid
; Topology: Linear
; US-08-780-562-2

Query Match 100.0%; Score 1165; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MICQFCVLLHMERIYVITAFNLSYPTPMRFKLSCMPNSTYDFLLPAGLSKNTSNS 60
Db 1 MICQFCVLLHMERIYVITAFNLSYPTPMRFKLSCMPNSTYDFLLPAGLSKNTSNS 60
Qy 61 NGHYETAPEKRNSSGTHSNLSKTFTHCCFERSBDRNCSLCADNIECKTFVSTNSLVF 120
Db 61 NGHYETAPEKRNSSGTHSNLSKTFTHCCFERSBDRNCSLCADNIECKTFVSTNSLVF 120
Qy 121 QOIDANMNIOCKLKGDLKFLICYVESLFRNFRNTNYKHLLYLPEVLDSPLVPQGS 180
Db 121 QOIDANMNIOCKLKGDLKFLICYVESLFRNFRNTNYKHLLYLPEVLDSPLVPQGS 180
Qy 181 FOMVANCNSVHECCBCLVLPVPTAKLNDTLMLCKITSGVIFOSPLMSVOPINMYKPPPP 240
Db 181 FOMVANCNSVHECCBCLVLPVPTAKLNDTLMLCKITSGVIFOSPLMSVOPINMYKPPPP 240
Qy 241 LGLHMETDDGGLKITSMSSPPLVPPLOYOVKYSNSTTIVREADKIVSATSLLVDSILP 300
Db 241 LGLHMETDDGGLKITSMSSPPLVPPLOYOVKYSNSTTIVREADKIVSATSLLVDSILP 300
Qy 301 GSSYEVQVGRKLDGPGIMSDMSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKEKNI 360
Db 301 GSSYEVQVGRKLDGPGIMSDMSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKEKNI 360

```



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Qy 361 VPSKEIWMMLAEKIPDOSOTDVSDHVSQVTFENLNETKRGKTTYDAVYCCNEHECH 420
Db 361 VPSKEIWMMLAEKIPDOSOTDVSDHVSQVTFENLNETKRGKTTYDAVYCCNEHECH 420
Qy 421 RYAEIYDVNINISCEFTDGLTKMTCRMSTSTIOSLAESTILOLTHRSLSYCSIPSH 480
Db 421 RYAEIYDVNINISCEFTDGLTKMTCRMSTSTIOSLAESTILOLTHRSLSYCSIPSH 480
Qy 481 PISEBKDCYLOSDGFECIFQPIFLLSGYTWIRINHSIGSLDSPPTCVLPDPSVVKPLPP 540
Db 481 PISEBKDCYLOSDGFECIFQPIFLLSGYTWIRINHSIGSLDSPPTCVLPDPSVVKPLPP 540
Qy 541 SSVKKEITINIGLTKISWEKPPFPENNLOFOIRGLSGKEVQMKWEYDAKSKVSLPV 600
Db 541 SSVKKEITINIGLTKISWEKPPFPENNLOFOIRGLSGKEVQMKWEYDAKSKVSLPV 600
Qy 601 PDLCAVAVQVRCRDLGIGYMSNPNPAYTVMDIKVPMRGPEFMRILINGTMRKENV 660
Db 601 PDLCAVAVQVRCRDLGIGYMSNPNPAYTVMDIKVPMRGPEFMRILINGTMRKENV 660
Qy 661 TLLMRPLMKNDLSCVQRYVINHHTSCNGTMSDEVGNHTKFTFELTQEAHTVTLAINSI 720
Db 661 TLLMRPLMKNDLSCVQRYVINHHTSCNGTMSDEVGNHTKFTFELTQEAHTVTLAINSI 720
Qy 721 GASVANFNLTSPMSKYNIVOSLSATPLNSCVIVSNLSBSYKLMFTTEKKNLMD 780
Db 721 GASVANFNLTSPMSKYNIVOSLSATPLNSCVIVSNLSBSYKLMFTTEKKNLMD 780
Qy 781 GEIKWLRISSSVKRYIYNDHFPIEKYOFSLYPIFMEGGRKTIINSFTODDIEKHSDA 840
Db 781 GEIKWLRISSSVKRYIYNDHFPIEKYOFSLYPIFMEGGRKTIINSFTODDIEKHSDA 840
Qy 841 GLYVIVPIYISSLILGTLTLLSHQRMKLFMEDVNPKNCSMAOGLNFQKPEFHEHLEFI 900
Db 841 GLYVIVPIYISSLILGTLTLLSHQRMKLFMEDVNPKNCSMAOGLNFQKPEFHEHLEFI 900
Qy 901 KHTASVTCGPILEPETSSEDISVDTSMKNKRDMMPTTVVSLSTTDLKSGVCSIDQDN 960
Db 901 KHTASVTCGPILEPETSSEDISVDTSMKNKRDMMPTTVVSLSTTDLKSGVCSIDQDN 960
Qy 961 SVNFSSEAGTEVTEDESGROPFVKATLINSKSPSETGEOGLINSVTKCFSSKNLPL 1020
Db 961 SVNFSSEAGTEVTEDESGROPFVKATLINSKSPSETGEOGLINSVTKCFSSKNLPL 1020
Qy 1021 KDSFNSSSWEIQAQAFILISDQHPNIIISPHTFSGLDLLEKGNFPRENNDKKSIYYL 1080
Db 1021 KDSFNSSSWEIQAQAFILISDQHPNIIISPHTFSGLDLLEKGNFPRENNDKKSIYYL 1080
Qy 1081 GVTSTKKRSGVLLDCKSVSCPPAPCLFDIRVLODSCSHFVENNINLGTSSKKTFS 1140
Db 1081 GVTSTKKRSGVLLDCKSVSCPPAPCLFDIRVLODSCSHFVENNINLGTSSKKTFS 1140
Qy 1141 YMPQFOTCSTQTKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTKIMENKMDLTV 1165

```

```

RESULT 9
: Sequence 4, Application us/09094410
: GENERAL INFORMATION:

```

```

: APPLICANT: Tartaglia, Louis A.
: APPLICANT: Tepper, Robert I.
: APPLICANT: Culpepper, Janice A.
: APPLICANT: White, David W.
: TITLE OF INVENTION: THE OR RECEPTOR AND METHODS FOR
: TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.
: STREET: 225 Franklin Street
: CITY: Boston

```

```

: STATE: MA
: COUNTRY: US
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/094,410
: FILING DATE: 09-JUN-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/864,564
: FILING DATE: 28-MAY-1997
: APPLICATION NUMBER: 08/708,123
: FILING DATE: 03-SEP-1996
: APPLICATION NUMBER: 08/638,524
: FILING DATE: 26-APR-1996
: APPLICATION NUMBER: 08/599,455
: FILING DATE: 22-JAN-1996
: APPLICATION NUMBER: 08/583,153
: FILING DATE: 28-DEC-1995
: APPLICATION NUMBER: 08/570,142
: FILING DATE: 11-DEC-1995
: APPLICATION NUMBER: 08/569,485
: FILING DATE: 08-DEC-1995
: APPLICATION NUMBER: 08/566,622
: FILING DATE: 04-DEC-1995
: APPLICATION NUMBER: 08/562,663
: FILING DATE: 27-NOV-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Melkiojohn, Ph.D., Anita L.
: REGISTRATION NUMBER: 35,283
: REFERENCE/DOCKET NUMBER: 07334/019003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-542-5070
: TELEFAX: 617-542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: FRAGMENT TYPE: Internal
: US-09-094-410-4

```

```

Query Match 100.0% Score 1165: DB 14: Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MICQKFCVLLHMERIYVITAFNLISYPIPMRFKLSCMPPNSTYDFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHMERIYVITAFNLISYPIPMRFKLSCMPPNSTYDFLLPAGLSKNTSNS 60
Qy 61 NGHYETAVEPKFNSSGTHESNLKSTTFHCCFRSEEDRNCSLCADNIEGTFEVSNSLVF 120
Db 61 NGHYETAVEPKFNSSGTHESNLKSTTFHCCFRSEEDRNCSLCADNIEGTFEVSNSLVF 120
Qy 121 QOIDANMNIOCKLKGDKLFTCYVESLFKNLFRNNRYKXHLIYVLEVEDSPLYPOKGS 180
Db 121 QOIDANMNIOCKLKGDKLFTCYVESLFKNLFRNNRYKXHLIYVLEVEDSPLYPOKGS 180
Qy 181 FQMVHNCNSVHECCGCLVVPVPAKINDTLMLCKLITSGGVIFQSPLMISVQPINMYKPPDP 240
Db 181 FQMVHNCNSVHECCGCLVVPVPAKINDTLMLCKLITSGGVIFQSPLMISVQPINMYKPPDP 240
Qy 241 LGLHMEITDDGNLKLISWSSPLVPPLOQYVYKYSNSTVIVIEAKQIVSATSLSLVDSILP 300
Db 241 LGLHMEITDDGNLKLISWSSPLVPPLOQYVYKYSNSTVIVIEAKQIVSATSLSLVDSILP 300
Qy 301 GSYTEVQVGRKLDGPGIWSMSTPRVFTTQVYIFPPKILTSVGSNVSFHCITAKKENKI 360

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|||||
Db 301 GSSYEYQVAGKRLDGGIMSDWSTPRVFTTODIYFPFKILTSVGSNVSFHCYKKENKI 360
QY 361 VPSKEIVMMNLAERIPQSOYDVSDHVSQVTFEENLEPKRGKGFYDAVYCCNEHECH 420
Db 361 VPSKEIVMMNLAERIPQSOYDVSDHVSQVTFEENLEPKRGKGFYDAVYCCNEHECH 420
QY 421 RAELVIVDWINISCEITGVLTKMCRWSTSTIOSLASTIOLRYHRSLSYCSIDPSIH 480
Db 421 RAELVIVDWINISCEITGVLTKMCRWSTSTIOSLASTIOLRYHRSLSYCSIDPSIH 480
QY 481 PISEPPDCYLOSDEYECEIFQPIFLLSGYTMIRINHSLGSLDSPPTCVLPDSVAKPLPP 540
Db 481 PISEPPDCYLOSDEYECEIFQPIFLLSGYTMIRINHSLGSLDSPPTCVLPDSVAKPLPP 540
QY 541 SSYKAEITINIGLKTSMKRPVPEENNIOFOIRYGLSGEKYQMKMEVDASKSYSLVP 600
Db 541 SSYKAEITINIGLKTSMKRPVPEENNIOFOIRYGLSGEKYQMKMEVDASKSYSLVP 600
QY 601 PDLCAVAVQVRCRKLDDGLGYSNMSNPAYTVVMDIKVPMRGPFEFRIINGDTMKKEKNV 660
Db 601 PDLCAVAVQVRCRKLDDGLGYSNMSNPAYTVVMDIKVPMRGPFEFRIINGDTMKKEKNV 660
QY 661 TLLMKRLMKNDSLCYQRYVINHHTSCNGTWSDEVGNNHTKFTFLMTEQAHYTVLAINSI 720
Db 661 TLLMKRLMKNDSLCYQRYVINHHTSCNGTWSDEVGNNHTKFTFLMTEQAHYTVLAINSI 720
QY 721 GASVANFTLFSWPMKSVINIOSLSAYPLNNSCVIYSWITLSPDYKLMFTIEMKRLNED 780
Db 721 GASVANFTLFSWPMKSVINIOSLSAYPLNNSCVIYSWITLSPDYKLMFTIEMKRLNED 780
QY 781 GEIKMLRISSSVKKYXIHDFIPRIEKYQFSLYPIEMEGVGPRIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSSVKKYXIHDFIPRIEKYQFSLYPIEMEGVGPRIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSWAGCLNOKRPFTEHFLT 900
Db 841 GLYVIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSWAGCLNOKRPFTEHFLT 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTJDLKSGSVCISIDQFN 960
Db 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTJDLKSGSVCISIDQFN 960
QY 961 SVNFSAEETEVYEDESQRPVYATLLINSKPSSETGEEOGLINSVYTKCFSSKNSPL 1020
Db 961 SVNFSAEETEVYEDESQRPVYATLLINSKPSSETGEEOGLINSVYTKCFSSKNSPL 1020
QY 1021 KDSFSSSWEIEAOAFILLSDQHPNIIISPLTFSEGLDELKLEGNFPEENNDRKSIYVL 1080
Db 1021 KDSFSSSWEIEAOAFILLSDQHPNIIISPLTFSEGLDELKLEGNFPEENNDRKSIYVL 1080
QY 1081 GYTSIKRRSGVLLDNDKSHVSCFPAPCLFTDIRVLQDSCSHFVENNINILGTSKKTFFAS 1140
Db 1081 GYTSIKRRSGVLLDNDKSHVSCFPAPCLFTDIRVLQDSCSHFVENNINILGTSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKCDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKCDLTV 1165

```

```

ADDRESSER: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137.132
FILING DATE: 18-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejoh, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-137-132-4

Query Match 100.0%; Score 1165; DB 15; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTCQRCVYLLHMEFYITAFNLSPITPWRFKLSGMPNSTYDVFLLPAGLSKRTS 60
Db 1 MTCQRCVYLLHMEFYITAFNLSPITPWRFKLSGMPNSTYDVFLLPAGLSKRTS 60
QY 61 NGHYETAPEKPNSSGTHFSNLKTTFFHCCTFSBODRNCSLCADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAPEKPNSSGTHFSNLKTTFFHCCTFSBODRNCSLCADNIEGTFVSTVNSLVF 120
QY 121 QOIDANMNIOCMKGLDKLFICYVSLFKNLFRNRYKVHLLYVLEVLDSPLVPQKS 180
Db 121 QOIDANMNIOCMKGLDKLFICYVSLFKNLFRNRYKVHLLYVLEVLDSPLVPQKS 180
QY 181 FQWVHCNCSVHECCLELVVPTAKLNDTLLMCLKITSQVIFQSPLSVQPIINMKVPPDP 240
Db 181 FQWVHCNCSVHECCLELVVPTAKLNDTLLMCLKITSQVIFQSPLSVQPIINMKVPPDP 240
QY 241 LGLHWEITDGNLKTISWSSPVLVPPLOYQVYSENSTVIREAKYVATSLDVSILP 300

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Db      241  LGLHETIDDCNLMKISMSPPPLVPPPLDYQVKSNSNTTVIREADKIYSATSLVDLSILP  300
QY      301  GSSIEVOYGRKRLDGPGLWSDMSTPRVFTTODVITYFPKILTSVGSNVSFHCITYKKENKI  360
Db      301  GSSYEVQVRGRKLDOPGLMSDMSTPRVFTTODVITYFPKILTSVGSNVSFHCITYKKENKI  360
QY      361  VPSKEIYMMNMLAEKIPOSQDYVDVSHYKVFENLNENKPRGKFTTYAVVCCNHECHH  420
Db      361  VPSKEIYMMNMLAEKIPOSQDYVDVSHYKVFENLNENKPRGKFTTYAVVCCNHECHH  420
QY      421  RYAEELYIDVNNINISCEFDGYLTAKMTCKWSTSTISLAESTQLQRYHRSSLYCSDIPSIH  480
Db      421  RYAEELYIDVNNINISCEFDGYLTAKMTCKWSTSTISLAESTQLQRYHRSSLYCSDIPSIH  480
QY      481  PISEFKDCYLOSDFGTECIPQPIFLLSGTYMKIRINHSIGSLDSDPPCYLPDPSVYKPLPP  540
Db      481  PISEFKDCYLOSDFGTECIPQPIFLLSGTYMKIRINHSIGSLDSDPPCYLPDPSVYKPLPP  540
QY      541  SSVKKEITINIGLKLISNEKPYFEPENNIOFOIRYBLSGGEYQWKVEYVDASKSVSLPV  600
Db      541  SSVKKEITINIGLKLISNEKPYFEPENNIOFOIRYBLSGGEYQWKVEYVDASKSVSLPV  600
QY      601  PDLCAVVAVOYRCKRLDGLGYWSNMNSNPAYTVVMDIKYPMRGPPEWRIINCGDTMKKEKNV  660
Db      601  PDLCAVVAVOYRCKRLDGLGYWSNMNSNPAYTVVMDIKYPMRGPPEWRIINCGDTMKKEKNV  660
QY      661  TLLMKPLMKNDLSGVORYVINHHTSCNGTWSDEVDGNHTKFTFLMEQAHVTYVLAINSI  720
Db      661  TLLMKPLMKNDLSGVORYVINHHTSCNGTWSDEVDGNHTKFTFLMEQAHVTYVLAINSI  720
QY      721  GASVANFNLTFEPWPSKYNIVOSLSAYPLNSSCVYVSWTSLSDVKLWFIIEKNLNED  780
Db      721  GASVANFNLTFEPWPSKYNIVOSLSAYPLNSSCVYVSWTSLSDVKLWFIIEKNLNED  780
QY      781  GEIKMLRTISSYKYYIHDFEPIEKYOFSLPIFMEGKGRKIINSFQODIEKHOSDA  840
Db      781  GEIKMLRTISSYKYYIHDFEPIEKYOFSLPIFMEGKGRKIINSFQODIEKHOSDA  840
QY      841  GLYIVIPVYIISSSILLGLTLISHQRMKLFMEDVDPNPKNSCMAOGLNFQKPEFHEHFT  900
Db      841  GLYIVIPVYIISSSILLGLTLISHQRMKLFMEDVDPNPKNSCMAOGLNFQKPEFHEHFT  900
QY      901  KHTASVTCGPLLREPTISEDISVDTSMKNKNDMPPTVYSLSTTDLEKGSVCISDQCN  960
Db      901  KHTASVTCGPLLREPTISEDISVDTSMKNKNDMPPTVYSLSTTDLEKGSVCISDQCN  960
QY      961  SVNFSEAGTEVYTYDEDESORPFRVYATPLINSKRKSETGEBOGLINSSVTKCFSSKNSPU  1020
Db      961  SVNFSEAGTEVYTYDEDESORPFRVYATPLINSKRKSETGEBOGLINSSVTKCFSSKNSPU  1020
QY      1021  KDSFNSNMSEIEAOAFLLSDQHPINISPHLTFSEGDLDELTKLEGNFPENNDDKSIYVL  1080
Db      1021  KDSFNSNMSEIEAOAFLLSDQHPINISPHLTFSEGDLDELTKLEGNFPENNDDKSIYVL  1080
QY      1081  GVTSTKKRESGYLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFEVENNINLGTSSKKTFAAS  1140
Db      1081  GVTSTKKRESGYLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFEVENNINLGTSSKKTFAAS  1140
QY      1141  YMPQFQTCSTQTHKTENKMDLTV  1165
Db      1141  YMPQFQTCSTQTHKTENKMDLTV  1165

RESULT 11
US-09-950-149-4
: Sequence 4, Application US/09950149
: GENERAL INFORMATION:
:   APPLICANT: Tartaglia, Louis A.
:   :
:   :   Tepper, Robert I.
:   :   Culpepper, Janice A.
:   :   White, David W.
:   TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR BODY WEIGHT DISORDERS.
:   THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS.

```

```

1      NUMBER OF SEQUENCES: 50      INCLUDING OBESITY AND CACHEXIA
2      CORRESPONDENCE ADDRESS:
3      ADDRESSEE: Fish & Richardson, P.C.
4      STREET: 225 Franklin Street
5      CITY: Boston
6      STATE: MA
7      COUNTRY: US
8      ZIP: 02110-2804
9
10     COMPUTER READABLE FORM:
11     MEDIUM TYPE: Diskette
12     COMPUTER: IBM Compatible
13     OPERATING SYSTEM: Windows95
14     SOFTWARE: FASTSEQ for Windows Version 2.0
15
16     CURRENT APPLICATION DATA:
17     APPLICATION NUMBER: US/09/950,149
18     FILING DATE: 10-Sep-2001
19
20     PRIOR APPLICATION DATA:
21     APPLICATION NUMBER: 09/069,781
22     FILING DATE: <unknown>
23     APPLICATION NUMBER: US 08/708,123
24     FILING DATE: 03-SEP-1996
25     APPLICATION NUMBER: US 08/638,524
26     FILING DATE: 26-APR-1996
27     APPLICATION NUMBER: US 08/559,455
28     FILING DATE: 22-JAN-1996
29     APPLICATION NUMBER: US 08/583,153
30     FILING DATE: 28-DEC-1995
31     APPLICATION NUMBER: US 08/570,142
32     FILING DATE: 11-DEC-1995
33     APPLICATION NUMBER: US 08/569,485
34     FILING DATE: 08-DEC-1995
35     APPLICATION NUMBER: US 08/566,622
36     FILING DATE: 04-DEC-1995
37     APPLICATION NUMBER: US 08/562,663
38     FILING DATE: 27-NOV-1995
39
40     ATTORNEY/AGENT INFORMATION:
41     NAME: Weikiejohn, Ph.D., Anita L.
42     REGISTRATION NUMBER: 35,283
43     REFERENCE/DOCKET NUMBER: 07334/082001
44     TELECOMMUNICATION INFORMATION:
45     TELEPHONE: (617) 542-5070
46     TELEFAX: (617) 542-8906
47     TELEX: 200154
48
49     INFORMATION FOR SEQ ID NO: 4:
50     SEQUENCE CHARACTERISTICS:
51     LENGTH: 1165 amino acids
52     TYPE: amino acid
53     TOPOLOGY: unknown
54     MOLECULE TYPE: protein
55     FRAGMENT TYPE: internal
56     SEQUENCE DESCRIPTION: SEQ ID NO: 4:
57
58     US-09-950-149-4
59
60     Query Match      100.0%; Score 1165; DB 23; Length 1165;
61     Best Local Similarity 100.0%; Pred. No. 0;
62     Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0
63
64     1 MICOFCVVLHWEIYYTAFNLSYPTIPWPKFKLSCEPNSYDYFLLPAGISKNTSNS 60
65     1 MICOFCVVLHWEIYYTAFNLSYPTIPWPKFKLSCEPNSYDYFLLPAGISKNTSNS 60
66
67     61 NCHYETAPEPRNNSGTHRSNLSKTFTHCCFPRSEODRNSLCADNTEGKTFVSTVSLVF 120
68     61 NCHYETAPEPRNNSGTHRSNLSKTFTHCCFPRSEODRNSLCADNTEGKTFVSTVSLVF 120
69
70     121 QOIDANMNINQCLAKDCLKFICYVESLFEKNLEFRNRYKVKHLIYVLPVEVLEDSPLVPQKS 180
71     121 QOIDANMNINQCLAKDCLKFICYVESLFEKNLEFRNRYKVKHLIYVLPVEVLEDSPLVPQKS 180
72
73     181 FOMVHNCNSVHECCGLVLPVPTAKLNDTLMLCKLTSGGVIFQCSPLMSVQPINNVAKDDP 240
74

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Db 181 FQWVHNCNVHECCLELVPPAKLNDTLMLCKITSGVIFQSPLMVSQPIINMKPDP 240
Qy 241 LGHMEITDGNLKISSMSSPLVPLOYOVKSENSSTVIREADKIVSATSLVLSIIP 300
Db 241 LGHMEITDGNLKISSMSSPLVPLOYOVKSENSSTVIREADKIVSATSLVLSIIP 300
Qy 301 GSSYEVOVGRKRLDGGIMSDMSTPRVFTTQDVYIFPPKILTVSGSNVSFHCIIYKKNKI 360
Db 301 GSSYEVOVGRKRLDGGIMSDMSTPRVFTTQDVYIFPPKILTVSGSNVSFHCIIYKKNKI 360
Qy 361 VPSKEIVMMNMLAEKIPQSOYDVSDHVSQVFFNLNETKPRGKFTYDAVYCNEHECHH 420
Db 361 VPSKEIVMMNMLAEKIPQSOYDVSDHVSQVFFNLNETKPRGKFTYDAVYCNEHECHH 420
Qy 421 RYAEIYVDVNNINISCEITDGYLTAKMCRWSTSTIOSLAESTIOLRYHRSLSYCSIPSIH 480
Db 421 RYAEIYVDVNNINISCEITDGYLTAKMCRWSTSTIOSLAESTIOLRYHRSLSYCSIPSIH 480
Qy 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVYKPLPP 540
Db 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVYKPLPP 540
Qy 541 SSVKAEITINIGLKIISWEKVPVPENNLOFOIRYGLSGKEVOMKVEYDARKSVSLPV 600
Db 541 SSVKAEITINIGLKIISWEKVPVPENNLOFOIRYGLSGKEVOMKVEYDARKSVSLPV 600
Qy 601 PDLCAVAYAVOVRCKRLDGLGYMSMNSPAYTVVMDIKVMPRGPEFWRJINGDTMKKEKNV 660
Db 601 PDLCAVAYAVOVRCKRLDGLGYMSMNSPAYTVVMDIKVMPRGPEFWRJINGDTMKKEKNV 660
Qy 661 TILMKRLMKNDSICQVORYINHTSCNGTWSGVNHTKFTFLMEQAHYVLAINSI 720
Db 661 TILMKRLMKNDSICQVORYINHTSCNGTWSGVNHTKFTFLMEQAHYVLAINSI 720
Qy 721 GASVANFNLTFSWPMKRVNIQVSLASVPLNNSCIVISWILSPDYKLMFIIEMKMLNED 780
Db 721 GASVANFNLTFSWPMKRVNIQVSLASVPLNNSCIVISWILSPDYKLMFIIEMKMLNED 780
Qy 781 GEIKMLRISSSVKRYIHDHFIPIEKYQPSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRISSSVKRYIHDHFIPIEKYQPSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
Qy 841 GLVYIYVPIIISILLGLTLISHQRMKRLFWDVYPRNKCMAOGLNQKPTFFHLLT 900
Db 841 GLVYIYVPIIISILLGLTLISHQRMKRLFWDVYPRNKCMAOGLNQKPTFFHLLT 900
Qy 901 KHTASVTCGPLLEPETISEDIVDSMKNKDMMPTTVVSLSTDLKESVACISDOFN 960
Db 901 KHTASVTCGPLLEPETISEDIVDSMKNKDMMPTTVVSLSTDLKESVACISDOFN 960
Qy 961 SVNFSEAEGETEYVDEESOROPFVKYATLISNKPSETGEEOGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETEYVDEESOROPFVKYATLISNKPSETGEEOGLINSSVTKCFSSKNSPL 1020
Qy 1021 KQSFSSMWEIEAOAFILISDQHPNITSPHLTFSEGLDELKLEGNFPEENDKKTITVL 1080
Db 1021 KQSFSSMWEIEAOAFILISDQHPNITSPHLTFSEGLDELKLEGNFPEENDKKTITVL 1080
Qy 1081 GYVSIKRRSGVLLDTRSKRSCFPAPCLFTDIRVLQDSCSHFVENNINILGTSKKTFFAS 1140
Db 1081 GYVSIKRRSGVLLDTRSKRSCFPAPCLFTDIRVLQDSCSHFVENNINILGTSKKTFFAS 1140
Qy 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

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RESULT 12
US-08-774-414-7
; Sequence 7-7, Application us/08774414
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: WELCHER, ANDREW A.

```

```

; APPLICANT: FLETCHER, FREDERICK A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,414
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382-A
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1216 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-774-414-7

Query Match 100.0%; Score 1165; DB 11; Length 1216;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTCQKFCVLLHMEFIYVITAENLSTPTPMWRKLSCMPNSTYDFLLPAGLSKNTS 60
Db 1 MTCQKFCVLLHMEFIYVITAENLSTPTPMWRKLSCMPNSTYDFLLPAGLSKNTS 60
Qy 61 NGHYETAVPEKNSGTHSNLSKTFHCFCPSBEDRNCSLCADNTEGTFVSTNSLVE 120
Db 61 NGHYETAVPEKNSGTHSNLSKTFHCFCPSBEDRNCSLCADNTEGTFVSTNSLVE 120
Qy 121 QOIDANMNIQCMKGLDKLFIYVESLFRNLFNNYKVALHLYVLPVLEDSPLVPOKS 180
Db 121 QOIDANMNIQCMKGLDKLFIYVESLFRNLFNNYKVALHLYVLPVLEDSPLVPOKS 180
Qy 181 FQWVHNCNVHECCLELVPPAKLNDTLMLCKITSGVIFQSPLMVSQPIINMKPDP 240
Db 181 FQWVHNCNVHECCLELVPPAKLNDTLMLCKITSGVIFQSPLMVSQPIINMKPDP 240
Qy 241 LGHMEITDGNLKISSMSSPLVPLOYOVKSENSSTVIREADKIVSATSLVLSIIP 300
Db 241 LGHMEITDGNLKISSMSSPLVPLOYOVKSENSSTVIREADKIVSATSLVLSIIP 300
Qy 301 GSSYEVOVGRKRLDGGIMSDMSTPRVFTTQDVYIFPPKILTVSGSNVSFHCIIYKKNKI 360
Db 301 GSSYEVOVGRKRLDGGIMSDMSTPRVFTTQDVYIFPPKILTVSGSNVSFHCIIYKKNKI 360
Qy 361 VPSKEIVMMNMLAEKIPQSOYDVSDHVSQVFFNLNETKPRGKFTYDAVYCNEHECHH 420
Db 361 VPSKEIVMMNMLAEKIPQSOYDVSDHVSQVFFNLNETKPRGKFTYDAVYCNEHECHH 420
Qy 421 RYAEIYVDVNNINISCEITDGYLTAKMCRWSTSTIOSLAESTIOLRYHRSLSYCSIPSIH 480
Db 421 RYAEIYVDVNNINISCEITDGYLTAKMCRWSTSTIOSLAESTIOLRYHRSLSYCSIPSIH 480
Qy 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVYKPLPP 540
Db 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVYKPLPP 540

```

QY 541 SSYKAEITINIGLKTSWEKPVPENNLOFOIRYGLSGKEVQKMEVYDAKSKSVLPV 600
DB 541 SSYKAEITINIGLKTSWEKPVPENNLOFOIRYGLSGKEVQKMEVYDAKSKSVLPV 600
QY 601 PDLCAVAVOVRCKRLDGLGYWMSNMPATVYMDIKVPMRGEPRIINGDMKKEKNV 660
DB 601 PDLCAVAVOVRCKRLDGLGYWMSNMPATVYMDIKVPMRGEPRIINGDMKKEKNV 660
QY 661 TLIMKPLMKNDISCSVQRYVINHHTSNGTWSVDGNHRTFTFLMTEQAHVTVLAINST 720
DB 661 TLIMKPLMKNDISCSVQRYVINHHTSNGTWSVDGNHRTFTFLMTEQAHVTVLAINST 720
QY 721 GASVANFNLFSPMPSKVNIVQSLAVPLNSSCVIYSWILSPDYKLMFTIEMKNLNE 780
DB 721 GASVANFNLFSPMPSKVNIVQSLAVPLNSSCVIYSWILSPDYKLMFTIEMKNLNE 780
QY 781 GEIKMLRISSSVKKYYIHHDFPIEIKYQFSFLPIFMGVGKPKIINSFTODDIEKHOSDA 840
DB 781 GEIKMLRISSSVKKYYIHHDFPIEIKYQFSFLPIFMGVGKPKIINSFTODDIEKHOSDA 840
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKLLWEDVNPKNCSWAQGLNFQKPEFELFI 900
DB 841 GLYVIVPVIISSSILLGLTLLISHQRMKLLWEDVNPKNCSWAQGLNFQKPEFELFI 900
QY 901 KHTASTCGRPLLEPETSIEDISVDTSNKKDKEMPTVYSLSTDLEKGSVCISQEN 960
DB 901 KHTASTCGRPLLEPETSIEDISVDTSNKKDKEMPTVYSLSTDLEKGSVCISQEN 960
QY 961 SVNFAEGEFTYEDESQHPFVKATILSNKPSPTGEQGLINSVTKCPSKNSPL 1020
DB 961 SVNFAEGEFTYEDESQHPFVKATILSNKPSPTGEQGLINSVTKCPSKNSPL 1020
QY 1021 KDSFSSNWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPERNDKSIYYL 1080
DB 1021 KDSFSSNWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPERNDKSIYYL 1080
QY 1081 GVTISIKREGVLLTDKSRKSCFPAPCLFTDIRVLQDSCSHVEVNNINIGTSKKTFA 1140
DB 1081 GVTISIKREGVLLTDKSRKSCFPAPCLFTDIRVLQDSCSHVEVNNINIGTSKKTFA 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 13
US-09-671-049-7
Sequence 7, Application US/09671049
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
FLETCHER, ANDREW A.
FLETCHER, FREDERICK A.
TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/671,049
FILING DATE: 27-Sep-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/774,414
FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER: A-382-A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1216 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-671-049-7

Query Match 100.0%; Score 1165; DB 20; Length 1216;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKRCVYLHMEFIYVITAFNLSTPIPTWRKLSGMPNSIYIFLLPAGLSKNTS 60
DB 1 MICQKRCVYLHMEFIYVITAFNLSTPIPTWRKLSGMPNSIYIFLLPAGLSKNTS 60
QY 61 NGHYETAVERKFNSSGTHFNSLKTFFHCCFRSEODRNCGLCADNIEGKTFVTSNLSV 120
DB 61 NGHYETAVERKFNSSGTHFNSLKTFFHCCFRSEODRNCGLCADNIEGKTFVTSNLSV 120
QY 121 QQIDAMNIOCWKRGDKLFICVESLFFKNLFRNYNKKVHLVYLPVLEDSPLVPOKGS 180
DB 121 QQIDAMNIOCWKRGDKLFICVESLFFKNLFRNYNKKVHLVYLPVLEDSPLVPOKGS 180
QY 181 FQWVHCNCSYHECCCLVVPYPAKLANDTLLMCKLITSGVIFQSPPLNSVOPIMVYKDP 240
DB 181 FQWVHCNCSYHECCCLVVPYPAKLANDTLLMCKLITSGVIFQSPPLNSVOPIMVYKDP 240
QY 241 LGLHMETDGNKIKISSSPPLVPLOVOYKSENSTVIYREADKIVSATSLVYOSILP 300
DB 241 LGLHMETDGNKIKISSSPPLVPLOVOYKSENSTVIYREADKIVSATSLVYOSILP 300
QY 301 GSSYEVQVRCKRLDQGIWSDMSTPRVFTYQDIYPPKILTSVGSNVSHCIYKKEKNI 360
DB 301 GSSYEVQVRCKRLDQGIWSDMSTPRVFTYQDIYPPKILTSVGSNVSHCIYKKEKNI 360
QY 361 VPSKEIYWMNLAELKIPQSOYDVVSDHVSQVTFPNLNETKPRKFTYYDAYVCCNEHECH 420
DB 361 VPSKEIYWMNLAELKIPQSOYDVVSDHVSQVTFPNLNETKPRKFTYYDAYVCCNEHECH 420
QY 421 RYAEIYVIVNINISCTDGYLTKMCRMSTIQSIAESTLRLRHRSLSYOSDPSIH 480
DB 421 RYAEIYVIVNINISCTDGYLTKMCRMSTIQSIAESTLRLRHRSLSYOSDPSIH 480
QY 481 PISEPKDYLQSDGFYECIPQPIFLLSGYTMWIRINHSLSLSPPTCVLPDSVVRPLP 540
DB 481 PISEPKDYLQSDGFYECIPQPIFLLSGYTMWIRINHSLSLSPPTCVLPDSVVRPLP 540
QY 541 SSYKAEITINIGLKTSWEKPVPENNLOFOIRYGLSGKAVQKMEVYDAKSKSVLPV 600
DB 541 SSYKAEITINIGLKTSWEKPVPENNLOFOIRYGLSGKAVQKMEVYDAKSKSVLPV 600
QY 601 PDLCAVAVOVRCKRLDGLGYWMSNMPATVYMDIKVPMRGEPRIINGDMKKEKNV 660
DB 601 PDLCAVAVOVRCKRLDGLGYWMSNMPATVYMDIKVPMRGEPRIINGDMKKEKNV 660
QY 661 TLIMKPLMKNDISCSVQRYVINHHTSNGTWSVDGNHRTFTFLMTEQAHVTVLAINST 720
DB 661 TLIMKPLMKNDISCSVQRYVINHHTSNGTWSVDGNHRTFTFLMTEQAHVTVLAINST 720
QY 721 GASVANFNLFSPMPSKVNIVQSLAVPLNSSCVIYSWILSPDYKLMFTIEMKNLNE 780
DB 721 GASVANFNLFSPMPSKVNIVQSLAVPLNSSCVIYSWILSPDYKLMFTIEMKNLNE 780
QY 781 GEIKMLRISSSVKKYYIHHDFPIEIKYQFSFLPIFMGVGKPKIINSFTODDIEKHOSDA 840
DB 781 GEIKMLRISSSVKKYYIHHDFPIEIKYQFSFLPIFMGVGKPKIINSFTODDIEKHOSDA 840

QY 841 GLYIVPVIISSILLGLTLLISHQRMKLLFWEDVNPKNCSMAOGLNFQKPETFEHLFI 900
DB 841 GLYIVPVIISSILLGLTLLISHQRMKLLFWEDVNPKNCSMAOGLNFQKPETFEHLFI 900
QY 901 KHTASVTCGPLLLEPEITISDVTSWKNKDEMPPTVYSLSTDLKSGVCSISDQFN 960
DB 901 KHTASVTCGPLLLEPEITISDVTSWKNKDEMPPTVYSLSTDLKSGVCSISDQFN 960
QY 961 SVNFSEAGTEVTYEDESQROPFVKATLISNKPSTGEQGLINSVYKCFSSKNSPL 1020
DB 961 SVNFSEAGTEVTYEDESQROPFVKATLISNKPSTGEQGLINSVYKCFSSKNSPL 1020
QY 1021 KDSFSSNMEIEAOAFILSDQHPNITSPHLTSEGLDELKLGNEPPEENNDKSTIYL 1080
DB 1021 KDSFSSNMEIEAOAFILSDQHPNITSPHLTSEGLDELKLGNEPPEENNDKSTIYL 1080
QY 1081 GVSIRKREGVLLTDKSRVSCPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
DB 1081 GVSIRKREGVLLTDKSRVSCPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMCIDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMCIDLTV 1165

RESULT 14
US-08-599-974C-56
: Sequence 56, Application US/08599974C
: GENERAL INFORMATION:
: APPLICANT: Friedman, Jeffrey M.
: APPLICANT: Lee, Gwo-Hua
: APPLICANT: Proenca, Ricardo
: TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
: NUMBER OF SEQUENCES: 56
: ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/599,974C
: FILING DATE: 14-FEB-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/586,594
: FILING DATE: 16-JAN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 600-1-162 CPL
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 56:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: ORIGINAL SOURCE:

ORGANISM: Homo sapiens
US-08-599-974C-56
Query Match 91.3%; Score 1064; DB 9; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MICQFCVYLHMEFTYVTAENLSYPIPWREKLSGMPNPNSTYDVELLPAGLSKNTSNS 60
DB 1 MICQFCVYLHMEFTYVTAENLSYPIPWREKLSGMPNPNSTYDVELLPAGLSKNTSNS 60
QY 61 NGHYETAPEKPNSSGTHSNLSKTTFHCCFNSQDQKNSCLADNLEKTFVSTVNSLYF 120
DB 61 NGHYETAPEKPNSSGTHSNLSKTTFHCCFNSQDQKNSCLADNLEKTFVSTVNSLYF 120
QY 121 QQIDAMNNTQCMPLKGLKLFICVESLFRNLFENYKHLVYLPEVELEDSPLVQKKS 180
DB 121 QQIDAMNNTQCMPLKGLKLFICVESLFRNLFENYKHLVYLPEVELEDSPLVQKKS 180
QY 181 FQWVHCNCSVHECCCLVPPYPAKLNDTLMLCKITSGGVIEQSPIMSVQPIIMVPRDPP 240
DB 181 FQWVHCNCSVHECCCLVPPYPAKLNDTLMLCKITSGGVIEQSPIMSVQPIIMVPRDPP 240
QY 241 LGIHMETDDGNLKISWSSPPLVPPLOYOVKXSENSTVIRPADIVSATSLVDSILP 300
DB 241 LGIHMETDDGNLKISWSSPPLVPPLOYOVKXSENSTVIRPADIVSATSLVDSILP 300
QY 301 GSSYEYQVGRKRLDGGIISDMSTPRVFTQDVIYPPKILTSVGSNVSFHCYKKENKI 360
DB 301 GSSYEYQVGRKRLDGGIISDMSTPRVFTQDVIYPPKILTSVGSNVSFHCYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCCH 420
DB 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCCH 420
QY 421 RYAEIYVIDVNIINISCEFTGVLTKMCRWSTSIQSLASTLOLRHRSLSVCSDIPISTH 480
DB 421 RYAEIYVIDVNIINISCEFTGVLTKMCRWSTSIQSLASTLOLRHRSLSVCSDIPISTH 480
QY 481 PISEPKCYLQSDGFECIFQPIFELLSGYTMIRIHSLGSLDSPPTCVLPDSVVRPLP 540
DB 481 PISEPKCYLQSDGFECIFQPIFELLSGYTMIRIHSLGSLDSPPTCVLPDSVVRPLP 540
QY 541 SSYKAEITTNIGLKITSWEKVPENNLQOLRYGSLGFEVQKKYEVYDANSKSYSLPV 600
DB 541 SSYKAEITTNIGLKITSWEKVPENNLQOLRYGSLGFEVQKKYEVYDANSKSYSLPV 600
QY 601 PDLCAVYAVQVRCRKLDDGLGYSNMSNPAYTYVMDIKVPMRGPEFRIINGDTMKKEKRY 660
DB 601 PDLCAVYAVQVRCRKLDDGLGYSNMSNPAYTYVMDIKVPMRGPEFRIINGDTMKKEKRY 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEEDVGNHTKFTFLMEQAHYTVLAINSI 720
DB 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEEDVGNHTKFTFLMEQAHYTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIYOSLSAYPLNSSCVIYSWILSPDYKLMFTIEMKRLND 780
DB 721 GASVANFNLTFSWPMKSVNIYOSLSAYPLNSSCVIYSWILSPDYKLMFTIEMKRLND 780
QY 781 GEFKMLRISSVKKYIHDHFPIEKYQSLPIFMEGVGKRIINSFQODIEKHQSDA 840
DB 781 GEFKMLRISSVKKYIHDHFPIEKYQSLPIFMEGVGKRIINSFQODIEKHQSDA 840
QY 841 GLYIVPVIISSILLGLTLLISHQRMKLLFWEDVNPKNCSMAOGLNFQKPETFEHLFI 900
DB 841 GLYIVPVIISSILLGLTLLISHQRMKLLFWEDVNPKNCSMAOGLNFQKPETFEHLFI 900
QY 901 KHTASVTCGPLLLEPEITISDVTSWKNKDEMPPTVYSLSTDLKSGVCSISDQFN 960
DB 901 KHTASVTCGPLLLEPEITISDVTSWKNKDEMPPTVYSLSTDLKSGVCSISDQFN 960
QY 961 SVNFSEAGTEVTYEDESQROPFVKATLISNKPSTGEQGLINSVYKCFSSKNSPL 1020

Db 961 SNFSEAEGETEYVEAESQROPVKYATLISNSKPSETEEOGLINSVTKCFSSKNSPL 1020
Qy 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPENNDRKSIYYL 1080
Db 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPENNDRKSIYYL 1080
Qy 1081 GYTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKRTFAS 1140
Db 1081 GYTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKRTFAS 1140
Qy 1141 YMPQFOTCSTQTHKIMENKCDLT 1165
Db 1141 YMPQFOTCSTQTHKIMENKCDLT 1165
RESULT 15
US-08-713-296-11
Sequence 11, Application US/08713296
GENERAL INFORMATION:
APPLICANT: Shodgrass, H. Ralph
APPLICANT: Clodfi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
APPLICANT: Mikhail, Adel A.
APPLICANT: Barut, Bruce A.
TITLE OF INVENTION: METHODS FOR USING THE OBES
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,296
FILING DATE: 13-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0039-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-713-296-11
Query Match 91.3%; Score 1064; DB 11: Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MICQKCVVLLHMEFIVITAFNLSYPTIPWRKLSOMPNSYDYVFLPAGLSKNTS 60
|||||

Db 1 MICQKCVVLLHMEFIVITAFNLSYPTIPWRKLSOMPNSYDYVFLPAGLSKNTS 60
Qy 61 NGHYETAVERPENSSCTHRSNLKTTFFHCCFRSEQDRNSICADNTEGTFVSTVSLVF 120
Db 61 NGHYETAVERPENSSCTHRSNLKTTFFHCCFRSEQDRNSICADNTEGTFVSTVSLVF 120
Qy 121 QOIDANMNIOCKLGDPLFICVESLFKNLFRNYKXHLVLYPEVLEDSPVPOKGS 180
Db 121 QOIDANMNIOCKLGDPLFICVESLFKNLFRNYKXHLVLYPEVLEDSPVPOKGS 180
Qy 181 FQWVHNCGVHCECELVPPVPAKLNDTLMLCKITSGGVTECSPLNSVOPTIMVRRDP 240
Db 181 FQWVHNCGVHCECELVPPVPAKLNDTLMLCKITSGGVTECSPLNSVOPTIMVRRDP 240
Qy 241 LGLHMETDGNLKLISMSSEPLVPFLOQOVKSENSTVIREAKIVSATSLVDSILP 300
Db 241 LGLHMETDGNLKLISMSSEPLVPFLOQOVKSENSTVIREAKIVSATSLVDSILP 300
Qy 301 GGSYEVQVRGKRLDGPGLMSDMSTPRVFTTODVYIPPKILISVGSNVSEHCYKKEKNI 360
Db 301 GGSYEVQVRGKRLDGPGLMSDMSTPRVFTTODVYIPPKILISVGSNVSEHCYKKEKNI 360
Qy 361 VPSKEIVMMNIAEKTIPOSOYDVVSDHVSQVPEFNLETRPKFTYDAYVCCNEHCHH 420
Db 361 VPSKEIVMMNIAEKTIPOSOYDVVSDHVSQVPEFNLETRPKFTYDAYVCCNEHCHH 420
Qy 421 RYAEVLYVIDNINISCESTDGILTKMTCRMSTYQISLAESTLQURHRSLSYCSDPISIH 480
Db 421 RYAEVLYVIDNINISCESTDGILTKMTCRMSTYQISLAESTLQURHRSLSYCSDPISIH 480
Qy 481 PISEPKDCYIQSDGFYECIFOPIFLLSGTYMIRINHSLSLSDSPICVLPDSVVRPLP 540
Db 481 PISEPKDCYIQSDGFYECIFOPIFLLSGTYMIRINHSLSLSDSPICVLPDSVVRPLP 540
Qy 541 SSYKAEITINIGLKISWEKVPENNLOFOIRYGLSGKEVOKMYEVYPAKSKSYLPV 600
Db 541 SSYKAEITINIGLKISWEKVPENNLOFOIRYGLSGKEVOKMYEVYPAKSKSYLPV 600
Qy 601 PDLCAVAVOVRCRRLDGLGYSNWSNPAYTVVMDIKVRPGEFPAKILINDGTMRKEKV 660
Db 601 PDLCAVAVOVRCRRLDGLGYSNWSNPAYTVVMDIKVRPGEFPAKILINDGTMRKEKV 660
Qy 661 TLAKPLMKNDISLCSVQRYVINHTSCNGTWSVDYNGHRTFTLKTBOATTVVLAINSI 720
Db 661 TLAKPLMKNDISLCSVQRYVINHTSCNGTWSVDYNGHRTFTLKTBOATTVVLAINSI 720
Qy 721 GASVANDNLTFSWPMKSVNIYQSLSAVPLNSCVIYSWILSPDYKLMYFIEMKNLNE 780
Db 721 GASVANDNLTFSWPMKSVNIYQSLSAVPLNSCVIYSWILSPDYKLMYFIEMKNLNE 780
Qy 781 GEIKMLRISSSVKRYIHDHFIDIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSSVKRYIHDHFIDIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840
Qy 841 GLVYIVPVIISSSITLLGTLIIHQRRKLTWEDVPRPKNCWAGGINFGRPTPEHLFT 900
Db 841 GLVYIVPVIISSSITLLGTLIIHQRRKLTWEDVPRPKNCWAGGINFGRPTPEHLFT 900
Qy 901 KHTASVTCGPLLEPETISDIDVTSMKNKDEMPPTVYSLSTJDLKSGVCSIDQFN 960
Db 901 KHTASVTCGPLLEPETISDIDVTSMKNKDEMPPTVYSLSTJDLKSGVCSIDQFN 960
Qy 961 SNFSEAEGETEYVEAESQROPVKYATLISNSKPSETEEOGLINSVTKCFSSKNSPL 1020
Db 961 SNFSEAEGETEYVEAESQROPVKYATLISNSKPSETEEOGLINSVTKCFSSKNSPL 1020
Qy 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPENNDRKSIYYL 1080
Db 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPENNDRKSIYYL 1080
Qy 1081 GYTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKRTFAS 1140
Db 1081 GYTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKRTFAS 1140

QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
 DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 16

US-08-961-809-4
 ; Sequence 4, Application US/08961809
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Cai
 ; APPLICANT: Friedman, Jeffrey M.
 ; TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS THAT
 ; NUMBER OF INVENTION: MODULATE LEPTIN ACTIVITY
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue, 4th Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/961,809
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-205
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1165 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-08-961-809-4

Query Match 91.3% Score 1064; DB 13; Length 1165;
 Best Local Similarity 99.9% Pred No. 0;
 Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKCEVLLHMEFLYITAFNLSPITPWRKILSCMPNPNSTYDFLLPAGLSKNTS 60
 DB 1 MICQKCEVLLHMEFLYITAFNLSPITPWRKILSCMPNPNSTYDFLLPAGLSKNTS 60
 QY 61 NGHYEAVPKNRSSTGTHSNLSKTTFHCCFPRSEODRNCSLCADNIEGTFSTVNSLVF 120
 DB 61 NGHYEAVPKNRSSTGTHSNLSKTTFHCCFPRSEODRNCSLCADNIEGTFSTVNSLVF 120
 QY 121 QOIDAMNINOCMLKGDJLKFICYVESLFRNLFPRNRYKVHLVYLPBEVLEDSPLVPQKS 180
 DB 121 QOIDAMNINOCMLKGDJLKFICYVESLFRNLFPRNRYKVHLVYLPBEVLEDSPLVPQKS 180
 QY 181 FQMVHNCNVHCCCECLVDPPTAKLNDTLIMCLKITSQGVIFQSPILMSVQPINMXPDP 240
 DB 181 FQMVHNCNVHCCCECLVDPPTAKLNDTLIMCLKITSQGVIFQSPILMSVQPINMXPDP 240
 QY 241 LGLHMETTDGNGLKISWSSPPLVPPLOVQVYKSENSTIVIREADKIVSATSLDVSILP 300

DB 241 LGLHMETTDGNGLKISWSSPPLVPPLOVQVYKSENSTIVIREADKIVSATSLDVSILP 300
 QY 301 GSSYEYQVGRKRLDGGIMSDMSTPRVFTQDVIYPPKILTSVCSNVEFHCYKKENKI 360
 DB 301 GSSYEYQVGRKRLDGGIMSDMSTPRVFTQDVIYPPKILTSVCSNVEFHCYKKENKI 360
 QY 361 VPSKETVMMNIAEKIPQSDVDVSDHVSQVTFPNLNETKPNKPTVDAVCCNEHECH 420
 DB 361 VPSKETVMMNIAEKIPQSDVDVSDHVSQVTFPNLNETKPNKPTVDAVCCNEHECH 420
 QY 421 RAELVIVDININISCTETGVLTKMCRWSTSTIOSLASTIQLRHRBSLVCSDIPIH 480
 DB 421 RAELVIVDININISCTETGVLTKMCRWSTSTIOSLASTIQLRHRBSLVCSDIPIH 480
 QY 481 PISEPKDYLQSDGFECIFOPIFLLSGTMMIRINHSGLSDSPICVLPDSVYKPLP 540
 DB 481 PISEPKDYLQSDGFECIFOPIFLLSGTMMIRINHSGLSDSPICVLPDSVYKPLP 540
 QY 541 SSVKAEITINIGLTKISWEKPVPEPENNLOFOIRYGLSGKEVQMKYEVYDAKSKSVLPV 600
 DB 541 SSVKAEITINIGLTKISWEKPVPEPENNLOFOIRYGLSGKEVQMKYEVYDAKSKSVLPV 600
 QY 601 PDLCAVYAVQVGRKRLDGLGYMSNMPAYIVYMDIKVPMRGEFWRILINGDMKREKV 660
 DB 601 PDLCAVYAVQVGRKRLDGLGYMSNMPAYIVYMDIKVPMRGEFWRILINGDMKREKV 660
 QY 661 TLLMKPLMNDLSQVORVIVNHHTSCNCTWSEDNHTKFTFLTEQAHVTYLAINSI 720
 DB 661 TLLMKPLMNDLSQVORVIVNHHTSCNCTWSEDNHTKFTFLTEQAHVTYLAINSI 720
 QY 721 GASVANFNLTFSWPMKVINIVOSLAVPINSSCVIWSLSPSDIKLMTFIEMKNLND 780
 DB 721 GASVANFNLTFSWPMKVINIVOSLAVPINSSCVIWSLSPSDIKLMTFIEMKNLND 780
 QY 781 GELKWLRISSVKKYIHHFPIEKYOFSLPIPEWEGKPKIINSFTODDIEKHQSDA 840
 DB 781 GELKWLRISSVKKYIHHFPIEKYOFSLPIPEWEGKPKIINSFTODDIEKHQSDA 840
 QY 841 GLYIVIPVITSSIIILGLTILSHQRMKILFMEVDPNPNCSWAGSLNFQKPEFELPI 900
 DB 841 GLYIVIPVITSSIIILGLTILSHQRMKILFMEVDPNPNCSWAGSLNFQKPEFELPI 900
 QY 901 KHTASVTCGPLLEPTEISDVSVDTSWKNKDEMPPTVAVSLSTOLEKGSVCISDQFN 960
 DB 901 KHTASVTCGPLLEPTEISDVSVDTSWKNKDEMPPTVAVSLSTOLEKGSVCISDQFN 960
 QY 961 SVNFSAEGETEYTYEASQROPVVKATLINSKPSETEEOGLNLSVTKCFSSKNSPL 1020
 DB 961 SVNFSAEGETEYTYEASQROPVVKATLINSKPSETEEOGLNLSVTKCFSSKNSPL 1020
 QY 1021 KDSFNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKKSITYL 1080
 DB 1021 KDSFNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKKSITYL 1080
 QY 1081 GVTSLIKKRESVGLLDKSVSCPPAPCLFTDIRVLQDSCSHFVNINILGTSKKTFFAS 1140
 DB 1081 GVTSLIKKRESVGLLDKSVSCPPAPCLFTDIRVLQDSCSHFVNINILGTSKKTFFAS 1140
 QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
 DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 17

US-08-178-691-4
 ; Sequence 4, Application US/09178691
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Cai
 ; APPLICANT: Friedman, Jeffrey M.
 ; TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS THAT MODULATE LEPTIN
 ; FILE REFERENCE: 600-1-205 N

;; CURRENT APPLICATION NUMBER: US/09/178,691
;; CURRENT FILING DATE: 1998-10-26
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 4
;; LENGTH: 1165
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-178-691-4

Query Match 91.3%; Score 1064; DB 15; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQFCVLLHMEFIYVITAFNLSTPTPMRFKLSCMPNSTYDYFLLPAGLSKNTS 60
DB 1 MICQFCVLLHMEFIYVITAFNLSTPTPMRFKLSCMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVERPKNSGTHSNLSKTTFHCCFSEODRNCSLCADNIEGTFVSTVSLVF 120
DB 61 NGHYETAVERPKNSGTHSNLSKTTFHCCFSEODRNCSLCADNIEGTFVSTVSLVF 120
QY 121 QOIIDANMNIOCMKGLDKLFIQVYESLFKNLFRNRYKXHLIYLPVELEDSPLYPOKGS 180
DB 121 QOIIDANMNIOCMKGLDKLFIQVYESLFKNLFRNRYKXHLIYLPVELEDSPLYPOKGS 180
QY 181 FQMVHNCNSVHECCCECLVVPPTAKLNDTLMLCKITSGGIVFQSPPLMSVQPINMVKPDP 240
DB 181 FQMVHNCNSVHECCCECLVVPPTAKLNDTLMLCKITSGGIVFQSPPLMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKIWSMSPPLVPPLOYQVYKSENSTVIREADKIVATSILVDSILP 300
DB 241 LGLHMEITDDGNLKIWSMSPPLVPPLOYQVYKSENSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEYQVAGKRLDGGIMSDMSTPRVFTTQDYIYPPPKILTVSGNSVSEFHCITYKKENKI 360
DB 301 GSSYEYQVAGKRLDGGIMSDMSTPRVFTTQDYIYPPPKILTVSGNSVSEFHCITYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSAYVFENLNETKPRGKFFDYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSAYVFENLNETKPRGKFFDYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNNISCEITDGYITKMTCRMSTSTIOSLAESTIQLRHRSLSYCSIDPSTH 480
DB 421 RYAEIYVIDVNNISCEITDGYITKMTCRMSTSTIOSLAESTIQLRHRSLSYCSIDPSTH 480
QY 481 PISEPRDCVLOSDFEECTFEOPIFILSGITMNRINHSLGSLDSEPTCYLPDSVAPPLP 540
DB 481 PISEPRDCVLOSDFEECTFEOPIFILSGITMNRINHSLGSLDSEPTCYLPDSVAPPLP 540
QY 541 SSVKAEITINISLKIWSKPVFPENNLOFQIRYGLSGKEVQMKMYEVDASKSVSLPV 600
DB 541 SSVKAEITINISLKIWSKPVFPENNLOFQIRYGLSGKEVQMKMYEVDASKSVSLPV 600
QY 601 PDLCAVYAVQVCKRDLGIGYWSNNSPAYVYMDIKVPMRGDEFRIRINDGTMKKEKNV 660
DB 601 PDLCAVYAVQVCKRDLGIGYWSNNSPAYVYMDIKVPMRGDEFRIRINDGTMKKEKNV 660
QY 661 TLLMKPLMNDLSQVQRYVINHHSTSCNGTWSBDVGNHKKFFFLMEQAHYVVALINSI 720
DB 661 TLLMKPLMNDLSQVQRYVINHHSTSCNGTWSBDVGNHKKFFFLMEQAHYVVALINSI 720
QY 721 GASVANFNLTFSMPKSVNIQSLAYPLNNSCVIYSLTSPDYFLMYFIEEMKLNED 780
DB 721 GASVANFNLTFSMPKSVNIQSLAYPLNNSCVIYSLTSPDYFLMYFIEEMKLNED 780
QY 781 GEIKWLRISSSVKKYKHIDHFIPIEKYQSPLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKWLRISSSVKKYKHIDHFIPIEKYQSPLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYIVYPIIISILLGLTLLISHQRMKLFMEDVAPNPKNSAOCNLNOKPPTFEHLFI 900
DB 841 GLYIVYPIIISILLGLTLLISHQRMKLFMEDVAPNPKNSAOCNLNOKPPTFEHLFI 900

DB 841 GLYIVYPIIISILLGLTLLISHQRMKLFMEDVAPNPKNSAOCNLNOKPPTFEHLFI 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSMKKNKDMPTTVVSLSTTDLEKGSVCISDQFN 960
DB 901 KHTASVTCGPLLEPETISEDISVDTSMKKNKDMPTTVVSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFSEABEGTEVYDESOQROPVKKYATLISNSKPSGEGEGLINSSVTKCFSSKNSPL 1020
DB 961 SVNFSEABEGTEVYDESOQROPVKKYATLISNSKPSGEGEGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSSWEIEAOAFELISDQHPNLSPHLTFESGIDELKLEGNFPEENNDKKSITYL 1080
DB 1021 KDSFSSWEIEAOAFELISDQHPNLSPHLTFESGIDELKLEGNFPEENNDKKSITYL 1080
QY 1081 GVTSIKRRSGVLLTDKSRVSCPAPCLFTDIRVLQDSCSHFVNINMLGTSKKTFAS 1140
DB 1081 GVTSIKRRSGVLLTDKSRVSCPAPCLFTDIRVLQDSCSHFVNINMLGTSKKTFAS 1140
QY 1141 YMPQOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQOTCSTQTHKIMENKMDLTV 1165

RESULT 18
US-09-700-813-10
; Sequence 10, Application US/09700813
; GENERAL INFORMATION:
; APPLICANT: SIERRA-HONIGMANN, Rocio
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND WOUND HEALING
; FILE REFERENCE: 044574-5029
; CURRENT APPLICATION NUMBER: US/09/700,813
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: PCT/US99/11209
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 60/086,354
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-700-813-10

Query Match 91.3%; Score 1064; DB 21; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQFCVLLHMEFIYVITAFNLSTPTPMRFKLSCMPNSTYDYFLLPAGLSKNTS 60
DB 1 MICQFCVLLHMEFIYVITAFNLSTPTPMRFKLSCMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVERPKNSGTHSNLSKTTFHCCFSEODRNCSLCADNIEGTFVSTVSLVF 120
DB 61 NGHYETAVERPKNSGTHSNLSKTTFHCCFSEODRNCSLCADNIEGTFVSTVSLVF 120
QY 121 QOIIDANMNIOCMKGLDKLFIQVYESLFKNLFRNRYKXHLIYLPVELEDSPLYPOKGS 180
DB 121 QOIIDANMNIOCMKGLDKLFIQVYESLFKNLFRNRYKXHLIYLPVELEDSPLYPOKGS 180
QY 181 FQMVHNCNSVHECCCECLVVPPTAKLNDTLMLCKITSGGIVFQSPPLMSVQPINMVKPDP 240
DB 181 FQMVHNCNSVHECCCECLVVPPTAKLNDTLMLCKITSGGIVFQSPPLMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKIWSMSPPLVPPLOYQVYKSENSTVIREADKIVATSILVDSILP 300
DB 241 LGLHMEITDDGNLKIWSMSPPLVPPLOYQVYKSENSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEYQVAGKRLDGGIMSDMSTPRVFTTQDYIYPPPKILTVSGNSVSEFHCITYKKENKI 360
DB 301 GSSYEYQVAGKRLDGGIMSDMSTPRVFTTQDYIYPPPKILTVSGNSVSEFHCITYKKENKI 360

QY 361 VPSKETVMMNNALEKIPQSDYDVSDHVSXVTFPNLNETKPRGKPTYYDAVYCCNEHECHH 420
DB 361 VPSKETVMMNNALEKIPQSDYDVSDHVSXVTFPNLNETKPRGKPTYYDAVYCCNEHECHH 420
QY 421 RYAEIVIDVNIINISCTEGYLTAKMCRWSTSTIOSLAESTIOLRHRSSLYCSDIPSIH 480
DB 421 RYAEIVIDVNIINISCTEGYLTAKMCRWSTSTIOSLAESTIOLRHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGFECEIFQPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVYKPLRP 540
DB 481 PISEPKDCYLOSDGFECEIFQPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVYKPLRP 540
QY 541 SSYKAEITINIGLKISWEKPVFPENNLOFOIRYGLSGKEVOMKMEYVDASKSVSLPV 600
DB 541 SSYKAEITINIGLKISWEKPVFPENNLOFOIRYGLSGKEVOMKMEYVDASKSVSLPV 600
QY 601 PDLCAVYAVOVRCKRLDGLGYMSNMSNPAYTYVMDIKVPMRGPFRRIINGDTMKKEKNV 660
DB 601 PDLCAVYAVOVRCKRLDGLGYMSNMSNPAYTYVMDIKVPMRGPFRRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVORYVNIHNTSCNGTWSHEDVGNHTKFEFLMTEQAHVTVLAINSI 720
DB 661 TLLMKPLMKNDLSQVORYVNIHNTSCNGTWSHEDVGNHTKFEFLMTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPSDYKLMFIIEMKNLND 780
DB 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPSDYKLMFIIEMKNLND 780
QY 781 GEIKMLRISSSVKYYIHDFIPIEKYQSLYPIFMEGVGKPKIINSFODDIEKHOSDA 840
DB 781 GEIKMLRISSSVKYYIHDFIPIEKYQSLYPIFMEGVGKPKIINSFODDIEKHOSDA 840
QY 841 GLYIVPVYIISSTILLGLTLLISHQRMKLLFWEDEVNPKNCWAGLNFQKPEFHEHFI 900
DB 841 GLYIVPVYIISSTILLGLTLLISHQRMKLLFWEDEVNPKNCWAGLNFQKPEFHEHFI 900
QY 901 KHTASVTCGPLLEPPTISEDISVDTSMKNKDEMPPTVYSLSTDLKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLEPPTISEDISVDTSMKNKDEMPPTVYSLSTDLKSGVCSIDQFN 960
QY 961 SVNFSAEGETEYVTEDESOROPFVKYATLISNKPSETGEEOGLINSYATKCFSSKNSPL 1020
DB 961 SVNFSAEGETEYVTEDESOROPFVKYATLISNKPSETGEEOGLINSYATKCFSSKNSPL 1020
QY 1021 KOSFSNWSWEIEAOAFIISDOHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIIYL 1080
DB 1021 KOSFSNWSWEIEAOAFIISDOHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIIYL 1080
QY 1081 GYTSIKKRESGVLLTDKSHVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
DB 1081 GYTSIKKRESGVLLTDKSHVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMQFOTCSTQTHKIMENKMDLTV 1165

RESULT 19
US-09-948-933-256
; Sequence 256, Application us/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; FILE REFERENCE: C1000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256

LENGTH: 1165
; TYPE: PRT
; ORGANISM: Human
US-09-948-933-256

Query Match 91.3%; Score 1064; DB 23; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICORCVALLHMEFIYVTAFLNLSYPIPMWPKLSCMPNPNYUVELLPAGLSKNTS 60
DB 1 MICORCVALLHMEFIYVTAFLNLSYPIPMWPKLSCMPNPNYUVELLPAGLSKNTS 60
QY 61 NGHYEAVPEKNSSGTTHSNLSKTFHCCFSEODRNCSLCADNIEGTFTVNSLVF 120
DB 61 NGHYEAVPEKNSSGTTHSNLSKTFHCCFSEODRNCSLCADNIEGTFTVNSLVF 120
QY 121 QOIDANNIQCWLKGDLCFICVESLFKNLPRNRYKVHLLYVLPVLEDSPLVPQKS 180
DB 121 QOIDANNIQCWLKGDLCFICVESLFKNLPRNRYKVHLLYVLPVLEDSPLVPQKS 180
QY 181 FQWVHNCNVHCCBCLVVPRAKINDTLMLCKITSGGVITQSPILMSVOPINMKAPDPP 240
DB 181 FQWVHNCNVHCCBCLVVPRAKINDTLMLCKITSGGVITQSPILMSVOPINMKAPDPP 240
QY 241 LGIHEMTDGNLKTISWSSPPLVPPLOQYVYSENSVIVREADKIVATSILVDSILP 300
DB 241 LGIHEMTDGNLKTISWSSPPLVPPLOQYVYSENSVIVREADKIVATSILVDSILP 300
QY 301 GSSYEQVQGRKLDGFGTSDMSTRVFTTOYIYFPPKILSVGSVNSFHCITYKKNKI 360
DB 301 GSSYEQVQGRKLDGFGTSDMSTRVFTTOYIYFPPKILSVGSVNSFHCITYKKNKI 360
QY 361 VPSKETVMMNNALEKIPQSDYDVSDHVSXVTFPNLNETKPRGKPTYYDAVYCCNEHECHH 420
DB 361 VPSKETVMMNNALEKIPQSDYDVSDHVSXVTFPNLNETKPRGKPTYYDAVYCCNEHECHH 420
QY 421 RYAEIVIDVNIINISCTEGYLTAKMCRWSTSTIOSLAESTIOLRHRSSLYCSDIPSIH 480
DB 421 RYAEIVIDVNIINISCTEGYLTAKMCRWSTSTIOSLAESTIOLRHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGFECEIFQPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVYKPLRP 540
DB 481 PISEPKDCYLOSDGFECEIFQPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVYKPLRP 540
QY 541 SSYKAEITINIGLKISWEKPVFPENNLOFOIRYGLSGKEVOMKMEYVDASKSVSLPV 600
DB 541 SSYKAEITINIGLKISWEKPVFPENNLOFOIRYGLSGKEVOMKMEYVDASKSVSLPV 600
QY 601 PDLCAVYAVOVRCKRLDGLGYMSNMSNPAYTYVMDIKVPMRGPFRRIINGDTMKKEKNV 660
DB 601 PDLCAVYAVOVRCKRLDGLGYMSNMSNPAYTYVMDIKVPMRGPFRRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVORYVNIHNTSCNGTWSHEDVGNHTKFEFLMTEQAHVTVLAINSI 720
DB 661 TLLMKPLMKNDLSQVORYVNIHNTSCNGTWSHEDVGNHTKFEFLMTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPSDYKLMFIIEMKNLND 780
DB 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPSDYKLMFIIEMKNLND 780
QY 781 GEIKMLRISSSVKYYIHDFIPIEKYQSLYPIFMEGVGKPKIINSFODDIEKHOSDA 840
DB 781 GEIKMLRISSSVKYYIHDFIPIEKYQSLYPIFMEGVGKPKIINSFODDIEKHOSDA 840
QY 841 GLYIVPVYIISSTILLGLTLLISHQRMKLLFWEDEVNPKNCWAGLNFQKPEFHEHFI 900
DB 841 GLYIVPVYIISSTILLGLTLLISHQRMKLLFWEDEVNPKNCWAGLNFQKPEFHEHFI 900
QY 901 KHTASVTCGPLLEPPTISEDISVDTSMKNKDEMPPTVYSLSTDLKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLEPPTISEDISVDTSMKNKDEMPPTVYSLSTDLKSGVCSIDQFN 960

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Qy 961 SVNSEAGTEVYEDSROPEFVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNSEAGTEVYEDSROPEFVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020
Qy 1021 KDSFNSSEWEIEAOAFLLSDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKRSIYLL 1080
Db 1021 KDSFNSSEWEIEAOAFLLSDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKRSIYLL 1080
Qy 1081 GVTSIKKRESGVLLTDKRSVSCPPAPCLFTDIRVLQDSCSHFENNINLTGSSKRTFAS 1140
Db 1081 GVTSIKKRESGVLLTDKRSVSCPPAPCLFTDIRVLQDSCSHFENNINLTGSSKRTFAS 1140
Qy 1141 YMPQOTCSTQTHKIMENKMDLTIV 1165
Db 1141 YMPQOTCSTQTHKIMENKMDLTIV 1165

RESULT 20
US-09-948-947-73
; Sequence 73, Application US/09948947
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO00786
; CURRENT APPLICATION NUMBER: US/09/948, 947
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Human
US-09-948-947-73

Query Match          91.3%; Score 1064; DB 23; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MICQKFCVALLHMERIYITAFNLSTPTPMRFKLSGMPNSTYDFELIPAGLSKNTS 60
Db 1 MICQKFCVALLHMERIYITAFNLSTPTPMRFKLSGMPNSTYDFELIPAGLSKNTS 60
Qy 61 NGHYETAEPKFNSSGTHPSNLSTTFHCCFSEODRNCISLADNIEGTFVSTVNSLIV 120
Db 61 NGHYETAEPKFNSSGTHPSNLSTTFHCCFSEODRNCISLADNIEGTFVSTVNSLIV 120
Qy 121 QOIDANMNIQCLWLGDKLFICVYESLFRNRYNYKHLHYLPEVLEDSPLVPQKGS 180
Db 121 QOIDANMNIQCLWLGDKLFICVYESLFRNRYNYKHLHYLPEVLEDSPLVPQKGS 180
Qy 181 FQMVHNCNSVHECCCECLVVPPTAKINDLLMCLKITSGGVIFQSPIMSVQPTNMVKPDP 240
Db 181 FQMVHNCNSVHECCCECLVVPPTAKINDLLMCLKITSGGVIFQSPIMSVQPTNMVKPDP 240
Qy 241 LGLHMEITDDGMLKISWSSPPLVPPLOYQVKSSENSSTTVIREADKIVATSILVDSILP 300
Db 241 LGLHMEITDDGMLKISWSSPPLVPPLOYQVKSSENSSTTVIREADKIVATSILVDSILP 300
Qy 301 GSSYEVQYGRKLDGPGIMSDSTPRVFTTQDVIEFPKILTSVGSNSVFFHCITYKKENKI 360
Db 301 GSSYEVQYGRKLDGPGIMSDSTPRVFTTQDVIEFPKILTSVGSNSVFFHCITYKKENKI 360
Qy 361 VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFNLNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RRAELVYIDVYNINISCEFDGILTKMTCKRMSSTIOSLAESTIQLKXHRSLYCSIDIPSIH 480

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Db 421 RRAELVYIDVYNINISCEFDGILTKMTCKRMSSTIOSLAESTIQLKXHRSLYCSIDIPSIH 480
Qy 481 PISEKDCVLOSDFGEYECIFOPIFLLSGTMMIRINHSLSUSPPTCVLPDSYVKPLPP 540
Db 481 PISEKDCVLOSDFGEYECIFOPIFLLSGTMMIRINHSLSUSPPTCVLPDSYVKPLPP 540
Qy 541 SSVKAETINIGLKI SWKPVFPEENNLOFOIRYGLSGREVOYKRYEYDANKSASVSLPV 600
Db 541 SSVKAETINIGLKI SWKPVFPEENNLOFOIRYGLSGREVOYKRYEYDANKSASVSLPV 600
Qy 601 PDLCAVYAVQVCKRLDGLGYSNMSNPAYTVVMDIKVPMRGPETWRIITNGTAKKEKV 660
Db 601 PDLCAVYAVQVCKRLDGLGYSNMSNPAYTVVMDIKVPMRGPETWRIITNGTAKKEKV 660
Qy 661 TLIMKPLMKNDLSGVORVYINHTSCNQTSEEDVGNHRTKFTFLVTEQAHYTVLAINSI 720
Db 661 TLIMKPLMKNDLSGVORVYINHTSCNQTSEEDVGNHRTKFTFLVTEQAHYTVLAINSI 720
Qy 721 GASVANFNLTFESWPMKSVNIYOSLSAYPLNSSCVIYSWILSPSDYKLMYFIEMKNLND 780
Db 721 GASVANFNLTFESWPMKSVNIYOSLSAYPLNSSCVIYSWILSPSDYKLMYFIEMKNLND 780
Qy 781 GEIKMLRISSSVKYYIHDFPIEKYQSLPIFMEGGRKIIINSTQODDIEKHQSDA 840
Db 781 GEIKMLRISSSVKYYIHDFPIEKYQSLPIFMEGGRKIIINSTQODDIEKHQSDA 840
Qy 841 GLYVIVPVISSSILLGLTLLSHQMKLFMEDVNPANCMAOGLNFKPTEFEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLSHQMKLFMEDVNPANCMAOGLNFKPTEFEHLFI 900
Qy 901 KHTASVTCGPLLEPBTISEDISVDTSMKNKDEMPYTVVSLSTDTLEKGSVCISDOFN 960
Db 901 KHTASVTCGPLLEPBTISEDISVDTSMKNKDEMPYTVVSLSTDTLEKGSVCISDOFN 960
Qy 961 SVNSEAGTEVYEDSROPEFVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNSEAGTEVYEDSROPEFVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020
Qy 1021 KDSFNSSEWEIEAOAFLLSDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKRSIYLL 1080
Db 1021 KDSFNSSEWEIEAOAFLLSDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKRSIYLL 1080
Qy 1081 GVTSIKKRESGVLLTDKRSVSCPPAPCLFTDIRVLQDSCSHFENNINLTGSSKRTFAS 1140
Db 1081 GVTSIKKRESGVLLTDKRSVSCPPAPCLFTDIRVLQDSCSHFENNINLTGSSKRTFAS 1140
Qy 1141 YMPQOTCSTQTHKIMENKMDLTIV 1165
Db 1141 YMPQOTCSTQTHKIMENKMDLTIV 1165

RESULT 21
US-10-095-929-11
; Sequence 11, Application US/10095929
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; Cioffi, Joseph
; Zupancic, Thomas Joel
; Shafer, Alan Wayne
; TITLE OF INVENTION: METHODS FOR USING THE OBES
; GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
; DEVELOPMENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,929
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,957
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-095-929-11

Query Match 91.3%; Score 1064; DB 24; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFYVTAFLNSLYITPMRFKLSQMPNSTYDFLLPAGLSKNTS 60
DB 1 MICQKFCVLLHMEFYVTAFLNSLYITPMRFKLSQMPNSTYDFLLPAGLSKNTS 60
QY 61 NGHTEFAVPEKNSSTHNSLSTKTHCCFSEODRNCSCADNIEGTEVSTNSLVF 120
DB 61 NGHTEFAVPEKNSSTHNSLSTKTHCCFSEODRNCSCADNIEGTEVSTNSLVF 120
QY 121 QOIDANMNIOGKLDKLFICYVESLFRNRYKYHLLYVLEVEDSLVPQKGS 180
DB 121 QOIDANMNIOGKLDKLFICYVESLFRNRYKYHLLYVLEVEDSLVPQKGS 180
QY 181 FQMVHNCSEVHCECELVPTAKLNDLLMCLKITSGVIFQSPIMSVQPIINMKPDP 240
DB 181 FQMVHNCSEVHCECELVPTAKLNDLLMCLKITSGVIFQSPIMSVQPIINMKPDP 240
QY 241 LGLHMEITDDGMLKISMSPLVPPLOYQVYKSESTVIREADKIYASATSLVDSILP 300
DB 241 LGLHMEITDDGMLKISMSPLVPPLOYQVYKSESTVIREADKIYASATSLVDSILP 300
QY 301 GSSYEYQVAGKRLDGPGLSDMSTPRVFTTQDVIYFPKILTSVGSNVSFHCILYKKEKI 360
DB 301 GSSYEYQVAGKRLDGPGLSDMSTPRVFTTQDVIYFPKILTSVGSNVSFHCILYKKEKI 360
QY 361 VPSKEIVMMNLAEKIPQSQYVVSVDHVSKVTFPNLNETKPRGKFTYDAVYCNEHECHH 420
DB 361 VPSKEIVMMNLAEKIPQSQYVVSVDHVSKVTFPNLNETKPRGKFTYDAVYCNEHECHH 420
QY 421 RYAEIYVIVDNNINISCTGTYLTKMTCRWSSTIQSLASTIQLRHRSLYCSIDIPSIH 480
DB 421 RYAEIYVIVDNNINISCTGTYLTKMTCRWSSTIQSLASTIQLRHRSLYCSIDIPSIH 480
QY 481 PISEPKDCYLOSDGFECIFQPIFLISGTYMIRINHSGLSDSPPTCVLPQSVYKPLPP 540
DB 481 PISEPKDCYLOSDGFECIFQPIFLISGTYMIRINHSGLSDSPPTCVLPQSVYKPLPP 540
QY 541 SSVKAEITINIGLTKISWEKPVFPENNIOFOIRYGLSGREYQWKVEYVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLTKISWEKPVFPENNIOFOIRYGLSGREYQWKVEYVDAKSKSVSLPV 600

QY 601 PDLCAVAYAVQVCKRLDGLGYSNMNSNPAYTVYMDIKVPMRGPFWRIINGDTMKKKNV 660
DB 601 PDLCAVAYAVQVCKRLDGLGYSNMNSNPAYTVYMDIKVPMRGPFWRIINGDTMKKKNV 660
QY 661 TLLMKPLKNDLSQVQRYVNHHTSCNCTWSEDNHKKFFFLTEQAHYTVYLAINSI 720
DB 661 TLLMKPLKNDLSQVQRYVNHHTSCNCTWSEDNHKKFFFLTEQAHYTVYLAINSI 720
QY 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYMWISPSDYKLMFIEMKNLND 780
DB 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYMWISPSDYKLMFIEMKNLND 780
QY 781 GEIKMLRISSSVKYYIHDFPIIEKYQSLYPIFMEGVGKPKINSFTODDIEKHQSDA 840
DB 781 GEIKMLRISSSVKYYIHDFPIIEKYQSLYPIFMEGVGKPKINSFTODDIEKHQSDA 840
QY 841 GLYIVPVYISSLILGLTLLSHORMKLEWEDVNPNCNAGLNFQKPEFHEHFT 900
DB 841 GLYIVPVYISSLILGLTLLSHORMKLEWEDVNPNCNAGLNFQKPEFHEHFT 900
QY 901 KHTASVTCGPLLEPETISEDIVDSVDMKNKDEMPPTVVSLLSTDLKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLEPETISEDIVDSVDMKNKDEMPPTVVSLLSTDLKSGVCSIDQFN 960
QY 961 SYNFEAEGETEYTYEDESQROPVYKATLISNKSSETEBQGLNNSVTKCFSSKNSE 1020
DB 961 SYNFEAEGETEYTYEDESQROPVYKATLISNKSSETEBQGLNNSVTKCFSSKNSE 1020
QY 1021 KDSFNSWEIEAQAFFILSDQHPNISPILTFESGLDELKLEGNFPEENDKRSIYL 1080
DB 1021 KDSFNSWEIEAQAFFILSDQHPNISPILTFESGLDELKLEGNFPEENDKRSIYL 1080
QY 1081 GYTSIKRRESGVLLTDKSVSCFPAPCLFTDIRVLQDSCHFVNNINLGTSSKRTFAS 1140
DB 1081 GYTSIKRRESGVLLTDKSVSCFPAPCLFTDIRVLQDSCHFVNNINLGTSSKRTFAS 1140
QY 1141 YMPFOFOTCSTQTHKIMENKCDLTV 1165
DB 1141 YMPFOFOTCSTQTHKIMENKCDLTV 1165

RESULT 22
US-08-583-153-4
Sequence 4, Application US/08583153
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,153
FILING DATE: 28-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-050
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1165 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-583-153-4

Query Match 82.7% Score 963; DB 9; Length 1165;
 Best Local Similarity 99.8% Pred. No. 0;
 Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMERIYITAFNLISYPTIPMRFKLSCHMPNSTYDYFLPAGLSKNTS 60
 Db 1 MICQKFCVLLHMERIYITAFNLISYPTIPMRFKLSCHMPNSTYDYFLPAGLSKNTS 60
 QY 61 NGHETAVEPKFNSSGTHFNSLSKTTFHCCFSEODRNCSLCADNIECKTFVTSNLSVF 120
 Db 61 NGHETAVEPKFNSSGTHFNSLSKTTFHCCFSEODRNCSLCADNIECKTFVTSNLSVF 120
 QY 121 QOIDANNNIQCWLKGDLLFTCYVESLEKRNLFRRNTNKHVHLIYLPVELDESPLYPOKGS 180
 Db 121 QOIDANNNIQCWLKGDLLFTCYVESLEKRNLFRRNTNKHVHLIYLPVELDESPLYPOKGS 180
 QY 181 FOMVHCNCSVHECCCELPVPFPAKINDTLIMGLKTTSGVITFOSPLMSVOPINMVKPDPP 240
 Db 181 FOMVHCNCSVHECCCELPVPFPAKINDTLIMGLKTTSGVITFOSPLMSVOPINMVKPDPP 240
 QY 241 LGLHMEITDDGKLTISWSSPLVPPLOQYVKSSENSTVIREADKIYSATSLVDSILP 300
 Db 241 LGLHMEITDDGKLTISWSSPLVPPLOQYVKSSENSTVIREADKIYSATSLVDSILP 300
 QY 301 GSSYEVQYGRKRLDGPGLWSMDSTPRVFTTODVYTFPPKILTSVGSNVSFHCIYKKNKI 360
 Db 301 GSSYEVQYGRKRLDGPGLWSMDSTPRVFTTODVYTFPPKILTSVGSNVSFHCIYKKNKI 360
 QY 361 VPSKETVMMNLAEKIPQSOYDVSDHSAKVFENLNETKPRGKFYDVAVYCCNEHECH 420
 Db 361 VPSKETVMMNLAEKIPQSOYDVSDHSAKVFENLNETKPRGKFYDVAVYCCNEHECH 420
 QY 421 RYAEIYDVNINISCETDGYLTMTKCRWSTSTIOSLAESTQLRYHRSSLYCSDIPSIH 480
 Db 421 RYAEIYDVNINISCETDGYLTMTKCRWSTSTIOSLAESTQLRYHRSSLYCSDIPSIH 480
 QY 481 PISEPKDCYLOSDFYECPFPIPLISGYTMMIRINHSLSGLSDSPPTCYLPDSVVKPLPP 540
 Db 481 PISEPKDCYLOSDFYECPFPIPLISGYTMMIRINHSLSGLSDSPPTCYLPDSVVKPLPP 540
 QY 541 SSVKAEITINIGLKTISMEKPYEPENNLOFOLRYGLSGEYQMKWEYVDASKSISLPV 600
 Db 541 SSVKAEITINIGLKTISMEKPYEPENNLOFOLRYGLSGEYQMKWEYVDASKSISLPV 600
 QY 601 PDLCAVAVQYRCKRLDGLGYSWMSNPAYTYVMDIKYPMRGPEEFRIINGDTMKKEKNV 660
 Db 601 PDLCAVAVQYRCKRLDGLGYSWMSNPAYTYVMDIKYPMRGPEEFRIINGDTMKKEKNV 660
 QY 661 TLLMKPLKNDLSGVORYVINHHTSCNGTSEDVGNHTKFFFLTMEQAHVTVLAINSI 720
 Db 661 TLLMKPLKNDLSGVORYVINHHTSCNGTSEDVGNHTKFFFLTMEQAHVTVLAINSI 720
 QY 721 GASVANFNLTSPWPSKYNIVOSLSAYPLNSSCVIWSLSPSDKILMFTIEKKNLND 780
 Db 721 GASVANFNLTSPWPSKYNIVOSLSAYPLNSSCVIWSLSPSDKILMFTIEKKNLND 780
 QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
 Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
 QY 841 GLIYIVPVIYISSILLGLTLLISHQRMKLFWEDEVNPNKNCMAOGLNOKETFEHLFI 900

Db 841 GLIYIVPVIYISSILLGLTLLISHQRMKLFWEDEVNPNKNCMAOGLNOKETFEHLFI 900
 QY 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVVSILSTDLEKGSYCIDQFN 960
 Db 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVVSILSTDLEKGSYCIDQFN 960
 QY 961 SVNFSAEGETEYTEDESOROPPVKATLISNSKPSGTGBOGLINSYTKCFSSKN SPL 1020
 Db 961 SVNFSAEGETEYTEDESOROPPVKATLISNSKPSGTGBOGLINSYTKCFSSKN SPL 1020
 QY 1021 KDSFSSWEIEQAFFILSDQHPNIIISPHFSEGLDELTKEGNFPENNDRKSIYYL 1080
 Db 1021 KDSFSSWEIEQAFFILSDQHPNIIISPHFSEGLDELTKEGNFPENNDRKSIYYL 1080
 QY 1081 GYTSIKRRESGYLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFENNINLGTSKKTFAS 1140
 Db 1081 GYTSIKRRESGYLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFENNINLGTSKKTFAS 1140
 QY 1141 YMPQFOTCSTQTHKIMENKRCDLTV 1165
 Db 1141 YMPQFOTCSTQTHKIMENKRCDLTV 1165

RESULT 23
 US-08-599-455A-4
 : Sequence 4, Application us//08599455A
 : GENERAL INFORMATION:
 : APPLICANT: Tartaglia, Louis A.
 : APPLICANT: Tepper, Robert T.
 : APPLICANT: Calpepper, Janice A.
 : TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
 : NUMBER OF SEQUENCES: 44
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Fish & Richardson, P.C.
 : STREET: 225 Franklin Street
 : CITY: Boston
 : STATE: MA
 : COUNTRY: US
 : ZIP: 02110-2804
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: Windows95
 : SOFTWARE: FastSeq for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/599,455A
 : FILING DATE: 22-JAN-1996
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/583,153
 : FILING DATE: 28-DEC-1995
 : APPLICATION NUMBER: 08/570,142
 : FILING DATE: 11-DEC-1995
 : APPLICATION NUMBER: 08/569,485
 : FILING DATE: 08-DEC-1995
 : APPLICATION NUMBER: 08/566,622
 : FILING DATE: 04-DEC-1995
 : APPLICATION NUMBER: 08/562,663
 : FILING DATE: 11-NOV-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Melkielejohn, Ph.D., Anita L.
 : REGISTRATION NUMBER: 35,283
 : REFERENCE/DOCKET NUMBER: 07334/017001
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-542-5070
 : TELEFAX: 617-542-8906
 : TELE: 200154
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1165 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-599-455A-4

Query Match 82.7%; Score 963; DB 9; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFYVTAFLNLSYPTIPWREKLSGMPNPNSTYDVELLPAGLSKNTS 60
DB 1 MICQKFCVLLHMEFYVTAFLNLSYPTIPWREKLSGMPNPNSTYDVELLPAGLSKNTS 60
QY 61 NGHYETAPEPKFNSSGTHESNLSTKTFHCCFRSEODRNCSLCADNIEGKTPVSTVNSLVE 120
DB 61 NGHYETAPEPKFNSSGTHESNLSTKTFHCCFRSEODRNCSLCADNIEGKTPVSTVNSLVE 120
QY 121 QOIDAMNMQCKGDKLKFICYVESLFKNLFRNRYKXHLVLEPEVLEDSFLVPOKGS 180
DB 121 QOIDAMNMQCKGDKLKFICYVESLFKNLFRNRYKXHLVLEPEVLEDSFLVPOKGS 180
QY 181 FQWVHNCSEVHECCLELVPTAKLNDTLMLKITSQVIFQSPIMSVOPIMVAPDP 240
DB 181 FQWVHNCSEVHECCLELVPTAKLNDTLMLKITSQVIFQSPIMSVOPIMVAPDP 240
QY 241 LGLHMEITDDGNLKSWSPPPLVPEPLQYQVXSENSSTVIREADKIVSATSLVDSTLP 300
DB 241 LGLHMEITDDGNLKSWSPPPLVPEPLQYQVXSENSSTVIREADKIVSATSLVDSTLP 300
QY 301 GSSYEYQVGRKLDGPGIMSDMSTPRVETODVIFPPKILTSVGSNSVGFHCYKKEKNI 360
DB 301 GSSYEYQVGRKLDGPGIMSDMSTPRVETODVIFPPKILTSVGSNSVGFHCYKKEKNI 360
QY 361 VPSKEIVMMNLAERKIPQSOYDVSDVSKVTFENLNETKPRGKTFYDVAVCCNEHECH 420
DB 361 VPSKEIVMMNLAERKIPQSOYDVSDVSKVTFENLNETKPRGKTFYDVAVCCNEHECH 420
QY 421 RYAEIYVIDVNNINISCTEGYLTMTKCRWSTSTIOSLASTIOLRYHRSLSYCSIDPSIH 480
DB 421 RYAEIYVIDVNNINISCTEGYLTMTKCRWSTSTIOSLASTIOLRYHRSLSYCSIDPSIH 480
QY 481 PISEPKDCYLOSDFEFCIFOPITFLSGTYMIRINHSGLSDSPPTCYLPDSVVPRLP 540
DB 481 PISEPKDCYLOSDFEFCIFOPITFLSGTYMIRINHSGLSDSPPTCYLPDSVVPRLP 540
QY 541 SSVKAEITINIGLKSISWEKPYFPENNLOFOIRYGLSGKEVOMKMEYVDASKSYSLPV 600
DB 541 SSVKAEITINIGLKSISWEKPYFPENNLOFOIRYGLSGKEVOMKMEYVDASKSYSLPV 600
QY 601 POLCAVYAVQVCKRLDGLGYMSNPNPAYTVVMDIKVPRGDEPRRIINGDTMKKEKNV 660
DB 601 POLCAVYAVQVCKRLDGLGYMSNPNPAYTVVMDIKVPRGDEPRRIINGDTMKKEKNV 660
QY 661 TLLMPLKMNDSLCGYORVYVNHHTSCNGTMSDGNHRTKFTFLMEQAHYTVLAINSI 720
DB 661 TLLMPLKMNDSLCGYORVYVNHHTSCNGTMSDGNHRTKFTFLMEQAHYTVLAINSI 720
QY 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPDYKLMFIEEMKLNED 780
DB 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPDYKLMFIEEMKLNED 780
QY 781 GEIKMLRISSSVKYYIHDFIPIEKYQPSLYPIEMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKMLRISSSVKYYIHDFIPIEKYQPSLYPIEMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVYVPISSILLGLLLSHQRMKLFMEDVNPKNCSMAOGLNQKRETFEHLFI 900
DB 841 GLYIVYVPISSILLGLLLSHQRMKLFMEDVNPKNCSMAOGLNQKRETFEHLFI 900
QY 901 KHTASVTCGPIILPEPTISEDIVPTSMKNKDEMMPTTVVSLSTTDLKGSVCISDQPN 960
DB 901 KHTASVTCGPIILPEPTISEDIVPTSMKNKDEMMPTTVVSLSTTDLKGSVCISDQPN 960

QY 961 SVNFEAEGETEYVEDESOROPFVKYATLISNSKPSFTEGEOGLJNSSVTKCRFSKNSPL 1020
DB 961 SVNFEAEGETEYVEDESOROPFVKYATLISNSKPSFTEGEOGLJNSSVTKCRFSKNSPL 1020
QY 1021 KDSFNSSWTEIAQAFIILSDQHPNITSPHLTSEGLDELKLEGNFPEENNKKSTIYL 1080
DB 1021 KDSFNSSWTEIAQAFIILSDQHPNITSPHLTSEGLDELKLEGNFPEENNKKSTIYL 1080
QY 1081 GYTSIKKRESGYLLTDRSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140
DB 1081 GYTSIKKRESGYLLTDRSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKWCULTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKWCULTV 1165

RESULT 24
US-08-638-524A-4
Sequence 4, Application US/08638524A
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 021001-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,524A
FILING DATE: 26-APR-1996
CLASSIFICATION: 336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids

TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-638-524A-4

Query Match 82.7%; Score 963; DB 10; Length 1165;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCOQFCVLLHMERIYVTAENLSPITPMWRKLSKMPNNTYDVELLPAGLSKNTS 60
 DB 1 MCOQFCVLLHMERIYVTAENLSPITPMWRKLSKMPNNTYDVELLPAGLSKNTS 60
 QY 61 NGHETAAVEPKNSGTHNSLKTFFHCCFSEODRNCSLADNTEGTFVSTVSLVF 120
 DB 61 NGHETAAVEPKNSGTHNSLKTFFHCCFSEODRNCSLADNTEGTFVSTVSLVF 120
 QY 121 QOIDANMNIQCLWKGDCLKFICVESLFKNLFRNRYKYVHLLVLEPEVEDSPLVPQKGS 180
 DB 121 QOIDANMNIQCLWKGDCLKFICVESLFKNLFRNRYKYVHLLVLEPEVEDSPLVPQKGS 180
 QY 181 FQMVHNCNSVHCCCEGLVVPVPAKINDTLMLKITSGGVITQSPMLSVQIPMMKPDPP 240
 DB 181 FQMVHNCNSVHCCCEGLVVPVPAKINDTLMLKITSGGVITQSPMLSVQIPMMKPDPP 240
 QY 241 LGLHMETDDGNLKISWSSPLVPPLOQVQVYSENSTVIREADKIVATSLLVDSILP 300
 DB 241 LGLHMETDDGNLKISWSSPLVPPLOQVQVYSENSTVIREADKIVATSLLVDSILP 300
 QY 301 GSSYEYQVAGKRLDGGTMSDSTPRVFTTODVYTPPKILTSVGSNVSEHCILYKKEKNI 360
 DB 301 GSSYEYQVAGKRLDGGTMSDSTPRVFTTODVYTPPKILTSVGSNVSEHCILYKKEKNI 360
 QY 361 VPSKETIYVMMANLAERKIPQSOQYDVSDHVSQVTFENLNETKPRCKFTYDAVCCNEHECH 420
 DB 361 VPSKETIYVMMANLAERKIPQSOQYDVSDHVSQVTFENLNETKPRCKFTYDAVCCNEHECH 420
 QY 421 RYAEIVYDVNINISGETDGYLTRKTCRWSTSTIOSLAESTLOLRHRSLSYCSIDPSIH 480
 DB 421 RYAEIVYDVNINISGETDGYLTRKTCRWSTSTIOSLAESTLOLRHRSLSYCSIDPSIH 480
 QY 481 PISEPRDCLQSDGFECFICFQPIFLISGTYMTMRINHSLSGSDSPPTCYLPDSVAPLPP 540
 DB 481 PISEPRDCLQSDGFECFICFQPIFLISGTYMTMRINHSLSGSDSPPTCYLPDSVAPLPP 540
 QY 541 SSVKAEITINIGLKISWKEPPEPENNLOFOIRYGLSGKEVOMKMEVDAAKSKSLPV 600
 DB 541 SSVKAEITINIGLKISWKEPPEPENNLOFOIRYGLSGKEVOMKMEVDAAKSKSLPV 600
 QY 601 PDLCAVYAVQVRCRLDGLGYWSNMSNPATVYVMDIKVPRGPEFWRILINGDTMKREKNV 660
 DB 601 PDLCAVYAVQVRCRLDGLGYWSNMSNPATVYVMDIKVPRGPEFWRILINGDTMKREKNV 660
 QY 661 TLLMKPLMNDLSQVQRYVINHTSCNGTWSGDVGNHRTKFTPLMTBOATFVVLAINST 720
 DB 661 TLLMKPLMNDLSQVQRYVINHTSCNGTWSGDVGNHRTKFTPLMTBOATFVVLAINST 720
 QY 721 GASVANFNLTFSWPMKSVINVOISLAVPLNSCIVISWILSPSDYKIMLYFIIMKMLNED 780
 DB 721 GASVANFNLTFSWPMKSVINVOISLAVPLNSCIVISWILSPSDYKIMLYFIIMKMLNED 780
 QY 781 GEIKWLRISSSVAKKYYIHDFIPIEKYQPSLPIEMEGVGKPKIINSFODDIEKHQSDA 840
 DB 781 GEIKWLRISSSVAKKYYIHDFIPIEKYQPSLPIEMEGVGKPKIINSFODDIEKHQSDA 840
 QY 841 GLVIVPVISSILLGLTLLSHORMKKLEWEDVNPKNCSMAOGINPKOPEFHEFLT 900
 DB 841 GLVIVPVISSILLGLTLLSHORMKKLEWEDVNPKNCSMAOGINPKOPEFHEFLT 900
 QY 901 KHTASVTCGPLLEPPTISSEDSVDTSMKNKDEMPPTVVSLSTDLDEGSCVCSIDQFN 960
 DB 901 KHTASVTCGPLLEPPTISSEDSVDTSMKNKDEMPPTVVSLSTDLDEGSCVCSIDQFN 960

QY 961 SVNFSEAEGETVYEDESQROPEVKYATLINSKPSPTGEQGLINSVTKCFSSKNSPL 1020
 DB 961 SVNFSEAEGETVYEDESQROPEVKYATLINSKPSPTGEQGLINSVTKCFSSKNSPL 1020
 QY 1021 KDSFNSSWEIEQAFFILSDQHPNITSPHLTSEGLDELKLEGNFPEENNKKSTIYL 1080
 DB 1021 KDSFNSSWEIEQAFFILSDQHPNITSPHLTSEGLDELKLEGNFPEENNKKSTIYL 1080
 QY 1081 GVSIRKRESGYLTDKSRVSCPEPAPCLFTDIRVODSCSHFVENNINLGTSSKRTFAS 1140
 DB 1081 GVSIRKRESGYLTDKSRVSCPEPAPCLFTDIRVODSCSHFVENNINLGTSSKRTFAS 1140
 QY 1141 YMPQOTCSTQTHKIMENKMCIDLTV 1165
 DB 1141 YMPQOTCSTQTHKIMENKMCIDLTV 1165

RESULT 25

US-08-708-123C-4

Sequence 4, Application US/08708123C

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpeper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHOD FOR

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TITLE OF INVENTION: THE OB RECEPTOR AND METHOD FOR

TITLE OF INVENTION: THE OB RECEPTOR AND METHOD FOR

TITLE OF INVENTION: THE OB RECEPTOR AND METHOD FOR

TITLE OF INVENTION: THE OB RECEPTOR AND METHOD FOR

TOPOLOGY: unknown
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-708-123C-4

Query Match 82.7%; Score 963; DB 11; Length 1165;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MICOKFCVLLHMEFYITVTAFLNLSYPTIPMRKLSGMPNPNSTYDFELLPAGLSKNTS 60
 DB 1 MICOKFCVLLHMEFYITVTAFLNLSYPTIPMRKLSGMPNPNSTYDFELLPAGLSKNTS 60
 OY 61 NGHYETAVERKENSSTHPSNLSKTFPHCCFSEODRNCSLCADNTEGKTFVSTVSLVF 120
 DB 61 NGHYETAVERKENSSTHPSNLSKTFPHCCFSEODRNCSLCADNTEGKTFVSTVSLVF 120
 OY 121 QOQDAMNNTQCMKGLDLKFLICVSESLFKNLFRNRYKHLVLPREVLEDSPLVPQGS 180
 DB 121 QOQDAMNNTQCMKGLDLKFLICVSESLFKNLFRNRYKHLVLPREVLEDSPLVPQGS 180
 OY 181 FQWVHCNCSVHECCCECLVPPPTAKLNDTLMLCKITSGGYIFQSPPLMSYQPIIMVBDPP 240
 DB 181 FQWVHCNCSVHECCCECLVPPPTAKLNDTLMLCKITSGGYIFQSPPLMSYQPIIMVBDPP 240
 OY 241 LGLHMEITDGNLKLISWSSPPLVPPLOQVKSSENSTVIRBADIIVSATSLVDSTLP 300
 DB 241 LGLHMEITDGNLKLISWSSPPLVPPLOQVKSSENSTVIRBADIIVSATSLVDSTLP 300
 OY 301 GSSYEYQVQGRKLDGPGISDMSTPRVFTTQDYIYPPKILTSVGSNVSFHCYKKEKNT 360
 DB 301 GSSYEYQVQGRKLDGPGISDMSTPRVFTTQDYIYPPKILTSVGSNVSFHCYKKEKNT 360
 OY 361 VPSKEIYVMMNLAERKIPQSOYDVVSDHVSKEVPEFNLETKPRCKFTYDAYVCCNECHH 420
 DB 361 VPSKEIYVMMNLAERKIPQSOYDVVSDHVSKEVPEFNLETKPRCKFTYDAYVCCNECHH 420
 OY 421 RYAEIYVIVNINISCTGDTYLRKTCRMSTSTIQLASTIOLRYHRSLSYCDIPSIH 480
 DB 421 RYAEIYVIVNINISCTGDTYLRKTCRMSTSTIQLASTIOLRYHRSLSYCDIPSIH 480
 OY 481 PISEPDCTLOSDGEYECIFQPIFLISGYTMIRINHSGLSDSPYCVLPDSVVPPLP 540
 DB 481 PISEPDCTLOSDGEYECIFQPIFLISGYTMIRINHSGLSDSPYCVLPDSVVPPLP 540
 OY 541 SSVKAEITINIGLKLISWEKPVFENNLOFOIRYGLSGKEVQKMEYVDAAKSKVSLPV 600
 DB 541 SSVKAEITINIGLKLISWEKPVFENNLOFOIRYGLSGKEVQKMEYVDAAKSKVSLPV 600
 OY 601 PDLCAVYAVQVRCRKLIDGLGYWSNMSNPAYTVMDIKVPMRGPENRIINGDTMKKEKNV 660
 DB 601 PDLCAVYAVQVRCRKLIDGLGYWSNMSNPAYTVMDIKVPMRGPENRIINGDTMKKEKNV 660
 OY 661 TILMRKLMNDLSICVQRYVINHTSCNGTMSDVGNNHTKFTPLMTQOAHYTVLAINSI 720
 DB 661 TILMRKLMNDLSICVQRYVINHTSCNGTMSDVGNNHTKFTPLMTQOAHYTVLAINSI 720
 OY 721 GASVANFNLTFSWPMKSVINIVOSLAVPLNNSCVIYSLTSPDYKLMFIIEKMLNED 780
 DB 721 GASVANFNLTFSWPMKSVINIVOSLAVPLNNSCVIYSLTSPDYKLMFIIEKMLNED 780
 OY 781 GEIKMLRISSSVKYYIHDFIPIEKYQFSLPVIFMEGVGKPRIINSFQDDIEKIQSDA 840
 DB 781 GEIKMLRISSSVKYYIHDFIPIEKYQFSLPVIFMEGVGKPRIINSFQDDIEKIQSDA 840
 OY 841 GLYIVYPIVYISSLILGLLISHQMKLTFMEDVNPKNCSAOCGLNQKPTFEHLPI 900
 DB 841 GLYIVYPIVYISSLILGLLISHQMKLTFMEDVNPKNCSAOCGLNQKPTFEHLPI 900
 OY 901 KHTASVTCGPLLEPETSIEDISVDTSKKNKDEMMPTVYVSLSTDLKGSVCISDQPN 960
 DB 901 KHTASVTCGPLLEPETSIEDISVDTSKKNKDEMMPTVYVSLSTDLKGSVCISDQPN 960

OY 961 SVNFSEAGTEVYIYEDESQROPEVKYATLISNSKPSFTEGEOGLINSYTKCFSSKNSPL 1020
 DB 961 SVNFSEAGTEVYIYEDESQROPEVKYATLISNSKPSFTEGEOGLINSYTKCFSSKNSPL 1020
 OY 1021 KDSFNSMTEIENQAFILSDQHPNITSPHLTSEGLDELKLEGNPEENNOKKSTIYL 1080
 DB 1021 KDSFNSMTEIENQAFILSDQHPNITSPHLTSEGLDELKLEGNPEENNOKKSTIYL 1080
 OY 1081 GVSIIKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140
 DB 1081 GVSIIKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140
 OY 1141 YMPQFOTCSTQTHKIMENKMCIDLTV 1165
 DB 1141 YMPQFOTCSTQTHKIMENKMCIDLTV 1165

RESULT 26
 US-08-864-564A-4
 Sequence 4, Application US/08864564A
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 APPLICANT: Tepper, Robert I.
 APPLICANT: Cuiper, Janice A.
 APPLICANT: White, David W.
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
 TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
 NUMBER OF SEQUENCES: 50.
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P. C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/864,564A
 FILING DATE: 28-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/708,123
 FILING DATE: 03-SEP-1996
 APPLICATION NUMBER: 08/638,524
 FILING DATE: 26-APR-1996
 APPLICATION NUMBER: 08/599,455
 FILING DATE: 22-JAN-1996
 APPLICATION NUMBER: 08/583,153
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: 08/570,142
 FILING DATE: 11-DEC-1995
 APPLICATION NUMBER: 08/569,485
 FILING DATE: 08-DEC-1995
 APPLICATION NUMBER: 08/566,622
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/562,663
 FILING DATE: 27-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Melkielejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/019002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1165 amino acids


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; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-864-564A-4

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Query Match      82.7%; Score 963; DB 12; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MICOFCVLLHMERIVYITAFNLISYPTLPMPFKLSGMPNNTYQYFLIPALSKNTS 60
DB 1 MICOFCVLLHMERIVYITAFNLISYPTLPMPFKLSGMPNNTYQYFLIPALSKNTS 60
QY 61 NGHYETAEPKFNSSGTFHNSLTKTFFHCCFSEODRNCSLCADNIEGTFSTVSLVF 120
DB 61 NGHYETAEPKFNSSGTFHNSLTKTFFHCCFSEODRNCSLCADNIEGTFSTVSLVF 120
QY 121 QOIDANNNIQCMLKGDLLFCITYESLSFKNLFRRNNYKVVHLLVLPVLEDSPLVPQKS 180
DB 121 QOIDANNNIQCMLKGDLLFCITYESLSFKNLFRRNNYKVVHLLVLPVLEDSPLVPQKS 180
QY 181 FOMVHCNCSVHCCCECLVPYPTAKINDTLMLCKITSGGVTFOSPLMSYQPINMKPDP 240
DB 181 FOMVHCNCSVHCCCECLVPYPTAKINDTLMLCKITSGGVTFOSPLMSYQPINMKPDP 240
QY 241 LGLHMEITDDGMLKISWSPPPLVPEPLQYQVKSNSSTVIREADKIYATSLVDSILP 300
DB 241 LGLHMEITDDGMLKISWSPPPLVPEPLQYQVKSNSSTVIREADKIYATSLVDSILP 300
QY 301 GSSYEVQYGRKRLDPCGJMSDMSTPRVFTQDYIYPPKILTVSGSNSVFCILYKKENKI 360
DB 301 GSSYEVQYGRKRLDPCGJMSDMSTPRVFTQDYIYPPKILTVSGSNSVFCILYKKENKI 360
QY 361 VPSKEIYMMNLAERKIPQSOYDVSDHYSKVFPLNTEKPKGFYDVAVCCNEHECH 420
DB 361 VPSKEIYMMNLAERKIPQSOYDVSDHYSKVFPLNTEKPKGFYDVAVCCNEHECH 420
QY 421 RYAEYVIDVNNISCELDGYLTMTCRMSTSTIOSLAESTQLRYHRSLVCSIDIPSIH 480
DB 421 RYAEYVIDVNNISCELDGYLTMTCRMSTSTIOSLAESTQLRYHRSLVCSIDIPSIH 480
QY 481 PISEKDCYLOSDFEYECTFOPIFILSGTYMMIRINHSIGSLDSEPTCYLPDSVAKPLPP 540
DB 481 PISEKDCYLOSDFEYECTFOPIFILSGTYMMIRINHSIGSLDSEPTCYLPDSVAKPLPP 540
QY 541 SSVKAEITINIGLKTISMEKPYEPENNLOFOLRYGLSGKEVOMKMEYVDASKSVSLPV 600
DB 541 SSVKAEITINIGLKTISMEKPYEPENNLOFOLRYGLSGKEVOMKMEYVDASKSVSLPV 600
QY 601 PDLCAVYAVQVRCRKLDDGLGYWSNMSNPAYTYVMDIKVPMRGPEFWRINIGDTMKKEKNV 660
DB 601 PDLCAVYAVQVRCRKLDDGLGYWSNMSNPAYTYVMDIKVPMRGPEFWRINIGDTMKKEKNV 660
QY 661 TLKMPPLKKNDSLCVQRYVINHHSCNCTSEEDVGNHKTFFLQTEQAHYTVLAINSI 720
DB 661 TLKMPPLKKNDSLCVQRYVINHHSCNCTSEEDVGNHKTFFLQTEQAHYTVLAINSI 720
QY 721 GASVANFNLTFFPMPSKVINIOSLSAYPLNSSCVIYSWILSPSDYKLMFTIEKMLAND 780
DB 721 GASVANFNLTFFPMPSKVINIOSLSAYPLNSSCVIYSWILSPSDYKLMFTIEKMLAND 780
QY 781 GEIKWLRISSSVKYYIHDFPIPEKYQSLVPFMEGVGKPKIINSFQDDIEKHQSDA 840
DB 781 GEIKWLRISSSVKYYIHDFPIPEKYQSLVPFMEGVGKPKIINSFQDDIEKHQSDA 840
QY 841 GLYIVVPYIISILLGLTLLSHQRMKLFMEDVDPNPNKCSMAOGLNOKETPFHLTI 900
DB 841 GLYIVVPYIISILLGLTLLSHQRMKLFMEDVDPNPNKCSMAOGLNOKETPFHLTI 900
QY 901 KHTASVTCGPLLPEPTISEDISVDTSMKNKDEMPPTVYVSLSTLDLEKGSVCISDQPN 960
DB 901 KHTASVTCGPLLPEPTISEDISVDTSMKNKDEMPPTVYVSLSTLDLEKGSVCISDQPN 960

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DB 901 KHTASVTCGPLLPEPTISEDISVDTSMKNKDEMPPTVYVSLSTLDLEKGSVCISDQPN 960
QY 961 SYNFSAECESTEYTEDESOROPFVKYATLISNSKSETEGEOGLINSYTKCFSSKNSEPL 1020
DB 961 SYNFSAECESTEYTEDESOROPFVKYATLISNSKSETEGEOGLINSYTKCFSSKNSEPL 1020
QY 1021 KDSFNSNSWEIEAQAFFILSDHPNIISSPHLTFSEGLDELKLEGNFPEENNDRKSIYYL 1080
DB 1021 KDSFNSNSWEIEAQAFFILSDHPNIISSPHLTFSEGLDELKLEGNFPEENNDRKSIYYL 1080
QY 1081 GYTSIRKRSRGVLTMDKSVSCPPAPCLFTDIRYLODSCSHVENNINLGTSSKTFAS 1140
DB 1081 GYTSIRKRSRGVLTMDKSVSCPPAPCLFTDIRYLODSCSHVENNINLGTSSKTFAS 1140
QY 1141 YMPQFQTCSTQTKIMENKMDLTV 1165
DB 1141 YMPQFQTCSTQTKIMENKMDLTV 1165

RESULT 27
US-10-079-625-4
; Sequence 4, Application US/10079625
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,625
; FILING DATE: 2002-FEB-19
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D. Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

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; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1165 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-10-079-625-4

Query Match 82.7%; Score 963; DB 24; Length 1165;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTCQKFCVLLHMEFYVITAFNLSTYPTPWREKLSGMPNSTYDYFLPAGLSKNTS 60
 DB 1 MTCQKFCVLLHMEFYVITAFNLSTYPTPWREKLSGMPNSTYDYFLPAGLSKNTS 60
 QY 61 NGHYEFAVEPKFNSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVSLVF 120
 DB 61 NGHYEFAVEPKFNSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVSLVF 120
 QY 121 QOIDAMNITQCMWLGDKLFLICVYESLFKNLFERNYKYHLLVLEVELEDSPLVPOKGS 180
 DB 121 QOIDAMNITQCMWLGDKLFLICVYESLFKNLFERNYKYHLLVLEVELEDSPLVPOKGS 180
 QY 181 FQWVHCNCSVHECCLELVPPPAKLNDTLMLCKITSGVIFQSPPLMSVQPIIMVVRPDP 240
 DB 181 FQWVHCNCSVHECCLELVPPPAKLNDTLMLCKITSGVIFQSPPLMSVQPIIMVVRPDP 240
 QY 241 LGIHMETTDGNNKISWSSPPLVPPLOQVKSSENSTVIREADKIVSATSLLVDSILP 300
 DB 241 LGIHMETTDGNNKISWSSPPLVPPLOQVKSSENSTVIREADKIVSATSLLVDSILP 300
 QY 301 GSSYEVOVNGKRLDGPGLSDMSSTPRVFTTQDYIFPPKILTVSGNSVFHCILYKKEKNI 360
 DB 301 GSSYEVOVNGKRLDGPGLSDMSSTPRVFTTQDYIFPPKILTVSGNSVFHCILYKKEKNI 360
 QY 361 VPSKETIWMNNLAEKIPQSOQDYVSDHVSQVTFPNLNETKPRCKFTYDAVCCNEHCCH 420
 DB 361 VPSKETIWMNNLAEKIPQSOQDYVSDHVSQVTFPNLNETKPRCKFTYDAVCCNEHCCH 420
 QY 421 RYAEIYIVDNNINISCTGTYLTKMCRWSTSTIOSLASTIOLRHRSSLYSDIPSIH 480
 DB 421 RYAEIYIVDNNINISCTGTYLTKMCRWSTSTIOSLASTIOLRHRSSLYSDIPSIH 480
 QY 481 PISEPKDCLQSDGFECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVRPLP 540
 DB 481 PISEPKDCLQSDGFECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVRPLP 540
 QY 541 SSVKAEITINIGLTKISWEKVPFENNLOFOIRYGLSGREVOMKMEVYDAKSVSPLV 600
 DB 541 SSVKAEITINIGLTKISWEKVPFENNLOFOIRYGLSGREVOMKMEVYDAKSVSPLV 600
 QY 601 PDLCAVYAVOVRCKRLDGLGYSNMSNPATYVMDIKVPRGEPFRIIINGDMKKEKVV 660
 DB 601 PDLCAVYAVOVRCKRLDGLGYSNMSNPATYVMDIKVPRGEPFRIIINGDMKKEKVV 660
 QY 661 TLLMKPLKNDLSLSQVRYVINHTSCNGTSEDVGNHTKFTFLMEQAHVTVLAINSI 720
 DB 661 TLLMKPLKNDLSLSQVRYVINHTSCNGTSEDVGNHTKFTFLMEQAHVTVLAINSI 720
 QY 721 GASVANFNLTFSWPMKSVNIYOSLAVPLNSSCVIVSWILSPSDYKLMFIIEKKNLMD 780
 DB 721 GASVANFNLTFSWPMKSVNIYOSLAVPLNSSCVIVSWILSPSDYKLMFIIEKKNLMD 780
 QY 781 GELKMLRISSVKKYIHHFPIEIKYOSLPIFMEGKPKRIINSFODOI EKQOSA 840
 DB 781 GELKMLRISSVKKYIHHFPIEIKYOSLPIFMEGKPKRIINSFODOI EKQOSA 840
 QY 841 GLVIVPVISSSILLGLTLLISHORMKRLFWEDVNPKNCSMAOGLNFQKPETFEHLFI 900
 DB 841 GLVIVPVISSSILLGLTLLISHORMKRLFWEDVNPKNCSMAOGLNFQKPETFEHLFI 900

QY 901 KHTASVTCGPILLEPETISDIDSVTSWKNKDMPTTVVSLSTDLKSGVICSIDQFN 960
 DB 901 KHTASVTCGPILLEPETISDIDSVTSWKNKDMPTTVVSLSTDLKSGVICSIDQFN 960
 QY 961 SVNFEAEGETEYVEDSQOPFVKYATLISNKPSETGEGGLINSSVTKCFSSKN SPL 1020
 DB 961 SVNFEAEGETEYVEDSQOPFVKYATLISNKPSETGEGGLINSSVTKCFSSKN SPL 1020
 QY 1021 KDSFNSWEIEAOAFILSDOHPNITSPLTFSEGLDELKLEGNPEENNDKSTIYL 1080
 DB 1021 KDSFNSWEIEAOAFILSDOHPNITSPLTFSEGLDELKLEGNPEENNDKSTIYL 1080
 QY 1081 GYTSIKKRESGVLLTDKSRVSCPFPACLETDIRVLQDSCSHFVNNINIGTSKRTFAS 1140
 DB 1081 GYTSIKKRESGVLLTDKSRVSCPFPACLETDIRVLQDSCSHFVNNINIGTSKRTFAS 1140
 QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
 DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 28
 US-09-948-933-284
 ; Sequence 284, Application US/09948933
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL000787
 ; CURRENT APPLICATION NUMBER: US/09/948, 933
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: 60/231, 399
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 6404
 ; SOFTWARE: fastSeq for Windows Version 4.0
 ; SEQ ID NO 284
 ; LENGTH: 1167
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-948-933-284

Query Match 82.7%; Score 963; DB 23; Length 1167;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTCQKFCVLLHMEFYVITAFNLSTYPTPWREKLSGMPNSTYDYFLPAGLSKNTS 60
 DB 3 MTCQKFCVLLHMEFYVITAFNLSTYPTPWREKLSGMPNSTYDYFLPAGLSKNTS 62
 QY 61 NGHYEFAVEPKFNSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVSLVF 120
 DB 63 NGHYEFAVEPKFNSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVSLVF 122
 QY 121 QOIDAMNITQCMWLGDKLFLICVYESLFKNLFERNYKYHLLVLEVELEDSPLVPOKGS 180
 DB 123 QOIDAMNITQCMWLGDKLFLICVYESLFKNLFERNYKYHLLVLEVELEDSPLVPOKGS 182
 QY 181 FQWVHCNCSVHECCLELVPPPAKLNDTLMLCKITSGVIFQSPPLMSVQPIIMVVRPDP 240
 DB 183 FQWVHCNCSVHECCLELVPPPAKLNDTLMLCKITSGVIFQSPPLMSVQPIIMVVRPDP 242
 QY 241 LGIHMETTDGNNKISWSSPPLVPPLOQVKSSENSTVIREADKIVSATSLLVDSILP 300
 DB 243 LGIHMETTDGNNKISWSSPPLVPPLOQVKSSENSTVIREADKIVSATSLLVDSILP 302
 QY 301 GSSYEVOVNGKRLDGPGLSDMSSTPRVFTTQDYIFPPKILTVSGNSVFHCILYKKEKNI 360
 DB 303 GSSYEVOVNGKRLDGPGLSDMSSTPRVFTTQDYIFPPKILTVSGNSVFHCILYKKEKNI 362
 QY 361 VPSKETIWMNNLAEKIPQSOQDYVSDHVSQVTFPNLNETKPRCKFTYDAVCCNEHCCH 420

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Db 363 VPSKELVMMNLAEKIPQSQDYVSDHVSKVTFENLNETKPRGKFTYDVAVCCNEHECH 422
OY 421 RYAEIVYIDVNIINISCEIDGYLTKMTCRMSTSTIOSIAESTLOLRHRSLSYCSIDPSIH 480
Db 423 RYAEIVYIDVNIINISCEIDGYLTKMTCRMSTSTIOSIAESTLOLRHRSLSYCSIDPSIH 482
OY 481 PISEPKDCYLOSDFEECTIPQIFILSGYTMIRINHSLGSLDSPTCYLPDSVAVPLP 540
Db 483 PISEPKDCYLOSDFEECTIPQIFILSGYTMIRINHSLGSLDSPTCYLPDSVAVPLP 542
OY 541 SSYKAEITINIGLTKISWEKPVPEPENNLOFOIRYGLSGKEVOKMVEYDANKSVSLPV 600
Db 543 SSYKAEITINIGLTKISWEKPVPEPENNLOFOIRYGLSGKEVOKMVEYDANKSVSLPV 602
OY 601 PDLCAVYAVOVCKRDLGIGYWSNMPAYTYVMDIKVPMRGPEFMRINIGDTMKKEKNV 660
Db 603 PDLCAVYAVOVCKRDLGIGYWSNMPAYTYVMDIKVPMRGPEFMRINIGDTMKKEKNV 662
OY 661 TLLMKPLMKNDLSYQVORYVINHTSCNGTWSDEVDGNHKTFFLMTQAHVYVLAINSI 720
Db 663 TLLMKPLMKNDLSYQVORYVINHTSCNGTWSDEVDGNHKTFFLMTQAHVYVLAINSI 722
OY 721 GASVANFNLTFSPMKSVMIVOSLSAYPLNSCIVYMWILSPDYKLMYFIEMKMLNED 780
Db 723 GASVANFNLTFSPMKSVMIVOSLSAYPLNSCIVYMWILSPDYKLMYFIEMKMLNED 782
OY 781 GEIKWLRISSVKKYYIHDHFPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKWLRISSVKKYYIHDHFPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
OY 841 GLYVIVPVIISSILLGLTLLSHQMKKLFMEDVDPNPNKCSAOGILNQKPTFEHLFI 900
Db 843 GLYVIVPVIISSILLGLTLLSHQMKKLFMEDVDPNPNKCSAOGILNQKPTFEHLFI 902
OY 901 KKTASVTCGPLLEPETSIEDISVDTSMKNKDEMPITYVVISLSTDLKSGVCSIDQFN 960
Db 903 KKTASVTCGPLLEPETSIEDISVDTSMKNKDEMPITYVVISLSTDLKSGVCSIDQFN 962
OY 961 SVNFSEAECTEYTYEDESQROPEVYATLINSKPSSETGEEQGLINSVYTKCFSSKNSPL 1020
Db 963 SVNFSEAECTEYTYEDESQROPEVYATLINSKPSSETGEEQGLINSVYTKCFSSKNSPL 1022
OY 1021 KQSFNSMWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNPEPENNKKSIYYL 1080
Db 1023 KQSFNSMWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNPEPENNKKSIYYL 1082
OY 1081 GYTSIKKRESGVLLTFKSHVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
Db 1083 GYTSIKKRESGVLLTFKSHVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1142
OY 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165
Db 1143 YMPQFOTCSTQTHKIMENKMDLTIV 1167

RESULT 29
US-09-948-947-87
; Sequence 87, Application US/09948947
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; FILE REFERENCE: CLO00786
; CURRENT APPLICATION NUMBER: US/09/948,947
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,397
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1167

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; TYPE: PRF
; ORGANISM: Human
US-09-948-947-87

Query Match      82.7%; Score 963; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MIOCKPCVVLHMEFIYVITAFNLSPYIPFMRKLSQMPENSTYUVEFLPAGLSKNTS 60
Db 3 MIOCKPCVVLHMEFIYVITAFNLSPYIPFMRKLSQMPENSTYUVEFLPAGLSKNTS 62
OY 61 NGHYETAVERKENSNGTHSNLSKTFPHCCFRSDORNSCLADNIEGKTFVSTVSLV 120
Db 63 NGHYETAVERKENSNGTHSNLSKTFPHCCFRSDORNSCLADNIEGKTFVSTVSLV 122
OY 121 QQIDAMNNIOCMKLGDKLFCYVESLEFKNLFNRYKVALLVLEVEDSPVLPQKS 180
Db 123 QQIDAMNNIOCMKLGDKLFCYVESLEFKNLFNRYKVALLVLEVEDSPVLPQKS 182
OY 181 FQVHNCVSVECCGLVPVPTAKLNDTLMLCKITSGVYIFQSPPLMSVOPIMVKRDP 240
Db 183 FQVHNCVSVECCGLVPVPTAKLNDTLMLCKITSGVYIFQSPPLMSVOPIMVKRDP 242
OY 241 LGLHMETDGNLAKISNSRPVLPPLQYQVYKSENSTYVIRADKTVSATSLVDSILP 300
Db 243 LGLHMETDGNLAKISNSRPVLPPLQYQVYKSENSTYVIRADKTVSATSLVDSILP 302
OY 301 GSSYEVOVRKRLDQFQINDMSTPRVFTTQDIYFPFKILTSVGSVSPHCYKKNKI 360
Db 303 GSSYEVOVRKRLDQFQINDMSTPRVFTTQDIYFPFKILTSVGSVSPHCYKKNKI 362
OY 361 VPSKEIVMMNLAEKIPQSQDYVSDHVSKVTFENLNETKPRKFTYDAVCCNEHECH 420
Db 363 VPSKEIVMMNLAEKIPQSQDYVSDHVSKVTFENLNETKPRKFTYDAVCCNEHECH 422
OY 421 RYAEIVYIDVNIINISCEIDGYLTKMTCRMSTSTIOSIAESTLOLRHRSLSYCSIDPSIH 480
Db 423 RYAEIVYIDVNIINISCEIDGYLTKMTCRMSTSTIOSIAESTLOLRHRSLSYCSIDPSIH 482
OY 481 PISEPKDCYLOSDFEECTIPQIFILSGYTMIRINHSLGSLDSPTCYLPDSVAVPLP 540
Db 483 PISEPKDCYLOSDFEECTIPQIFILSGYTMIRINHSLGSLDSPTCYLPDSVAVPLP 542
OY 541 SSYKAEITINIGLTKISWEKPVPEPENNLOFOIRYGLSGKEVOKMVEYDANKSVSLPV 600
Db 543 SSYKAEITINIGLTKISWEKPVPEPENNLOFOIRYGLSGKEVOKMVEYDANKSVSLPV 602
OY 601 PDLCAVYAVOVCKRDLGIGYWSNMPAYTYVMDIKVPMRGPEFMRINIGDTMKKEKNV 660
Db 603 PDLCAVYAVOVCKRDLGIGYWSNMPAYTYVMDIKVPMRGPEFMRINIGDTMKKEKNV 662
OY 661 TLLMKPLMKNDLSYQVORYVINHTSCNGTWSDEVDGNHKTFFLMTQAHVYVLAINSI 720
Db 663 TLLMKPLMKNDLSYQVORYVINHTSCNGTWSDEVDGNHKTFFLMTQAHVYVLAINSI 722
OY 721 GASVANFNLTFSPMKSVMIVOSLSAYPLNSCIVYMWILSPDYKLMYFIEMKMLNED 780
Db 723 GASVANFNLTFSPMKSVMIVOSLSAYPLNSCIVYMWILSPDYKLMYFIEMKMLNED 782
OY 781 GEIKWLRISSVKKYYIHDHFPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKWLRISSVKKYYIHDHFPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
OY 841 GLYVIVPVIISSILLGLTLLSHQMKKLFMEDVDPNPNKCSAOGILNQKPTFEHLFI 900
Db 843 GLYVIVPVIISSILLGLTLLSHQMKKLFMEDVDPNPNKCSAOGILNQKPTFEHLFI 902
OY 901 KKTASVTCGPLLEPETSIEDISVDTSMKNKDEMPITYVVISLSTDLKSGVCSIDQFN 960
Db 903 KKTASVTCGPLLEPETSIEDISVDTSMKNKDEMPITYVVISLSTDLKSGVCSIDQFN 962

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QY 961 SVNFSEAEGETEYEDDESQOPFVKYATILSNKPSGTGEGLINSSTYKCFSSKNSPL 1020
DB 963 SVNFSEAEGETEYEDDESQOPFVKYATILSNKPSGTGEGLINSSTYKCFSSKNSPL 1022
QY 1021 KDSFSSNSWIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDKSIYYL 1080
DB 1023 KDSFSSNSWIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDKSIYYL 1082
QY 1081 GVSIRKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFEVNNINLTSSKKTFFAS 1140
DB 1083 GVSIRKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFEVNNINLTSSKKTFFAS 1142
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1143 YMPQFOTCSTQTHKIMENKMDLTV 1167

RESULT 30
US-08-570-142B-4
Sequence 4, Application US/08570142B
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Chiepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS
TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,142B
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-570-142B-4

Query Match 82.6%; Score 962; DB 9; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1162; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICOKECVLLHMEFIYVITAFNLSPITPWRKLSQMPNPNSTYVYFLPAGLSKNTSNS 60
DB 1 MICOKECVLLHMEFIYVITAFNLSPITPWRKLSQMPNPNSTYVYFLPAGLSKNTSNS 60
QY 61 NGHYETRAVEKRFSSSGHSENLSTKTHCCFSEODONCSLADNIEGKTFVSTVNSLVE 120
DB 61 NGHYETRAVEKRFSSSGHSENLSTKTHCCFSEODONCSLADNIEGKTFVSTVNSLVE 120
QY 121 QQIDAMNNICQMLGDLKLCYVESLTKNLNFNNYKVALLVLPVELDPSLPVPOKGS 180
DB 121 QQIDAMNNICQMLGDLKLCYVESLTKNLNFNNYKVALLVLPVELDPSLPVPOKGS 180
QY 181 FQWVHCNCSVHECCCECLVPVPAKNDTLLMCLKITSQVIFQSPMLSVOPINMKEDPP 240
DB 181 FQWVHCNCSVHECCCECLVPVPAKNDTLLMCLKITSQVIFQSPMLSVOPINMKEDPP 240
QY 241 LGIAMEITDDGNLKISWSSPPLVPFLOVOYKTSNSTVIREADKTVSATSLVDSILP 300
DB 241 LGIAMEITDDGNLKISWSSPPLVPFLOVOYKTSNSTVIREADKTVSATSLVDSILP 300
QY 301 GSSYEVOVRGRRLDGPQIMSDMSTPRVFTYQDVIYPPPKILTSVSNVSFHCYKKEKNI 360
DB 301 GSSYEVOVRGRRLDGPQIMSDMSTPRVFTYQDVIYPPPKILTSVSNVSFHCYKKEKNI 360
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSVTPEPNLNETKPRGKITVDVAVCCNEHCCH 420
DB 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSVTPEPNLNETKPRGKITVDVAVCCNEHCCH 420
QY 421 RYAEIYIDVININISCTEDYLTFRKNCRWSTSTQSLAESTLQIKHRSLSLSDIPSIH 480
DB 421 RYAEIYIDVININISCTEDYLTFRKNCRWSTSTQSLAESTLQIKHRSLSLSDIPSIH 480
QY 481 PISEPKDYLQSDGFYECIFQPIFLLSGYTMIRINHSLSLSDPPTCVLPDSVYRPLP 540
DB 481 PISEPKDYLQSDGFYECIFQPIFLLSGYTMIRINHSLSLSDPPTCVLPDSVYRPLP 540
QY 541 SSVKAETTINGLKTSMKPVPEPNLOIROIYIGSGKVOKMKNVYVYAKSKSVSLPV 600
DB 541 SSVKAETTINGLKTSMKPVPEPNLOIROIYIGSGKVOKMKNVYVYAKSKSVSLPV 600
QY 601 PDLCAVAVOVRGRRLDGLGYSWMSNPATVYVMDIVPARKGEFVRIINGDTMKKKNV 660
DB 601 PDLCAVAVOVRGRRLDGLGYSWMSNPATVYVMDIVPARKGEFVRIINGDTMKKKNV 660
QY 661 TLLMKPLMKNDLSLCSVORYIINHHTSCNGTMSDVGKHTFTFLTEQANTVYLAINST 720
DB 661 TLLMKPLMKNDLSLCSVORYIINHHTSCNGTMSDVGKHTFTFLTEQANTVYLAINST 720
QY 721 GASVAVANLTFESPMKSVNIVOSLSAYPLNNSCVIYVMIISPSDYKLMYFLIEKKNLNE 780
DB 721 GASVAVANLTFESPMKSVNIVOSLSAYPLNNSCVIYVMIISPSDYKLMYFLIEKKNLNE 780
QY 781 GEIKMLRISSSVKRYIHDHFIPIEKYQFSLPIFMGVGKPKIINSTODDIEKHSDA 840
DB 781 GEIKMLRISSSVKRYIHDHFIPIEKYQFSLPIFMGVGKPKIINSTODDIEKHSDA 840
QY 841 GLYIVIVPVIITSSILLGLTLLISHQRMKLFWEVDVPPKNCNMAQGLNFOKPEFHEFLT 900
DB 841 GLYIVIVPVIITSSILLGLTLLISHQRMKLFWEVDVPPKNCNMAQGLNFOKPEFHEFLT 900
QY 901 KHTASTYCGPLLEPEPISDISVIDVTSKKNKDEMPPTVYVSLSTDTLDEGSCISQFN 960
DB 901 KHTASTYCGPLLEPEPISDISVIDVTSKKNKDEMPPTVYVSLSTDTLDEGSCISQFN 960
QY 961 SVNFSEAEGETEYEDDESQOPFVKYATILSNKPSGTGEGLINSSTYKCFSSKNSPL 1020
DB 961 SVNFSEAEGETEYEDDESQOPFVKYATILSNKPSGTGEGLINSSTYKCFSSKNSPL 1020
QY 1021 KDSFSSNSWIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDKSIYYL 1080
DB 1021 KDSFSSNSWIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDKSIYYL 1080
QY 1081 GVSIRKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFEVNNINLTSSKKTFFAS 1140

DB 1081 GVTISIKKRESGVLITDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMCIDL 1164
DB 1141 YMPQFOTCSTQTHKIMENKMCIDL 1164

RESULT 31
US-08-570-142C-4
; Sequence 4, Application US/08570142C
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS
; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570.142C
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-570-142C-4

Query Match 82.6%; Score 962; DB 9; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1162; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICOKRCVLLHMEFIYVITAFNLSTPIPMWRKLSKMPNSTYDYFLPAGLSKNTSNS 60
DB 1 MICOKRCVLLHMEFIYVITAFNLSTPIPMWRKLSKMPNSTYDYFLPAGLSKNTSNS 60
QY 61 NGHYETAVERKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAVERKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDAMNNIOCMKLGDLKLFICYVESLFRNLFNNYNTKVLVLPVLEDSPLVPQKGS 180

DB 121 QQIDAMNNIOCMKLGDLKLFICYVESLFRNLFNNYNTKVLVLPVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCCECLVPPYPAKLANDTLMLCKITSGVIFGSPLSVOPINMKVDPDP 240
DB 181 FQWVHCNCSVHECCCECLVPPYPAKLANDTLMLCKITSGVIFGSPLSVOPINMKVDPDP 240
QY 241 LGLHMEITDGNLKISMSPPPLVPPLOVQKYSNSTYIYREADKIVSATSLLYDSILP 300
DB 241 LGLHMEITDGNLKISMSPPPLVPPLOVQKYSNSTYIYREADKIVSATSLLYDSILP 300
QY 301 GSSYEVOGRKRLDGPQIMSDMSTPRVFTQDYPPPKILTSGVSVSFHCITKKNKI 360
DB 301 GSSYEVOGRKRLDGPQIMSDMSTPRVFTQDYPPPKILTSGVSVSFHCITKKNKI 360
QY 361 VPSKEIYMMNNLAEKIPQSOYDVSDHVSRYTEFNLETPRGRFVDAVCCNEHCCH 420
DB 361 VPSKEIYMMNNLAEKIPQSOYDVSDHVSRYTEFNLETPRGRFVDAVCCNEHCCH 420
QY 421 RYAEIYVIDVNNISCTEDGYLTKMTCRWSSTIQLAESTLQLRHRSLSYCSDIPSIH 480
DB 421 RYAEIYVIDVNNISCTEDGYLTKMTCRWSSTIQLAESTLQLRHRSLSYCSDIPSIH 480
QY 481 PISPRKCYLQSDGFYECIFQPIFLLSGYTMMIRINSLSLDLPYCVLPDSVYKPLP 540
DB 481 PISPRKCYLQSDGFYECIFQPIFLLSGYTMMIRINSLSLDLPYCVLPDSVYKPLP 540
QY 541 SSVKAEITINIGLKLISMEKVPPENNLOFQIRGLSGKEVQMKMYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLKLISMEKVPPENNLOFQIRGLSGKEVQMKMYDAKSKSVSLPV 600
QY 601 PDLCAVYAVOVRCKRLDGLGYSWMSNPAYTVMDIKVPMGRPEVRIJINGDTMKKEKNV 660
DB 601 PDLCAVYAVOVRCKRLDGLGYSWMSNPAYTVMDIKVPMGRPEVRIJINGDTMKKEKNV 660
QY 661 TLMLKPLMKNDLSQVORYVYNNHTSCNGTMSDEVQHTKTELEAOAHVYLAINSI 720
DB 661 TLMLKPLMKNDLSQVORYVYNNHTSCNGTMSDEVQHTKTELEAOAHVYLAINSI 720
QY 721 GASVANEPLTFSPWMSKVNIYQSLASAYPLNSSCYIVSMILSPSYDKLMEYFIEKKNLNE 780
DB 721 GASVANEPLTFSPWMSKVNIYQSLASAYPLNSSCYIVSMILSPSYDKLMEYFIEKKNLNE 780
QY 781 GEIKMLRISSSVKKYYIHDHFIPLEKYOFSLYPIFMGVGPKIINSFTODDIEKHOSDA 840
DB 781 GEIKMLRISSSVKKYYIHDHFIPLEKYOFSLYPIFMGVGPKIINSFTODDIEKHOSDA 840
QY 841 GLVYIVPVIISSSTLLGLTLLISHQRMKLFWEDEVPMKNSMAQGLNFOAPETFEHLFI 900
DB 841 GLVYIVPVIISSSTLLGLTLLISHQRMKLFWEDEVPMKNSMAQGLNFOAPETFEHLFI 900
QY 901 KHTASVTCGPLLEPETISEDIVSTSMKNDKEMPTTVVSLSTTDLKSGVYCISQDFN 960
DB 901 KHTASVTCGPLLEPETISEDIVSTSMKNDKEMPTTVVSLSTTDLKSGVYCISQDFN 960
QY 961 SVNFSAEAGTEVYEDESQRPYKAVATLISNSKRPSETGEEGLINSVTRCFSSKNSPL 1020
DB 961 SVNFSAEAGTEVYEDESQRPYKAVATLISNSKRPSETGEEGLINSVTRCFSSKNSPL 1020
QY 1021 KDSFSNNSWELEAQAFTILSQHNPITSPHLTSESGDELKLECNPEENNDKKSIIYL 1080
DB 1021 KDSFSNNSWELEAQAFTILSQHNPITSPHLTSESGDELKLECNPEENNDKKSIIYL 1080
QY 1081 GVTISIKKRESGVLITDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
DB 1081 GVTISIKKRESGVLITDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMCIDL 1164
DB 1141 YMPQFOTCSTQTHKIMENKMCIDL 1164

RESULT 32

US-08-582-825-1
 ; Sequence 1, Application US/08582825
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 Dehavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/582,825
 ; FILING DATE: 04-JAN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pesslin, Karol M.
 ; REFERENCE/DOCKET NUMBER: A-382
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 896 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-582-825-1

Query Match 76.5%: Score 891; DB 9; Length 896;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFYITAFNLSTPTPMWRKLSCLMPNSTYDYLFLPAGLSKNTNS 60
 DB 1 MICQKFCVLLHMEFYITAFNLSTPTPMWRKLSCLMPNSTYDYLFLPAGLSKNTNS 60
 QY 61 NGHYEFAVEPKFNSGTHPSNLSTPTPHCCFSEODRNCSLCADNI ECKTFVSTVNSLVF 120
 DB 61 NGHYEFAVEPKFNSGTHPSNLSTPTPHCCFSEODRNCSLCADNI ECKTFVSTVNSLVF 120
 QY 121 QQIDAMNINOCWLGKDLKLFICVVESELFKNLPNNYKXHLVLPBVLDSPLVPOKGS 180
 DB 121 QQIDAMNINOCWLGKDLKLFICVVESELFKNLPNNYKXHLVLPBVLDSPLVPOKGS 180
 QY 181 FQVHNCNSVHECCLELVPPTAKLNDTLMLCKITSGVIFQSPPLMSVQPIWVPRDP 240
 DB 181 FQVHNCNSVHECCLELVPPTAKLNDTLMLCKITSGVIFQSPPLMSVQPIWVPRDP 240
 QY 241 LGLHMEITDGNLKISWSSPPLVPPLOQVKSSENSTVIRADKIVSATSLVDSILP 300
 DB 241 LGLHMEITDGNLKISWSSPPLVPPLOQVKSSENSTVIRADKIVSATSLVDSILP 300
 QY 301 GGSYEVOVGKRLDGLGINSWSTPRVFTTQDVIYPPKILTSVGSNVSFHCYKKEKNI 360
 DB 301 GGSYEVOVGKRLDGLGINSWSTPRVFTTQDVIYPPKILTSVGSNVSFHCYKKEKNI 360
 QY 361 VESKEIVMMNLAELIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECH 420
 DB 361 VESKEIVMMNLAELIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECH 420
 QY 421 RYAEIVYDVNINISCTDGYLTKMCRWSTSTIQLSLASTQLRHRSLYCSDPISIH 480
 DB 421 RYAEIVYDVNINISCTDGYLTKMCRWSTSTIQLSLASTQLRHRSLYCSDPISIH 480
 QY 481 PISEPRDCTLOSDGFECIFPPIFLLSGTYTMMIRINHSLGSLDSPPTCVLPDSVAKPLPP 540

DB 481 PISEPRDCTLOSDGFECIFPPIFLLSGTYTMMIRINHSLGSLDSPPTCVLPDSVAKPLPP 540
 QY 541 SSYKAETTINGLKLKISWEPENNLOFOIRYGLSGKEVOKMYEYVAKSKSVSLPV 600
 DB 541 SSYKAETTINGLKLKISWEPENNLOFOIRYGLSGKEVOKMYEYVAKSKSVSLPV 600
 QY 601 PDLCAVAVOVRCKRLDGLGYSWNSNPAYTVMDIKVPKRGFEFWIINGDTMKKEKNV 660
 DB 601 PDLCAVAVOVRCKRLDGLGYSWNSNPAYTVMDIKVPKRGFEFWIINGDTMKKEKNV 660
 QY 661 TLLMKPLMKNDLSLSVORYIYNHHTSCNGTWSDEYVGNHTFTFLTQCATVYVLAINSI 720
 DB 661 TLLMKPLMKNDLSLSVORYIYNHHTSCNGTWSDEYVGNHTFTFLTQCATVYVLAINSI 720
 QY 721 GASVAFNLTFSNPMKSVNIVOSLSAFLNSCIVYMIISPSDYKLMYETIEKKNLND 780
 DB 721 GASVAFNLTFSNPMKSVNIVOSLSAFLNSCIVYMIISPSDYKLMYETIEKKNLND 780
 QY 781 GEIKWLRISSSVKRYIHDHFIPEKYQFSLYPIFMGVGPKIINSFTODDIEKHQSDA 840
 DB 781 GEIKWLRISSSVKRYIHDHFIPEKYQFSLYPIFMGVGPKIINSFTODDIEKHQSDA 840
 QY 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVPRPKNSVAGGGINPQK 891
 DB 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVPRPKNSVAGGGINPQK 891

RESULT 33

US-08-582-825A-1
 ; Sequence 1, Application US/08582825A

; GENERAL INFORMATION:
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 Dehavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/582,825A
 ; FILING DATE: 04-JAN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pesslin, Karol M.
 ; REFERENCE/DOCKET NUMBER: A-382
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 896 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-582-825A-1

Query Match 76.5%: Score 891; DB 9; Length 896;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFYITAFNLSTPTPMWRKLSCLMPNSTYDYLFLPAGLSKNTNS 60
 DB 1 MICQKFCVLLHMEFYITAFNLSTPTPMWRKLSCLMPNSTYDYLFLPAGLSKNTNS 60


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Db 661 TLAKMLKNDLSQVORYINHTSCNGTSEDVGNHTKFTFLMEQAHVTVLAINST 720
QY 721 GASVANFNLFSPWPMKSVINVOISLAVPLNNSCVIYSWILSPDYKLMFTIEMKLNED 780
Db 722 GASVANFNLFSPWPMKSVINVOISLAVPLNNSCVIYSWILSPDYKLMFTIEMKLNED 780
QY 781 GEKMLRISSSVKKYIYHDFPIEKYOFSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEKMLRISSSVKKYIYHDFPIEKYOFSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSILLGLTLLISHORMKLFMEDVDPNPKKCSMAOGLNFOK 891
Db 841 GLYVIVPVISSILLGLTLLISHORMKLFMEDVDPNPKKCSMAOGLNFOK 891

RESULT 35
US-08-667-197-3
; Sequence 3, Application US/08667197
; GENERAL INFORMATION:
; APPLICANT: Mathews, William
; TITLE OF INVENTION: USES FOR WSX LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,197
; FILING DATE: 20-Jun-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0986P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-667-197-3

Query Match 76.5%; Score 891; DB 10; Length 896;
Best Local Similarity: 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 EQVHNCVSHCECECLVPPVAKLANDTLMCKITSGVIEVSPLNSVOPINMVKPDP 240
Db 181 EQVHNCVSHCECECLVPPVAKLANDTLMCKITSGVIEVSPLNSVOPINMVKPDP 240
QY 241 LGLHMETDGNLKISMSRPLVPFLQYOVAKISENTVIRKADKIVSATSLIYNISILP 300
Db 241 LGLHMETDGNLKISMSRPLVPFLQYOVAKISENTVIRKADKIVSATSLIYNISILP 300
QY 301 GSSYEVOVRGRKRLDGGIWSDMSTPRVFTQDVIYPPPKILTSVGSNVSPHCYKKNKI 360
Db 301 GSSYEVOVRGRKRLDGGIWSDMSTPRVFTQDVIYPPPKILTSVGSNVSPHCYKKNKI 360
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVKVTFPNLNETKPRCKFTYDAYVCCNEHC 420
Db 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVKVTFPNLNETKPRCKFTYDAYVCCNEHC 420
QY 421 RVALVIVDYNINISCTDGYLTKMCRWSTSTIOSLAESTLRLHRSLSLSDPSIH 480
Db 421 RVALVIVDYNINISCTDGYLTKMCRWSTSTIOSLAESTLRLHRSLSLSDPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYMMIRINHSLSLSDSPPTCVLPDSVYKPLP 540
Db 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYMMIRINHSLSLSDSPPTCVLPDSVYKPLP 540
QY 541 SSYKAETITNIGLKISWEKVPFPENNLOPQIRGLSGKAVQKKHIEYDAAKSKSYSLP 600
Db 541 SSYKAETITNIGLKISWEKVPFPENNLOPQIRGLSGKAVQKKHIEYDAAKSKSYSLP 600
QY 601 PDICAVAYAVOVRCKRLDGLYWSNMSNPATVYMDIKVPRGEPNRIINGDMKKEKNV 660
Db 601 PDICAVAYAVOVRCKRLDGLYWSNMSNPATVYMDIKVPRGEPNRIINGDMKKEKNV 660
QY 661 TLAKMLKNDLSQVORYINHTSCNGTSEDVGNHTKFTFLMEQAHVTVLAINST 720
Db 661 TLAKMLKNDLSQVORYINHTSCNGTSEDVGNHTKFTFLMEQAHVTVLAINST 720
QY 721 GASVANFNLFSPWPMKSVINVOISLAVPLNNSCVIYSWILSPDYKLMFTIEMKLNED 780
Db 721 GASVANFNLFSPWPMKSVINVOISLAVPLNNSCVIYSWILSPDYKLMFTIEMKLNED 780
QY 781 GEKMLRISSSVKKYIYHDFPIEKYOFSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEKMLRISSSVKKYIYHDFPIEKYOFSLPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSILLGLTLLISHORMKLFMEDVDPNPKKCSMAOGLNFOK 891
Db 841 GLYVIVPVISSILLGLTLLISHORMKLFMEDVDPNPKKCSMAOGLNFOK 891

RESULT 36
US-08-779-457-3
; Sequence 3, Application US/08779457
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Mathews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIHODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779.457
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-779-457-3

```

```

Query Match          76.5%; Score 891; DB 11; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MLCQKFCVLLHMEFYITAFNLSTPTPMWRKLSCLMPNSIYDVFLLPAGLSKNTS 60
DB 1 MLCQKFCVLLHMEFYITAFNLSTPTPMWRKLSCLMPNSIYDVFLLPAGLSKNTS 60
QY 61 NGHYETAPEKNSGTHSNLSKTFHCCFSEODRNCISLADNIEGTFVSTVSLVF 120
DB 61 NGHYETAPEKNSGTHSNLSKTFHCCFSEODRNCISLADNIEGTFVSTVSLVF 120
QY 121 QOIDANMNIOCMKGLDLFCYVESLFKNLFRNRYKVHLLYLVELEDSEPLVPQKS 180
DB 121 QOIDANMNIOCMKGLDLFCYVESLFKNLFRNRYKVHLLYLVELEDSEPLVPQKS 180
QY 181 FQWVHNCNVHGCCCLVAVPTAKLNDTLMLCKITSGVIRQSPILMSVQPIIMVAPDP 240
DB 181 FQWVHNCNVHGCCCLVAVPTAKLNDTLMLCKITSGVIRQSPILMSVQPIIMVAPDP 240
QY 241 LGLHMEITDGNLKLISMSPPVLPFPLOYQVYSENSTVIYRADKIVATSLVDSILP 300
DB 241 LGLHMEITDGNLKLISMSPPVLPFPLOYQVYSENSTVIYRADKIVATSLVDSILP 300
QY 301 GSSYEYQVRGKRLDGGIWSMSTPRVFTTQDIYPPKILTSVGSNVSFHCITYKKENKI 360
DB 301 GSSYEYQVRGKRLDGGIWSMSTPRVFTTQDIYPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIVVMNNLAERKIPQOYDVVSDHVSQVTFENLNKRPKRFYDAYVCCNEHECHH 420
DB 361 VPSKEIVVMNNLAERKIPQOYDVVSDHVSQVTFENLNKRPKRFYDAYVCCNEHECHH 420
QY 421 RYAEIVIVDVNINISCTGGYLTAKMCRMSTIQLSLAESTLQLRHRSLSYCSIDPSIH 480
DB 421 RYAEIVIVDVNINISCTGGYLTAKMCRMSTIQLSLAESTLQLRHRSLSYCSIDPSIH 480
QY 481 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVAPLPP 540
DB 481 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVAPLPP 540
QY 541 SSYKAEITINIGLKISWKPVPFPENNLOPIRYGLSGKEVQKMYEYDAKSKSVSLVP 600
DB 541 SSYKAEITINIGLKISWKPVPFPENNLOPIRYGLSGKEVQKMYEYDAKSKSVSLVP 600
QY 601 PDLCAVYAVQVCRKRLDGGYMSNMSPAYTVVMDIKVPMRGEPFRITINGDMKKEKNV 660
DB 601 PDLCAVYAVQVCRKRLDGGYMSNMSPAYTVVMDIKVPMRGEPFRITINGDMKKEKNV 660

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QY 661 TLMLKPLMKNDLSICVQRYVINHHSTSCNGTWSGNSHTKFTFLMTEQAHVTVALNSI 720
DB 661 TLMLKPLMKNDLSICVQRYVINHHSTSCNGTWSGNSHTKFTFLMTEQAHVTVALNSI 720
QY 721 GASVANFNITFSPMKSKVINVOISLAVPLNSSCVIYSLLSPDYKLMFTIEKMLNED 780
DB 721 GASVANFNITFSPMKSKVINVOISLAVPLNSSCVIYSLLSPDYKLMFTIEKMLNED 780
QY 781 GEIKMLRISSVKYYIHHPFIPIEYQFSLVPFMEGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKMLRISSVKYYIHHPFIPIEYQFSLVPFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYIVPVISSSILLGLTLLISHQMKRLFMEDVDPNPKNSVAGLNFQK 891
DB 841 GLYIVPVISSSILLGLTLLISHQMKRLFMEDVDPNPKNSVAGLNFQK 891

```

RESULT 37

```

US-08-780-562-3
Sequence 3, Application US/08780562
GENERAL INFORMATION:
APPLICANT: Matthews, William
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-562-3

```

```

Query Match          76.5%; Score 891; DB 11; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLCQKFCVLLHMEFYITAFNLSTPTPMWRKLSCLMPNSIYDVFLLPAGLSKNTS 60
DB 1 MLCQKFCVLLHMEFYITAFNLSTPTPMWRKLSCLMPNSIYDVFLLPAGLSKNTS 60
QY 61 NGHYETAPEKNSGTHSNLSKTFHCCFSEODRNCISLADNIEGTFVSTVSLVF 120

```

```

Db      | 120
Qy      | 180
Db      | 180
Qy      | 240
Db      | 240
Qy      | 300
Db      | 360
Qy      | 420
Db      | 420
Qy      | 480
Db      | 540
Qy      | 600
Db      | 600
Qy      | 660
Db      | 720
Qy      | 780
Db      | 840
Qy      | 891
Db      | 891

```

```

RESULT 38
US-08-585-005-4
: Sequence 4, Application US/08585005
: GENERAL INFORMATION:
: APPLICANT: Matthews, William
: APPLICANT: Bennett, Brian
: TITLE OF INVENTION: WSX RECEPTOR
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

```

```

: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/585.005
: FILING DATE: 08-Jan-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0986
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELETYPE: 910/371-7168
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 923 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-08-585-005-4

```

```

Query Match      76.5%; Score 891; DB 9; Length 923;
Best Local Similarity: 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      | 60
Db      | 60
Qy      | 120
Db      | 180
Qy      | 240
Db      | 240
Qy      | 300
Db      | 360
Qy      | 420
Db      | 480
Qy      | 540
Db      | 600
Qy      | 660
Db      | 720
Qy      | 780
Db      | 840
Qy      | 891
Db      | 891

```

Db 661 TLIMKPLMKNDLSCVQRYVINHHHTSCNGTSEDVGNHTKFTFLTEQAHVTVLAINSI 720
 QY 721 GASVANFNLTFSMPMSKVNIYOSLSAYPLNSSCVIYSWILSPSDYKLMFLEIMKRLNED 780
 Db 721 GASVANFNLTFSMPMSKVNIYOSLSAYPLNSSCVIYSWILSPSDYKLMFLEIMKRLNED 780
 QY 781 GEIKMLRISSSVKKYIYIHDFPIEKYQSLYPIFMEVGAKKIINSTFODDIEKHQSDA 840
 Db 781 GEIKMLRISSSVKKYIYIHDFPIEKYQSLYPIFMEVGAKKIINSTFODDIEKHQSDA 840
 QY 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVDPNPNKCSMAOGLNFK 891
 Db 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVDPNPNKCSMAOGLNFK 891

RESULT 39
 US-08-667-197-4
 ; Sequence 4, Application US/08667197
 ; GENERAL INFORMATION:
 ; APPLICANT: Matthews, William
 ; TITLE OF INVENTION: USES FOR WSX LIGANDS
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/667,197
 ; FILING DATE: 20-Jun-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/585005
 ; FILING DATE: 01/08/96
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: P-40,378
 ; REFERENCE/DOCKET NUMBER: P09866P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1994
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 923 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-667-197-4

Query Match 76.5%; Score 891; DB 10; Length 923;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMERIYVITAFNLSPITPMRFKLSCMPNSTDYDFLLPAGLSKNTNS 60
 Db 1 MICQKFCVLLHMERIYVITAFNLSPITPMRFKLSCMPNSTDYDFLLPAGLSKNTNS 60
 QY 61 NGHYETAVERKNSGTHNSNLSKTFHCCFRSEODRNSCLADNIEGTFTVSTNSLAF 120
 Db 61 NGHYETAVERKNSGTHNSNLSKTFHCCFRSEODRNSCLADNIEGTFTVSTNSLAF 120
 QY 121 QQIDANMNIOCMKGDKLFICYVESLFRNRYNYKHLIYLPVEVJEDSPLYPQKSS 180
 Db 121 QQIDANMNIOCMKGDKLFICYVESLFRNRYNYKHLIYLPVEVJEDSPLYPQKSS 180

QY 181 FQVHCNCSVHECCCECLYVPVPAKLNIDLMLCKLITSGCVIFQSLMSQVPINMKPPDP 240
 Db 181 FQVHCNCSVHECCCECLYVPVPAKLNIDLMLCKLITSGCVIFQSLMSQVPINMKPPDP 240
 QY 241 LGLHMEITDDGMLKISWSSPPLVPPLOYQVYSNSTVIREAKIYATSLDLSITP 300
 Db 241 LGLHMEITDDGMLKISWSSPPLVPPLOYQVYSNSTVIREAKIYATSLDLSITP 300
 QY 301 GSSYEVOYGRKRLDPGIMSDWSTPRVFTTQDVIYFPFKILTSVGSNVSFHCITYKKENKI 360
 Db 301 GSSYEVOYGRKRLDPGIMSDWSTPRVFTTQDVIYFPFKILTSVGSNVSFHCITYKKENKI 360
 QY 361 VPSKEIYMMNTAEKIPQSDYVSDHYSKTFPUNLNETKPPGKITTYDAYVCCNEHECH 420
 Db 361 VPSKEIYMMNTAEKIPQSDYVSDHYSKTFPUNLNETKPPGKITTYDAYVCCNEHECH 420
 QY 421 RYAEIYVIDVINISCEPTGYLTKMTCRMSTSTIOSLASTOLYHRSLKCSIDPSIH 480
 Db 421 RYAEIYVIDVINISCEPTGYLTKMTCRMSTSTIOSLASTOLYHRSLKCSIDPSIH 480
 QY 481 PISEPDCYLOSDGFYECIFOPIFLLSGYTMWIRINHSLSLDSHPPTCYLPDSYVKKPLPP 540
 Db 481 PISEPDCYLOSDGFYECIFOPIFLLSGYTMWIRINHSLSLDSHPPTCYLPDSYVKKPLPP 540
 QY 541 SSVKAEITINIGLKIISMKRPYFPENNLOFOIRYGLSGKEVOYMKHYEVDASKSVSLPV 600
 Db 541 SSVKAEITINIGLKIISMKRPYFPENNLOFOIRYGLSGKEVOYMKHYEVDASKSVSLPV 600
 QY 601 PDLCAVYAVQVCKRDLGIGYWSNNSNPAYTVYMDIKVMPRGPEFRIRINGDTMKREKV 660
 Db 601 PDLCAVYAVQVCKRDLGIGYWSNNSNPAYTVYMDIKVMPRGPEFRIRINGDTMKREKV 660
 QY 661 TLIMKPLMKNDLSCVQRYVINHHHTSCNGTSEDVGNHTKFTFLTEQAHVTVLAINSI 720
 Db 661 TLIMKPLMKNDLSCVQRYVINHHHTSCNGTSEDVGNHTKFTFLTEQAHVTVLAINSI 720
 QY 721 GASVANFNLTFSMPMSKVNIYOSLSAYPLNSSCVIYSWILSPSDYKLMFLEIMKRLNED 780
 Db 721 GASVANFNLTFSMPMSKVNIYOSLSAYPLNSSCVIYSWILSPSDYKLMFLEIMKRLNED 780
 QY 781 GEIKMLRISSSVKKYIYIHDFPIEKYQSLYPIFMEVGAKKIINSTFODDIEKHQSDA 840
 Db 781 GEIKMLRISSSVKKYIYIHDFPIEKYQSLYPIFMEVGAKKIINSTFODDIEKHQSDA 840
 QY 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVDPNPNKCSMAOGLNFK 891
 Db 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVDPNPNKCSMAOGLNFK 891

RESULT 40
 US-08-779-457-4
 ; Sequence 4, Application US/08779457
 ; GENERAL INFORMATION:
 ; APPLICANT: Carter, Paul J.
 ; APPLICANT: Chhang, Nancy Y.
 ; APPLICANT: Kyung, Jin Kim
 ; APPLICANT: Matthews, William
 ; APPLICANT: Rodrigues, Maria L.
 ; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/779,457
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-779-457-4

```

```

Query Match      76.5%; Score 891; DB 11; Length 923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MICQKFCVLLHMEFYITAFNLSPITPMRFKLSGMPNSTYDFLLPAGLSKNTS 60
DB 1 MICQKFCVLLHMEFYITAFNLSPITPMRFKLSGMPNSTYDFLLPAGLSKNTS 60
QY 61 NGHETAVEPKENSSGTHFSNLKTTFHCCFSESDRNCSLCADNIEGTFVSTVNSL 120
DB 61 NGHETAVEPKENSSGTHFSNLKTTFHCCFSESDRNCSLCADNIEGTFVSTVNSL 120
QY 121 QOIDANMNIOQWLKGLKLFICYVESLFKNLFERNYKXHLVLEPEVLEDSPLVQKS 180
DB 121 QOIDANMNIOQWLKGLKLFICYVESLFKNLFERNYKXHLVLEPEVLEDSPLVQKS 180
QY 181 FQMVHNCNVHGCCCECTLVPTAKLNDTLMLCKITSGSVIFQSPIMASQPIINMVPDP 240
DB 181 FQMVHNCNVHGCCCECTLVPTAKLNDTLMLCKITSGSVIFQSPIMASQPIINMVPDP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPELOYVXKXSENSTVIREADKIVSATSLVDLSP 300
DB 241 LGLHMEITDDGNLKISWSSPPLVPELOYVXKXSENSTVIREADKIVSATSLVDLSP 300
QY 301 GSSYEVOVGKRLDGPGLSDMSTPRVFTTODVYIFPRKILTSVGSNVSFHCITKKENKI 360
DB 301 GSSYEVOVGKRLDGPGLSDMSTPRVFTTODVYIFPRKILTSVGSNVSFHCITKKENKI 360
QY 361 VPSKEIIVMMNLAEKIPQSQDYVDSDHVSKVTFEFLNLEKPRGKFFYDVAVCCNEHECH 420
DB 361 VPSKEIIVMMNLAEKIPQSQDYVDSDHVSKVTFEFLNLEKPRGKFFYDVAVCCNEHECH 420
QY 421 RYAEIYVIDVINISGCTDGYLTAKMTCRWSTSTIOSLASTIQLRYHRSSLYCSDIPSIH 480
DB 421 RYAEIYVIDVINISGCTDGYLTAKMTCRWSTSTIOSLASTIQLRYHRSSLYCSDIPSIH 480
QY 481 PISEPRDCLOSDGFECECFOPIFLLSGTYMIRINHSLSGSDSPPTCYLPDSVAKPLRP 540
DB 481 PISEPRDCLOSDGFECECFOPIFLLSGTYMIRINHSLSGSDSPPTCYLPDSVAKPLRP 540
QY 541 SSVKAEITINISLKIEMKPEVPENNLOFOIRYGLSGEYOMKMYEVDASKSVSLPV 600
DB 541 SSVKAEITINISLKIEMKPEVPENNLOFOIRYGLSGEYOMKMYEVDASKSVSLPV 600
QY 601 PDLCAVYAVOVCKRLDGLGYWMSNPNAYTVVMDIKYPMRGPPEFRIIINGDTMKKEKNV 660
DB 601 PDLCAVYAVOVCKRLDGLGYWMSNPNAYTVVMDIKYPMRGPPEFRIIINGDTMKKEKNV 660

```

```

QY 661 TLIMPLKMNDSICVQRYVINHHNTSCNGTWSBDVGNHTRKFTFLTEQAHVTVLAINSI 720
DB 661 TLIMPLKMNDSICVQRYVINHHNTSCNGTWSBDVGNHTRKFTFLTEQAHVTVLAINSI 720
QY 721 GASVANENITFSPMSKVINIYOSLSAYPLNSSCVIYSWILSSDVKLMEFIEKMLND 780
DB 721 GASVANENITFSPMSKVINIYOSLSAYPLNSSCVIYSWILSSDVKLMEFIEKMLND 780
QY 781 GEIKMLRISSVKYKYYIHDFPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKMLRISSVKYKYYIHDFPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVPVIISSILLGLTLLSHQRMKLEMDVDPNPKNSMAQGLNFK 891
DB 841 GLYIVPVIISSILLGLTLLSHQRMKLEMDVDPNPKNSMAQGLNFK 891

```

RESULT 41

```

US-08-780-562-4
Sequence 4, Application US/08/780562
GENERAL INFORMATION:
APPLICANT: Mathews, William
TITLE OF INVENTION: MSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562

```

```

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-562-4

```

```

Query Match      76.5%; Score 891; DB 11; Length 923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MICQKFCVLLHMEFYITAFNLSPITPMRFKLSGMPNSTYDFLLPAGLSKNTS 60
DB 1 MICQKFCVLLHMEFYITAFNLSPITPMRFKLSGMPNSTYDFLLPAGLSKNTS 60
QY 61 NGHETAVEPKENSSGTHFSNLKTTFHCCFSESDRNCSLCADNIEGTFVSTVNSL 120
DB 61 NGHETAVEPKENSSGTHFSNLKTTFHCCFSESDRNCSLCADNIEGTFVSTVNSL 120

```

```

Db 61 NGHYETAVERKRNSSGTHSNLSKTTFFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120
Qy 121 QOIDANNNIQCWLKGDGLKLFICYVESLFEKNLFRNRYKYHLLYLPEVLEDSPLVPQKGS 180
Db 121 QOIDANNNIQCWLKGDGLKLFICYVESLFEKNLFRNRYKYHLLYLPEVLEDSPLVPQKGS 180
Qy 181 FQWVHCNCSVHECCCECLVPEVPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINMKVPRDP 240
Db 181 FQWVHCNCSVHECCCECLVPEVPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINMKVPRDP 240
Qy 241 LGLHMEITDDGNLKLISWSSPPLVPPLOQOVKYSNSTVIREADTVATSLVDSILP 300
Db 241 LGLHMEITDDGNLKLISWSSPPLVPPLOQOVKYSNSTVIREADTVATSLVDSILP 300
Qy 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTTODIYVPPKILTVSGSNVSFHCYKKEKNI 360
Db 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTTODIYVPPKILTVSGSNVSFHCYKKEKNI 360
Qy 361 VPSKEIVMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RAELVIVDYNINISCEGTGYLTKMTCRWSSTIOSLASTIOLRHRSLVCSODIPSIH 480
Db 421 RAELVIVDYNINISCEGTGYLTKMTCRWSSTIOSLASTIOLRHRSLVCSODIPSIH 480
Qy 481 PISEPKCYLQSDGFECIFQPIFLISGYTMMIRINHSLSGLSDSPFCVLPSVVPRLP 540
Db 481 PISEPKCYLQSDGFECIFQPIFLISGYTMMIRINHSLSGLSDSPFCVLPSVVPRLP 540
Qy 541 SSVKAEITINIGLKLISWKPVPENNLOPQIRYGLSGKEVQKMYEVDASKSVSLPV 600
Db 541 SSVKAEITINIGLKLISWKPVPENNLOPQIRYGLSGKEVQKMYEVDASKSVSLPV 600
Qy 601 PDLCAVYAVQVGRKLDGPGIWSMDSTPRVFTTODIYVPPKILTVSGSNVSFHCYKKEKNI 660
Db 601 PDLCAVYAVQVGRKLDGPGIWSMDSTPRVFTTODIYVPPKILTVSGSNVSFHCYKKEKNI 660
Qy 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSBDVGNHKTFFLMTQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSBDVGNHKTFFLMTQAHVTVLAINSI 720
Qy 721 GASVANFNITFSPMKVNIYOSLSAYPLNNSCVYLSLSPDYKLMFTIEMKMLND 780
Db 721 GASVANFNITFSPMKVNIYOSLSAYPLNNSCVYLSLSPDYKLMFTIEMKMLND 780
Qy 781 GEKMLRISSVKKYIHHFTPIEKYQSLYPIFMEGKPKIINSFTODDIEKHQSDA 840
Db 781 GEKMLRISSVKKYIHHFTPIEKYQSLYPIFMEGKPKIINSFTODDIEKHQSDA 840
Qy 841 GLYVIVPVIISSIIILLGTLILSHQRMKLFMEDVBNPKNCSWAQGLNFQK 891
Db 841 GLYVIVPVIISSIIILLGTLILSHQRMKLFMEDVBNPKNCSWAQGLNFQK 891

```

RESULT 42
US-08-774-414-1
Sequence 1, Application US/08774414

GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: WELCHER, ANDREW A.
APPLICANT: FLETCHER, FREDERICK A.
TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,414
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382-A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 965 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-774-414-1

```

Query Match 76.5%; Score 891; DB 11; length 965;

Best local similarity 100.0%; Pred. No. 0; Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MICQKFCVLLHMEFIYVITAFNLSTPITPMRFKLSCMPNNTYUYELLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHMEFIYVITAFNLSTPITPMRFKLSCMPNNTYUYELLPAGLSKNTSNS 60
Qy 61 NGHYETAVERKRNSSGTHSNLSKTTFFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAVERKRNSSGTHSNLSKTTFFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120
Qy 121 QOIDANNNIQCWLKGDGLKLFICYVESLFEKNLFRNRYKYHLLYLPEVLEDSPLVPQKGS 180
Db 121 QOIDANNNIQCWLKGDGLKLFICYVESLFEKNLFRNRYKYHLLYLPEVLEDSPLVPQKGS 180
Qy 181 FQWVHCNCSVHECCCECLVPEVPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINMKVPRDP 240
Db 181 FQWVHCNCSVHECCCECLVPEVPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINMKVPRDP 240
Qy 241 LGLHMEITDDGNLKLISWSSPPLVPPLOQOVKYSNSTVIREADTVATSLVDSILP 300
Db 241 LGLHMEITDDGNLKLISWSSPPLVPPLOQOVKYSNSTVIREADTVATSLVDSILP 300
Qy 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTTODIYVPPKILTVSGSNVSFHCYKKEKNI 360
Db 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTTODIYVPPKILTVSGSNVSFHCYKKEKNI 360
Qy 361 VPSKEIVMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RAELVIVDYNINISCEGTGYLTKMTCRWSSTIOSLASTIOLRHRSLVCSODIPSIH 480
Db 421 RAELVIVDYNINISCEGTGYLTKMTCRWSSTIOSLASTIOLRHRSLVCSODIPSIH 480
Qy 481 PISEPKCYLQSDGFECIFQPIFLISGYTMMIRINHSLSGLSDSPFCVLPSVVPRLP 540
Db 481 PISEPKCYLQSDGFECIFQPIFLISGYTMMIRINHSLSGLSDSPFCVLPSVVPRLP 540
Qy 541 SSVKAEITINIGLKLISWKPVPENNLOPQIRYGLSGKEVQKMYEVDASKSVSLPV 600
Db 541 SSVKAEITINIGLKLISWKPVPENNLOPQIRYGLSGKEVQKMYEVDASKSVSLPV 600
Qy 601 PDLCAVYAVQVGRKLDGPGIWSMDSTPRVFTTODIYVPPKILTVSGSNVSFHCYKKEKNI 660
Db 601 PDLCAVYAVQVGRKLDGPGIWSMDSTPRVFTTODIYVPPKILTVSGSNVSFHCYKKEKNI 660
Qy 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSBDVGNHKTFFLMTQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSBDVGNHKTFFLMTQAHVTVLAINSI 720

```

QY 721 GASVAFNLTFSMPMSKVINIVOSLSAYPLNSSCVIWSLSPSDYKLMYFIEMKNLND 780
 DB 721 GASVAFNLTFSMPMSKVINIVOSLSAYPLNSSCVIWSLSPSDYKLMYFIEMKNLND 780
 QY 781 GEIKWLRISSSVKYYIHDFIPIEKYOSLYPIFMEGVGKPKIINSFQDDEKHQSDA 840
 DB 781 GEIKWLRISSSVKYYIHDFIPIEKYOSLYPIFMEGVGKPKIINSFQDDEKHQSDA 840
 QY 841 GLVIVPVISSSILLGLTLLISHQRMKLFMEDVDPNPNKNCMAQGLNOK 891
 DB 841 GLVIVPVISSSILLGLTLLISHQRMKLFMEDVDPNPNKNCMAQGLNOK 891

RESULT 43

US-09-671-049-1
 ; Sequence 1, Application US/09671049
 ; GENERAL INFORMATION:
 ; APPLICANT: CHANG, MING-SHI
 ; FLETCHER, ANDREW A.
 ; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
 ; COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 Dehavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/671,049
 ; FILING DATE: 27-Sep-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/774,414
 ; FILING DATE: 31-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pessin, Karol M.
 ; REFERENCE/DOCKET NUMBER: A-382-A
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 965 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 ; US-09-671-049-1

Query Match 76.5%; Score 891; DB 20; Length 965;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCQKRCVLLHMEFYVTAFLSYPIIPWRFKLSGMPNSYDYELLPAIGSKTNS 60
 DB 1 MLCQKRCVLLHMEFYVTAFLSYPIIPWRFKLSGMPNSYDYELLPAIGSKTNS 60
 QY 61 NCHYEAVPEKFNSSGTHFSNLKTFHCFCFSEODRNSCLADNIEGKFTSVNSLVF 120
 DB 61 NCHYEAVPEKFNSSGTHFSNLKTFHCFCFSEODRNSCLADNIEGKFTSVNSLVF 120
 QY 121 QOIDANMNIOQWLKGLKPICTVESLEFNLFRNIVYKVLHLYLPEVLEDSPLVPQKS 180
 DB 121 QOIDANMNIOQWLKGLKPICTVESLEFNLFRNIVYKVLHLYLPEVLEDSPLVPQKS 180
 QY 181 PQMVHCNCSVHECCLELVVPTAKLNDTLMLKLTSGVITQSPLMASQPIINMKRPDP 240
 DB 181 PQMVHCNCSVHECCLELVVPTAKLNDTLMLKLTSGVITQSPLMASQPIINMKRPDP 240

DB 181 PQMVHCNCSVHECCLELVVPTAKLNDTLMLKLTSGVITQSPLMASQPIINMKRPDP 240
 QY 241 LGLHMEITDGNLTKISMSPPPLVPEPIQYQVYKSENSTVIREADKIVSATSLYDSILP 300
 DB 241 LGLHMEITDGNLTKISMSPPPLVPEPIQYQVYKSENSTVIREADKIVSATSLYDSILP 300
 QY 301 GSSYEVOVGKRLDGGIWSMDSTPRVFTTODVIFYPPKILTSVGSNVSFHCITYKKENKI 360
 DB 301 GSSYEVOVGKRLDGGIWSMDSTPRVFTTODVIFYPPKILTSVGSNVSFHCITYKKENKI 360
 QY 361 VPSKETVMMNLAEKIPQSOQYDVSDHVSQVTEFNLNETKPRGKFTYDAVCCNEHECHH 420
 DB 361 VPSKETVMMNLAEKIPQSOQYDVSDHVSQVTEFNLNETKPRGKFTYDAVCCNEHECHH 420
 QY 421 RYAEIYVIDVINISCEITDGYLTMTKCRNSTSTIOLASTIQLRYHRSLSYCSIPSIH 480
 DB 421 RYAEIYVIDVINISCEITDGYLTMTKCRNSTSTIOLASTIQLRYHRSLSYCSIPSIH 480
 QY 481 PISEPKDCYLOSDGFECEIFOPIFLISGYTMMIRINHSIGSLDSIPTCVLPDSVYKPLPP 540
 DB 481 PISEPKDCYLOSDGFECEIFOPIFLISGYTMMIRINHSIGSLDSIPTCVLPDSVYKPLPP 540
 QY 541 SSVKAEITINIGLTKISMEKPFEPENNLOFOIRYGLSGKEVOMKYEVYDAKSKSVSLPV 600
 DB 541 SSVKAEITINIGLTKISMEKPFEPENNLOFOIRYGLSGKEVOMKYEVYDAKSKSVSLPV 600
 QY 601 PDLCAVYAVQVQCKRLDGLGYWSNMSNPAYTVMDIKYMRGPETNRILINGDMKKEKNV 660
 DB 601 PDLCAVYAVQVQCKRLDGLGYWSNMSNPAYTVMDIKYMRGPETNRILINGDMKKEKNV 660
 QY 661 TLLMKPLKNDLSICVQRYVINHHHSNGTWSGSDGNNHKKFFLWTEQAHYTVLAINSI 720
 DB 661 TLLMKPLKNDLSICVQRYVINHHHSNGTWSGSDGNNHKKFFLWTEQAHYTVLAINSI 720
 QY 721 GASVAFNLTFSMPMSKVINIVOSLSAYPLNSSCVIWSLSPSDYKLMYFIEMKNLND 780
 DB 721 GASVAFNLTFSMPMSKVINIVOSLSAYPLNSSCVIWSLSPSDYKLMYFIEMKNLND 780
 QY 781 GEIKWLRISSSVKYYIHDFIPIEKYOSLYPIFMEGVGKPKIINSFQDDEKHQSDA 840
 DB 781 GEIKWLRISSSVKYYIHDFIPIEKYOSLYPIFMEGVGKPKIINSFQDDEKHQSDA 840
 QY 841 GLVIVPVISSSILLGLTLLISHQRMKLFMEDVDPNPNKNCMAQGLNOK 891
 DB 841 GLVIVPVISSSILLGLTLLISHQRMKLFMEDVDPNPNKNCMAQGLNOK 891

RESULT 44

US-08-582-825-5
 ; Sequence 5, Application US/08582825
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
 ; COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 Dehavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/582,825
 ; FILING DATE: 04-JAN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pessin, Karol M.

REFERENCE/DOCKET NUMBER: A-382
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 969 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-582-825-5

Query Match 76.5%; Score 891; DB 9; Length 969;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MICQKFCVLLHMEFIYTAFLNLSYPIIPWPKFKLSCMPNNTYDYFLLPAGLSKNTS 60
DB 1 MICQKFCVLLHMEFIYTAFLNLSYPIIPWPKFKLSCMPNNTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVERPKNSGTHFSNLKTTFHCCFSEODRNCSLCADNIEGKTFVSTNSLVF 120
DB 61 NGHYETAVERPKNSGTHFSNLKTTFHCCFSEODRNCSLCADNIEGKTFVSTNSLVF 120
QY 121 QOIDANMNIQCMKGLDKLFICYVESLFKNLFRNNYKHYLLVLPVLEDSPLVPQKGS 180
DB 121 QOIDANMNIQCMKGLDKLFICYVESLFKNLFRNNYKHYLLVLPVLEDSPLVPQKGS 180
QY 181 FQMVHNCNVHCECECLVVPPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPIINMVPDPP 240
DB 181 FQMVHNCNVHCECECLVVPPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPIINMVPDPP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPPLOYQVXKSENSTVIREADKIVATSILVDSILP 300
DB 241 LGLHMEITDDGNLKISWSSPPLVPPLOYQVXKSENSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEVOVAGKRLDGGIMSDSTPRVFTQDYIFPPKILTSVGSNVSFHCYKKEKNI 360
DB 301 GSSYEVOVAGKRLDGGIMSDSTPRVFTQDYIFPPKILTSVGSNVSFHCYKKEKNI 360
QY 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCEIDGYLTAKMTCRMSTSTIOSLAESTIQLRYHRSLSVCSIDPSIH 480
DB 421 RYAEIYVIDVNIINISCEIDGYLTAKMTCRMSTSTIOSLAESTIQLRYHRSLSVCSIDPSIH 480
QY 481 PISEPKDVLQSDGFECIFQPIFLLSGYTMIRLNHSLGSLDSPPTCVLPDSVYKPLRP 540
DB 481 PISEPKDVLQSDGFECIFQPIFLLSGYTMIRLNHSLGSLDSPPTCVLPDSVYKPLRP 540
QY 541 SSVKAEITINILKISWEKPVFPEENNLOFQIRYGLSGKEVOMKMEYVDAKSKSYSLPV 600
DB 541 SSVKAEITINILKISWEKPVFPEENNLOFQIRYGLSGKEVOMKMEYVDAKSKSYSLPV 600
QY 601 PDLCAVYAVOVCKRLDGLGYSNMSNPAYTVVMDIKVPMRGPEFWRINNGDTMKKEKNV 660
DB 601 PDLCAVYAVOVCKRLDGLGYSNMSNPAYTVVMDIKVPMRGPEFWRINNGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSGVORVYINHHSTSCNGTSEDVGNHKKFTFLMEQAHYTVVLAINSI 720
DB 661 TLLMKPLMKNDLSGVORVYINHHSTSCNGTSEDVGNHKKFTFLMEQAHYTVVLAINSI 720
QY 721 GASVANFNLTFSMPKSVKIVOSLSAYPLNSSCVIYSWILSPSDYILMEYIIEKMLNED 780
DB 721 GASVANFNLTFSMPKSVKIVOSLSAYPLNSSCVIYSWILSPSDYILMEYIIEKMLNED 780
QY 781 GEIKMLRISSSVKKYIYIDHFIPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKMLRISSSVKKYIYIDHFIPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVTPVLISSILLGLTLLSHQRMKLFMEDVDPNPKNCMAOGLNOK 891
DB 841 GLYIVTPVLISSILLGLTLLSHQRMKLFMEDVDPNPKNCMAOGLNOK 891

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DB 841 GLYIVTPVLISSILLGLTLLSHQRMKLFMEDVDPNPKNCMAOGLNOK 891

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RESULT 45
US-08-582-825A-5
; Sequence 5, Application US/08582825A
; GENERAL INFORMATION:
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,825A
; FILING DATE: 04-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-582-825A-5

```

Query Match 76.5%; Score 891; DB 9; Length 969;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MICQKFCVLLHMEFIYTAFLNLSYPIIPWPKFKLSCMPNNTYDYFLLPAGLSKNTS 60
DB 1 MICQKFCVLLHMEFIYTAFLNLSYPIIPWPKFKLSCMPNNTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVERPKNSGTHFSNLKTTFHCCFSEODRNCSLCADNIEGKTFVSTNSLVF 120
DB 61 NGHYETAVERPKNSGTHFSNLKTTFHCCFSEODRNCSLCADNIEGKTFVSTNSLVF 120
QY 121 QOIDANMNIQCMKGLDKLFICYVESLFKNLFRNNYKHYLLVLPVLEDSPLVPQKGS 180
DB 121 QOIDANMNIQCMKGLDKLFICYVESLFKNLFRNNYKHYLLVLPVLEDSPLVPQKGS 180
QY 181 FQMVHNCNVHCECECLVVPPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPIINMVPDPP 240
DB 181 FQMVHNCNVHCECECLVVPPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPIINMVPDPP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPPLOYQVXKSENSTVIREADKIVATSILVDSILP 300
DB 241 LGLHMEITDDGNLKISWSSPPLVPPLOYQVXKSENSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEVOVAGKRLDGGIMSDSTPRVFTQDYIFPPKILTSVGSNVSFHCYKKEKNI 360
DB 301 GSSYEVOVAGKRLDGGIMSDSTPRVFTQDYIFPPKILTSVGSNVSFHCYKKEKNI 360
QY 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCEIDGYLTAKMTCRMSTSTIOSLAESTIQLRYHRSLSVCSIDPSIH 480
DB 421 RYAEIYVIDVNIINISCEIDGYLTAKMTCRMSTSTIOSLAESTIQLRYHRSLSVCSIDPSIH 480

```

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Db 421 RAELVYIDVNIINISCEITGTLTKMTCRMSTSTQSLAESTLOLRHRSLSYCDIPSIH 480
QY 481 PISEPKDCYLOSDGFECECTFOPIFELLSGYTMMIRINHSGLSDSPPTCVLPDSVYAPLPP 540
Db 481 PISEPKDCYLOSDGFECECTFOPIFELLSGYTMMIRINHSGLSDSPPTCVLPDSVYAPLPP 540
QY 541 SSVKAEITINIGLKISWEKVPPENNLOFOIRYGLSGREVKMKMEYVDKSKSVSLPV 600
Db 541 SSVKAEITINIGLKISWEKVPPENNLOFOIRYGLSGREVKMKMEYVDKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATVYMDIKVPRGPEFRIIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATVYMDIKVPRGPEFRIIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSQVORYVINHHTSCNGTWSDEVGNHTKETFLMTQEAHTVVLAINSI 720
Db 661 TLLMKPLMKNDLSLCSQVORYVINHHTSCNGTWSDEVGNHTKETFLMTQEAHTVVLAINSI 720
QY 721 GASVANFNLTFSWPMKSKVINVOISLAYPLNSSCVIVSWILSPSDYKLMYFIEMKMLNED 780
Db 721 GASVANFNLTFSWPMKSKVINVOISLAYPLNSSCVIVSWILSPSDYKLMYFIEMKMLNED 780
QY 781 GEIKMLRISSSVKYYIHDFIPIEIKYQPSLYPIFMEGCGKPKIINSFTQODIEKHQSDA 840
Db 781 GEIKMLRISSSVKYYIHDFIPIEIKYQPSLYPIFMEGCGKPKIINSFTQODIEKHQSDA 840
QY 841 GLYVIVPVIISSILLGLTLLISHQRMKLFMEDVNPKNCSMAOGLNFOK 891
Db 841 GLYVIVPVIISSILLGLTLLISHQRMKLFMEDVNPKNCSMAOGLNFOK 891

```

RESULT 46
US-08-774-414-5

```

; Sequence 5, Application US/08774414
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: WELCHER, ANDREW A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774.414
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382-A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-774-414-5

```

Query Match 76.5%, Score 891; DB 11; Length 969;
Best Local Similarity 100.0%, Pred. No. 0;

	Matches	991; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY 1	MICOKFCVLLHWEFIYVTAENLSTYPTMREKLSGMPNNTYVFLPAGLSKNTNS	60				
Db 1	MICOKFCVLLHWEFIYVTAENLSTYPTMREKLSGMPNNTYVFLPAGLSKNTNS	60				
QY 61	NGHYEAVBEKENSSTHPSNLSKTTFHCCFNSQDRNCSLADNTEGTFVSTVNSLVF	120				
Db 61	NGHYEAVBEKENSSTHPSNLSKTTFHCCFNSQDRNCSLADNTEGTFVSTVNSLVF	120				
QY 121	QOIDANNINOCMLKGLDKLPICVESLFRNLPENYKVALHLYLVEDESPVQOKS	180				
Db 121	QOIDANNINOCMLKGLDKLPICVESLFRNLPENYKVALHLYLVEDESPVQOKS	180				
QY 181	FGVHNCNCSVHECCLELVVPTAKLNDTLMCKLITSGVIFQSPPLASVQPIVMVAPDP	240				
Db 181	FGVHNCNCSVHECCLELVVPTAKLNDTLMCKLITSGVIFQSPPLASVQPIVMVAPDP	240				
QY 241	LGHLMEITDDGNLKSISWSSPPLVPPLOYOVKYSNSTVIREADKIVSATSLVDSTLP	300				
Db 241	LGHLMEITDDGNLKSISWSSPPLVPPLOYOVKYSNSTVIREADKIVSATSLVDSTLP	300				
QY 301	GSSYEVOVGRKRLDGPISDMSTPRVFTTODVITPPKILISVGSNSVPHCIYKKEKNT	360				
Db 301	GSSYEVOVGRKRLDGPISDMSTPRVFTTODVITPPKILISVGSNSVPHCIYKKEKNT	360				
QY 361	VPSKEIYVMNNLAIEKIPQSOYDVSDHVKYTFEFLNETKPRGKTYDAVCCNEHECHH	420				
Db 361	VPSKEIYVMNNLAIEKIPQSOYDVSDHVKYTFEFLNETKPRGKTYDAVCCNEHECHH	420				
QY 421	RAELVYIDVNIINISCEITGTLTKMTCRMSTSTQSLAESTLOLRHRSLSYCDIPSIH	480				
Db 421	RAELVYIDVNIINISCEITGTLTKMTCRMSTSTQSLAESTLOLRHRSLSYCDIPSIH	480				
QY 481	PISEPKDCYLOSDGFECECTFOPIFELLSGYTMMIRINHSGLSDSPPTCVLPDSVYAPLPP	540				
Db 481	PISEPKDCYLOSDGFECECTFOPIFELLSGYTMMIRINHSGLSDSPPTCVLPDSVYAPLPP	540				
QY 541	SSVKAEITINIGLKISWEKVPPENNLOFOIRYGLSGREVKMKMEYVDKSKSVSLPV	600				
Db 541	SSVKAEITINIGLKISWEKVPPENNLOFOIRYGLSGREVKMKMEYVDKSKSVSLPV	600				
QY 601	PDLCAVYAVQVRCKRLDGLGYWSNMSNPATVYMDIKVPRGPEFRIIINGDTMKKEKNV	660				
Db 601	PDLCAVYAVQVRCKRLDGLGYWSNMSNPATVYMDIKVPRGPEFRIIINGDTMKKEKNV	660				
QY 661	TLLMKPLMKNDLSLCSQVORYVINHHTSCNGTWSDEVGNHTKETFLMTQEAHTVVLAINSI	720				
Db 661	TLLMKPLMKNDLSLCSQVORYVINHHTSCNGTWSDEVGNHTKETFLMTQEAHTVVLAINSI	720				
QY 721	GASVANFNLTFSWPMKSKVINVOISLAYPLNSSCVIVSWILSPSDYKLMYFIEMKMLNED	780				
Db 721	GASVANFNLTFSWPMKSKVINVOISLAYPLNSSCVIVSWILSPSDYKLMYFIEMKMLNED	780				
QY 781	GEIKMLRISSSVKYYIHDFIPIEIKYQPSLYPIFMEGCGKPKIINSFTQODIEKHQSDA	840				
Db 781	GEIKMLRISSSVKYYIHDFIPIEIKYQPSLYPIFMEGCGKPKIINSFTQODIEKHQSDA	840				
QY 841	GLYVIVPVIISSILLGLTLLISHQRMKLFMEDVNPKNCSMAOGLNFOK	891				
Db 841	GLYVIVPVIISSILLGLTLLISHQRMKLFMEDVNPKNCSMAOGLNFOK	891				

RESULT 47
US-08-774-414-6

```

; Sequence 6, Application US/08774414
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: WELCHER, ANDREW A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 33

```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: 1840 Dehavilland Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: USA
;; ZIP: 91320
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/774,414
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pessin, Karol M.
;; REFERENCE/DOCKET NUMBER: A-382-A
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 969 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-774-414-6

Query Match 76.5%; Score 891; DB 11; Length 969;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 891; Conservative 0;

QY 1 MICQKFCVLLHMEFYVTAENLSYPTIPWREKLSCEMPNSTYDYFLPAGLSKNTS 60
DB 1 MICQKFCVLLHMEFYVTAENLSYPTIPWREKLSCEMPNSTYDYFLPAGLSKNTS 60
QY 61 NGHYETAVERKNSGTHSNLSKTFPHCCFNSQDRNCSLADNTEGTFVSTVNSLVF 120
DB 61 NGHYETAVERKNSGTHSNLSKTFPHCCFNSQDRNCSLADNTEGTFVSTVNSLVF 120
QY 121 QOQDAMWNIQCMKGLDKLFCICVESLFRNPNYKVAHLVLPEDVLEDSPLVQKGS 180
DB 121 QOQDAMWNIQCMKGLDKLFCICVESLFRNPNYKVAHLVLPEDVLEDSPLVQKGS 180
QY 181 PQWVHNCNSVHECCSLVVPYPAKNDTLLMCKLITSGVIFQSPPLMSVQPIIMVPRDP 240
DB 181 PQWVHNCNSVHECCSLVVPYPAKNDTLLMCKLITSGVIFQSPPLMSVQPIIMVPRDP 240
QY 241 LGLHMEITDGNLKIWSSPPLVPPLOQVQKXSENSTVIRADKIVASTLSLVDSILP 300
DB 241 LGLHMEITDGNLKIWSSPPLVPPLOQVQKXSENSTVIRADKIVASTLSLVDSILP 300
QY 301 GGSYEYQVNGKRLDGGVMSDMSTPRVFTTODVYPPKILTVSGSNVSHCIYKKNKI 360
DB 301 GGSYEYQVNGKRLDGGVMSDMSTPRVFTTODVYPPKILTVSGSNVSHCIYKKNKI 360
QY 361 VPSKEIYVMMNLAETIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHCCH 420
DB 361 VPSKEIYVMMNLAETIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHCCH 420
QY 421 RYAEIYVIVNINISCEIDGYLTKMTCRMSTSTIQSLAESTLQLRHRSLSXCSDIPSIH 480
DB 421 RYAEIYVIVNINISCEIDGYLTKMTCRMSTSTIQSLAESTLQLRHRSLSXCSDIPSIH 480
QY 481 PISEPDVLOSQGEFECIFQPIFLLSGYTMIRINHSLSGSDSPRTCVLPDSVVRPLRP 540
DB 481 PISEPDVLOSQGEFECIFQPIFLLSGYTMIRINHSLSGSDSPRTCVLPDSVVRPLRP 540
QY 541 SSYKAEITINIGLKISMEKPVFPENNLOFQIRYGLSGKEVQKMEVYDAKSSVSLPV 600
DB 541 SSYKAEITINIGLKISMEKPVFPENNLOFQIRYGLSGKEVQKMEVYDAKSSVSLPV 600

QY 601 PDLCAVYAVQVRCRKLIDGLGYSNNSNPAYTVYMDIKVPRGEPVRIINGDTMKKEKV 660
DB 601 PDLCAVYAVQVRCRKLIDGLGYSNNSNPAYTVYMDIKVPRGEPVRIINGDTMKKEKV 660
QY 661 TLLMKPLMKNDISCSQVQVIVNHHTSCNGTSEDVGNHRTKFTLEQAHYTVLAINSI 720
DB 661 TLLMKPLMKNDISCSQVQVIVNHHTSCNGTSEDVGNHRTKFTLEQAHYTVLAINSI 720
QY 721 GASVANFNTFSWPMKVINVOISLAYPLNNSCVIYSWILSPSDYKLMYFIEMKMLND 780
DB 721 GASVANFNTFSWPMKVINVOISLAYPLNNSCVIYSWILSPSDYKLMYFIEMKMLND 780
QY 781 GEIKWLRISSVYKYYIHDFPIPEKYQSLYPIFMEGVGKPKINSFQODIEKHQSDA 840
DB 781 GEIKWLRISSVYKYYIHDFPIPEKYQSLYPIFMEGVGKPKINSFQODIEKHQSDA 840
QY 841 GLYVIVPVLISSILGLTLISHQRMKLFMEDVNPKNCSAOGLNQK 891
DB 841 GLYVIVPVLISSILGLTLISHQRMKLFMEDVNPKNCSAOGLNQK 891

RESULT 48

US-09-671-049-5

Sequence 5, Application US/09671049

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI

WELCHER, ANDREW A.

FLETCHER, FREDERICK A.

TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED

COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/671,049

FILING DATE: 27-Sep-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/774,414

FILING DATE: 31-Dec-1996

ATTORNEY/AGENT INFORMATION:

NAME: Pessin, Karol M.

REFERENCE/DOCKET NUMBER: A-382-A

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 969 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-671-049-5

Query Match 76.5%; Score 891; DB 20; Length 969;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 891; Conservative 0;

QY 1 MICQKFCVLLHMEFYVTAENLSYPTIPWREKLSCEMPNSTYDYFLPAGLSKNTS 60
DB 1 MICQKFCVLLHMEFYVTAENLSYPTIPWREKLSCEMPNSTYDYFLPAGLSKNTS 60
QY 61 NGHYETAVERKNSGTHSNLSKTFPHCCFNSQDRNCSLADNTEGTFVSTVNSLVF 120
DB 61 NGHYETAVERKNSGTHSNLSKTFPHCCFNSQDRNCSLADNTEGTFVSTVNSLVF 120

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Db 61 NGHETAVEPEKFNSSGTHESNLKSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDAMNINOCWMLKGLDLKLFICVYESLFKNLFNNYKXVLLVLPVLEDSPLVPQKS 180
Db 121 QQIDAMNINOCWMLKGLDLKLFICVYESLFKNLFNNYKXVLLVLPVLEDSPLVPQKS 180
QY 181 FQWVHCNCSVHECCCELVVPVAKLNDTLMLCKLITSGVIFOSPLMSVQPINMKVPRDP 240
Db 181 FQWVHCNCSVHECCCELVVPVAKLNDTLMLCKLITSGVIFOSPLMSVQPINMKVPRDP 240
QY 241 LGHMETIDGKNCIKISMSPPLVPFLOQYVKTSNSTVYIRADKIVSATSLVDSILP 300
Db 241 LGHMETIDGKNCIKISMSPPLVPFLOQYVKTSNSTVYIRADKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKRLDGPIMSDMSTPRVFTTQDYIYFPFKLITSGSVNSFHCIYKKEKNI 360
Db 301 GSSYEVOVGRKRLDGPIMSDMSTPRVFTTQDYIYFPFKLITSGSVNSFHCIYKKEKNI 360
QY 361 VPSKEIYVMMNLAEKIPQSDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCCH 420
Db 361 VPSKEIYVMMNLAEKIPQSDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCCH 420
QY 421 RYAEIVIDVNIINISCEIDGYLTKMTCRMSTSTQSLAESTLQLRHRSLSYCSIDPSIH 480
Db 421 RYAEIVIDVNIINISCEIDGYLTKMTCRMSTSTQSLAESTLQLRHRSLSYCSIDPSIH 480
QY 481 PISEPKCYLQSDGFECIFOPIFLLSGYTMTRINHSLSGLSDSPPTCVLPDSVPRPLP 540
Db 481 PISEPKCYLQSDGFECIFOPIFLLSGYTMTRINHSLSGLSDSPPTCVLPDSVPRPLP 540
QY 541 SSKAETITINIGLKISWEKVPFENNLOFOIRYGLSGKVOXKMEVYDAKSKSVSLPV 600
Db 541 SSKAETITINIGLKISWEKVPFENNLOFOIRYGLSGKVOXKMEVYDAKSKSVSLPV 600
QY 601 PDICAVAYAVQVCKRLDGLGYMSNMSNPATYVMDIKVPRGRPEFRIRIINGDTMKKEKNV 660
Db 601 PDICAVAYAVQVCKRLDGLGYMSNMSNPATYVMDIKVPRGRPEFRIRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTQAHVTVLAINSI 720
QY 721 GASVAPNLTFSMPKMNVTVOISLAVPLNSSCVITVSWILSPDYKLMFTIEMKMLNED 780
Db 721 GASVAPNLTFSMPKMNVTVOISLAVPLNSSCVITVSWILSPDYKLMFTIEMKMLNED 780
QY 781 GEIKMLRISSSVAKKYYIHDFIPIEKYQPSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSSVAKKYYIHDFIPIEKYQPSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLXVIVPVIISSITLLGLTLLISHOMKCLFMDVDPNPKNCVAGGLNFOK 891
Db 841 GLXVIVPVIISSITLLGLTLLISHOMKCLFMDVDPNPKNCVAGGLNFOK 891

```

RESULT 49

US-09-671-049-6
Sequence 6, Application US/09671049

GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI

WELCHER, ANDREW A.
TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED

COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.

STREET: 1840 Delavalland Drive
CITY: Thousand Oaks

STATE: California
COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

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? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentia Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/671,049
? FILING DATE: 27-Sep-2000
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/774,414
? FILING DATE: 31-DEC-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Pesslin, Karol M.
? REFERENCE/DOCKET NUMBER: A-382-A
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 969 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-671-049-6

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Query Match 76.5%; Score 891; DB 20; length 969;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICOKFCVULLHMEFYIVTAFLSYPIIPWPRKLSGMPNSTRYDFLLPAGLSKRTSNS 60
Db 1 MICOKFCVULLHMEFYIVTAFLSYPIIPWPRKLSGMPNSTRYDFLLPAGLSKRTSNS 60
QY 61 NGHETAVEPEKFNSSGTHESNLKSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPEKFNSSGTHESNLKSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDAMNINOCWMLKGLDLKLFICVYESLFKNLFNNYKXVLLVLPVLEDSPLVPQKS 180
Db 121 QQIDAMNINOCWMLKGLDLKLFICVYESLFKNLFNNYKXVLLVLPVLEDSPLVPQKS 180
QY 181 FQWVHCNCSVHECCCELVVPVAKLNDTLMLCKLITSGVIFOSPLMSVQPINMKVPRDP 240
Db 181 FQWVHCNCSVHECCCELVVPVAKLNDTLMLCKLITSGVIFOSPLMSVQPINMKVPRDP 240
QY 241 LGHMETIDGKNCIKISMSPPLVPFLOQYVKTSNSTVYIRADKIVSATSLVDSILP 300
Db 241 LGHMETIDGKNCIKISMSPPLVPFLOQYVKTSNSTVYIRADKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKRLDGPIMSDMSTPRVFTTQDYIYFPFKLITSGSVNSFHCIYKKEKNI 360
Db 301 GSSYEVOVGRKRLDGPIMSDMSTPRVFTTQDYIYFPFKLITSGSVNSFHCIYKKEKNI 360
QY 361 VPSKEIYVMMNLAEKIPQSDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCCH 420
Db 361 VPSKEIYVMMNLAEKIPQSDYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCCH 420
QY 421 RYAEIVIDVNIINISCEIDGYLTKMTCRMSTSTQSLAESTLQLRHRSLSYCSIDPSIH 480
Db 421 RYAEIVIDVNIINISCEIDGYLTKMTCRMSTSTQSLAESTLQLRHRSLSYCSIDPSIH 480
QY 481 PISEPKCYLQSDGFECIFOPIFLLSGYTMTRINHSLSGLSDSPPTCVLPDSVPRPLP 540
Db 481 PISEPKCYLQSDGFECIFOPIFLLSGYTMTRINHSLSGLSDSPPTCVLPDSVPRPLP 540
QY 541 SSKAETITINIGLKISWEKVPFENNLOFOIRYGLSGKVOXKMEVYDAKSKSVSLPV 600
Db 541 SSKAETITINIGLKISWEKVPFENNLOFOIRYGLSGKVOXKMEVYDAKSKSVSLPV 600
QY 601 PDICAVAYAVQVCKRLDGLGYMSNMSNPATYVMDIKVPRGRPEFRIRIINGDTMKKEKNV 660
Db 601 PDICAVAYAVQVCKRLDGLGYMSNMSNPATYVMDIKVPRGRPEFRIRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTQAHVTVLAINSI 720

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Db 661 TLMKPLKNDLCSVQRYVINHHSCNGTWSGSEEDGNHFKFTFLTEQAHVTVLAINSI 720
Qy 721 GASVANFNLTFSMPMSKVNIVOSLSAYPLNNSCVIYSWILSPSDYKLMVFIEEMKNLND 780
Db 721 GASVANFNLTFSMPMSKVNIVOSLSAYPLNNSCVIYSWILSPSDYKLMVFIEEMKNLND 780
Qy 781 GEIKMLRISSSVKKYYIHDFPIEIKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSSVKKYYIHDFPIEIKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Qy 841 GLYIVPVISSISLLGLTLISHOQMKKLFMEDVNPKNCSMAOGLNFOK 891
Db 841 GLYIVPVISSISLLGLTLISHOQMKKLFMEDVNPKNCSMAOGLNFOK 891

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RESULT 50
US-08-582-825-3
: Sequence 3, Application US/08582825
: GENERAL INFORMATION:
: APPLICANT: Chang, Ming-Shi
: TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
: TITLE OF INVENTION: COMPOSITIONS AND METHODS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Inc.
: STREET: 1840 Dehavilland Drive
: CITY: Thousand Oaks
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 91320-1789
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/582,825
: FILING DATE: 04-JAN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Pessin, Karol M.
: REFERENCE/DOCKET NUMBER: A-382
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 995 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-582-825-3

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Query Match 76.5%; Score 891; DB 9; Length 995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTCQFCVLLHMERIYVTAFTNLSPITPMRFKLSCLMPNSTYDYFILPAGLSKNTSNS 60
Qy 61 NGHYETAPEKFNSSGTHFSNLKSTTFHCFCFRSEODRNCISLCADNIECKTFVSTVNSIYF 120
Db 61 NGHYETAPEKFNSSGTHFSNLKSTTFHCFCFRSEODRNCISLCADNIECKTFVSTVNSIYF 120
Qy 121 QOIIDANMNIOCKLKGDKLFCIYVESLFRNLFRNNYKHHLLYVBEVLDESDPLVPQKGS 180
Db 121 QOIIDANMNIOCKLKGDKLFCIYVESLFRNLFRNNYKHHLLYVBEVLDESDPLVPQKGS 180
Qy 181 FQMVHNCNSVHECCCEIYVPTAKINDTLIMCLKITSQGVIFQSPPLMSVQPINMVKPDP 240
Db 181 FQMVHNCNSVHECCCEIYVPTAKINDTLIMCLKITSQGVIFQSPPLMSVQPINMVKPDP 240

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Qy 241 LGLHMEITDDGNLTKISWSSPPLVPPLOYQVYKSENSTTVINEAKIKYSATSLDVSILP 300
Db 241 LGLHMEITDDGNLTKISWSSPPLVPPLOYQVYKSENSTTVINEAKIKYSATSLDVSILP 300
Qy 301 GSSYEVQYRGKRLDGPGLMSDMSPTPRVFTQDVYIEPPKILSVGSNSFHCITYKENKI 360
Db 301 GSSYEVQYRGKRLDGPGLMSDMSPTPRVFTQDVYIEPPKILSVGSNSFHCITYKENKI 360
Qy 361 VPSKEIYVMNNLAEKIPOSQYDVVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVMNNLAEKIPOSQYDVVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RYAEIYVDVNNINISCEFDGYITKMTCRMSTSTQSLASTIQLRHRSSILCSODIPSH 480
Db 421 RYAEIYVDVNNINISCEFDGYITKMTCRMSTSTQSLASTIQLRHRSSILCSODIPSH 480
Qy 481 PISEPKDCYLOSDGFYECCIFOPIFLLSGVTMMIRINHSIGSLDSPPTCVLPDSVYKPLPP 540
Db 481 PISEPKDCYLOSDGFYECCIFOPIFLLSGVTMMIRINHSIGSLDSPPTCVLPDSVYKPLPP 540
Qy 541 SSVKAEITINIGLKIISWEKPVFPENNLOFQIRYGLSGREYQWKVEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKIISWEKPVFPENNLOFQIRYGLSGREYQWKVEYVDAKSKSVSLPV 600
Qy 601 PDLCAVYAVQVCKRLDGLGYGYSNNSNPAYTYVMIDIKYPMRGPETWRIINGDTMKREKV 660
Db 601 PDLCAVYAVQVCKRLDGLGYGYSNNSNPAYTYVMIDIKYPMRGPETWRIINGDTMKREKV 660
Qy 661 TLMKPLKNDLCSVQRYVINHHSCNGTWSGSEEDGNHFKFTFLTEQAHVTVLAINSI 720
Db 661 TLMKPLKNDLCSVQRYVINHHSCNGTWSGSEEDGNHFKFTFLTEQAHVTVLAINSI 720
Qy 721 GASVANFNLTFSMPMSKVNIVOSLSAYPLNNSCVIYSWILSPSDYKLMVFIEEMKNLND 780
Db 721 GASVANFNLTFSMPMSKVNIVOSLSAYPLNNSCVIYSWILSPSDYKLMVFIEEMKNLND 780
Qy 781 GEIKMLRISSSVKKYYIHDFPIEIKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKMLRISSSVKKYYIHDFPIEIKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Qy 841 GLYIVPVISSISLLGLTLISHOQMKKLFMEDVNPKNCSMAOGLNFOK 891
Db 841 GLYIVPVISSISLLGLTLISHOQMKKLFMEDVNPKNCSMAOGLNFOK 891

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Search completed: May 18, 2002, 07:07:51
Job time: 350 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 07:02:51 ; Search time 13.83 Seconds
(without alignments)
2226.469 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 1165
Sequence: 1 MICQKFCVLLHMEFIYIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 107366 seqs, 26430961 residues

Word size : 0

Total number of hits satisfying chosen parameters: 107366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

Pending Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	2.0	23	US-09-991-548-6	Sequence 6, Appl1
2	8	0.7	102	US-09-540-209B-8563	Sequence 8563, Ap
3	8	0.7	1887	US-09-853-180-3	Sequence 13, Appl1
4	7	0.6	20	US-10-027-400-13	Sequence 770, App
5	7	0.6	50	PCT-US02-09188-770	Sequence 507, App
6	7	0.6	50	PCT-US02-09257-507	Sequence 800, App
7	7	0.6	50	PCT-US02-09370-800	Sequence 169, App
8	7	0.6	50	US-10-103-295-169	Sequence 6882, Ap
9	7	0.6	50	US-10-105-299-3604	Sequence 6912, Ap
10	7	0.6	64	US-09-540-209B-6882	Sequence 265, App
11	7	0.6	64	US-09-540-209B-6912	Sequence 616, App
12	7	0.6	81	US-10-103-295-265	Sequence 6470, Ap
13	7	0.6	86	PCT-US02-09921-616	Sequence 6272, Ap
14	7	0.6	122	US-09-620-393B-6470	Sequence 7726, Ap
15	7	0.6	127	US-10-106-698-6272	Sequence 282, App
16	7	0.6	134	US-10-106-698-7726	Sequence 456, App
17	7	0.6	176	PCT-US02-07826-282	Sequence 6320, Ap
18	7	0.6	176	US-10-097-340-282	Sequence 8108, Ap
19	7	0.6	197	US-10-125-540-456	Sequence 233, Appl1
20	7	0.6	206	US-10-106-698-620	Sequence 331, App
21	7	0.6	229	PCT-US01-46651-2	Sequence 294, App
22	7	0.6	259	US-09-540-209B-8108	
23	7	0.6	290	US-10-138-632-2	
24	7	0.6	293	US-10-115-123-233	
25	7	0.6	307	US-10-115-123-331	
26	7	0.6	358	US-10-125-540-294	

27	7	0.6	461	US-09-994-404-225	Sequence 225, App
28	7	0.6	470	US-09-994-404-28	Sequence 28, Appl
29	7	0.6	470	US-09-994-404-158	Sequence 158, App
30	7	0.6	473	PCT-US02-09944-442	Sequence 442, App
31	7	0.6	473	US-10-002-304-8	Sequence 8, Appl1
32	7	0.6	473	US-10-002-050-8	Sequence 8, Appl1
33	7	0.6	473	US-10-003-152-8	Sequence 158, App
34	7	0.6	490	US-10-115-123-158	Sequence 1433, App
35	7	0.6	504	US-10-115-123-332	Sequence 10008, A
36	7	0.6	578	US-09-573-655B-1433	Sequence 2, Appl1
37	7	0.6	642	US-09-540-209B-10008	Sequence 6, Appl1
38	7	0.6	663	PCT-US02-01339-2	Sequence 5548, Ap
39	7	0.6	788	US-10-002-304-6	Sequence 3585, Ap
40	7	0.6	788	US-10-002-050-6	Sequence 8585, App
41	7	0.6	788	US-10-003-152-6	Sequence 246, App
42	7	0.6	885	US-09-540-209B-5548	Sequence 17, Appl
43	7	0.6	951	US-09-573-655B-2349	Sequence 134, App
44	7	0.6	1018	US-10-128-714-3585	Sequence 4795, Ap
45	7	0.6	1018	US-10-128-714-8585	Sequence 5897, Ap
46	7	0.6	1185	US-09-895-913A-246	Sequence 129, App
47	7	0.6	1523	PCT-US02-09809-5	Sequence 5092, Ap
48	6	0.5	8	US-09-423-037A-17	Sequence 71, Appl
49	6	0.5	27	US-10-106-698-7746	Sequence 4356, Ap
50	6	0.5	30	US-09-623-799A-134	Sequence 1018, Ap
51	6	0.5	30	US-09-991-548-23	Sequence 938, App
52	6	0.5	33	US-09-620-393B-4795	Sequence 5700, Ap
53	6	0.5	35	US-10-105-299-5897	Sequence 4837, Ap
54	6	0.5	40	US-09-312-283B-129	Sequence 5, Appl1
55	6	0.5	43	US-09-620-393B-5092	Sequence 4356, Ap
56	6	0.5	44	US-09-554-354A-71	Sequence 1018, Ap
57	6	0.5	45	US-10-105-299-4456	Sequence 938, App
58	6	0.5	45	US-10-004-860-938	Sequence 5700, Ap
59	6	0.5	46	US-10-105-299-5700	Sequence 4837, Ap
60	6	0.5	47	US-10-089-903-45	Sequence 5, Appl1
61	6	0.5	51	US-10-105-299-4837	Sequence 4837, Ap
62	6	0.5	51	US-09-564-951A-5	Sequence 5, Appl1
63	6	0.5	53	US-09-564-951A-5	Sequence 4837, Ap
64	6	0.5	55	US-10-105-299-4835	Sequence 8923, Ap
65	6	0.5	55	US-09-620-393B-8923	Sequence 533, App
66	6	0.5	62	US-60-365-384-533	Sequence 5826, App
67	6	0.5	70	US-10-105-299-5826	Sequence 1035, Ap
68	6	0.5	72	US-09-620-393B-1035	Sequence 415, App
69	6	0.5	73	US-09-312-283B-415	Sequence 5468, App
70	6	0.5	73	US-10-106-698-5468	Sequence 5147, Ap
71	6	0.5	78	US-10-106-698-5147	Sequence 3679, App
72	6	0.5	79	US-09-620-393B-3679	Sequence 207, App
73	6	0.5	79	US-10-114-893-207	Sequence 233, App
74	6	0.5	80	PCT-US02-09105-233	Sequence 338, App
75	6	0.5	80	PCT-US02-09105-338	

ALIGNMENTS

RESULT 1
US-09-991-548-6
; Sequence 6, Application US/09991548
; GENERAL INFORMATION:
; APPLICANT: OLSOON, Iemart
; APPLICANT: NARANDA, Tatjana
; TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES AS MODULATORS
; FILE REFERENCE: 213542000101
; CURRENT APPLICATION NUMBER: US/09/991,548
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/028,937
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 08/788,820
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/701,382
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: 08/612,999
; PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for windows version 4.0
SEQ ID NO 6
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human leptin receptor
US-09-991-548-6

Query Match 2.0%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1,3e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 KKKNKIVPSKEIYMMNLAEKIP 377
|||||
Db 1 KKKNKIVPSKEIYMMNLAEKIP 23

RESULT 2
US-09-540-209B-8563
; Sequence 8563, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: 2709,1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 8563
; LENGTH: 102
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-8563

Query Match 0.7%; Score 8; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 655 KKKKNVTL 662
|||||
Db 27 KKKKNVTL 34

RESULT 3
US-09-853-180-3
; Sequence 3, Application US/09853180
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madaline
; APPLICANT: Parham, Christl L.
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074
; CURRENT APPLICATION NUMBER: US/09/853,180
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1887
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-180-3

Query Match 0.7%; Score 8; DB 5; Length 1887;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 GYWSNMSN 627
|||||
Db 1673 GYWSNMSN 1680

RESULT 4
US-10-027-400-13
; Sequence 13, Application US/10027400
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; TITLE OF INVENTION: ESCOBEDO, Jaime A.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/027,400
; FILING DATE: 19-Dec-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,917
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..20
; OTHER INFORMATION: /note="Peptide 7719p scrambled.
; Contains a phosphate group at position 15."
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-027-400-13

Query Match 0.6%; Score 7; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 634 MDIKVPM 640
|||||
Db 2 MDIKVPM 8

RESULT 5
PCT-US02-09188-770
; Sequence 770, Application PC/TRUS0209188
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins

```
FILE REFERENCE: PS952PCT
CURRENT APPLICATION NUMBER: PCT/US02/09188
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 1732
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 770
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09188-770
```

```
Query Match      0.6%; Score 7; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 521 SLDSPPT 527
Db 27 SLDSPPT 33
```

```
RESULT 6
PCT-US02-09257-507
Sequence 507, Application PC/TUS0209257
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS957PCT
CURRENT APPLICATION NUMBER: PCT/US02/09257
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 994
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 507
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09257-507
```

```
Query Match      0.6%; Score 7; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 521 SLDSPPT 527
Db 27 SLDSPPT 33
```

```
RESULT 7
PCT-US02-09370-800
Sequence 800, Application PC/TUS0209370
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS954PCT
CURRENT APPLICATION NUMBER: PCT/US02/09370
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR FILING DATE: 2001-09-12
```

```
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 1834
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 800
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09370-800
```

```
Query Match      0.6%; Score 7; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 521 SLDSPPT 527
Db 27 SLDSPPT 33
```

```
RESULT 8
US-10-103-295-169
Sequence 169, Application US/10103295
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P2
CURRENT APPLICATION NUMBER: US/10/103,295
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: PCT/US01/29871
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: PCT/US01/00911
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/234,925
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 417
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 169
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-295-169
```

```
Query Match      0.6%; Score 7; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 521 SLDSPPT 527
Db 27 SLDSPPT 33
```

```
RESULT 9
US-10-105-299-3604
Sequence 3604, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
```

;; Prior Application removed - See File Wrapper or Palm
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3604
;; LENGTH: 50
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-105-299-3604

Query Match 0.6%; Score 7; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 SLDSPPT 527
|||||||
DB 27 SLDSPPT 33

RESULT 10
US-09-540-209B-6882
; Sequence 6882, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 6882
; LENGTH: 64
; TYPE: PRT
; ORGANISM: B.frag111s
US-09-540-209B-6882

Query Match 0.6%; Score 7; DB 5; Length 64;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 847 PVISSS 853
|||||||
DB 32 PVISSS 38

RESULT 11
US-09-540-209B-6912
; Sequence 6912, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 6912
; LENGTH: 66
; TYPE: PRT
; ORGANISM: B.frag111s
US-09-540-209B-6912

Query Match 0.6%; Score 7; DB 5; Length 66;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 READKIV 288
|||||||
DB 60 READKIV 66

RESULT 12

US-10-103-295-265
; Sequence 265, Application US/10103295
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P2
; CURRENT APPLICATION NUMBER: US/10/103,295
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/US01/29871
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/00911
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/234,925
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 265
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-295-265

Query Match 0.6%; Score 7; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 SLDSPPT 527
|||||||
DB 58 SLDSPPT 64

RESULT 13
PCT-US02-09921-616
; Sequence 616, Application PC/TUS0209921
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFPO, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Dairyl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: HILMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHRY, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.
; APPLICANT: DAM, Tam C.
; APPLICANT: LIU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLEEFELD, Yael
; APPLICANT: GERSTIN JR., Edward H.
; APPLICANT: PERALTA, Careyna H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.

APPLICANT: PANZER, Scott R.
APPLICANT: HARRIS, Bernard
APPLICANT: FLORES, Vincent
APPLICANT: MARWAHA, Rakesh
APPLICANT: LO, Audrey
APPLICANT: LAN, Ruth Y.
APPLICANT: URASHKA, Michael
TITLE OF INVENTION: SECRETORY MOLECULES
FILE REFERENCE: PT-1232 PCT
CURRENT APPLICATION NUMBER: PCT/US02/09921
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/280,067; 60/280,068; 60/291,280; 60/291,849;
60/291,829; 60/299,428; 60/300,001; 60/299,776
PRIOR FILING DATE: 2001-03-29; 2001-03-29; 2001-05-16; 2001-05-17;
2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
NUMBER OF SEQ ID NOS: 1146
SOFTWARE: PERL Program
SEQ ID NO: 616
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: LG:001923.1.orf3a:2001MAR30
PCT-US02-09921-616

Query Match 0.6%; Score 7; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 LPDSVVK 536
|||||

DB 29 LPDSVVK 35

RESULT 14
US-09-620-393B-6470
Sequence 6470, Application US/09620393B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1068P
CURRENT APPLICATION NUMBER: US/09/620,393B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 6470
LENGTH: 122
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..122
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..122
OTHER INFORMATION: Ceres Seq. ID 1392769
US-09-620-393B-6470

Query Match 0.6%; Score 7; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1080 LGVTSIK 1086
|||||

DB 32 LGVTSIK 38

RESULT 15

US-10-106-698-6272
Sequence 6272, Application US/10106698
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280.
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO: 6272
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
US-10-106-698-6272

Query Match 0.6%; Score 7; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 LLISHOR 866
|||||

DB 116 LLISHOR 122

RESULT 16
US-10-106-698-7726
Sequence 7726, Application US/10106698
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO: 7726
LENGTH: 134
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (10)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (17)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (20)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (39)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (56)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (107)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7726

Query Match 0.6%; Score 7; DB 6; Length 134;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 597 SLRPDL 603
 DB 70 SLRPDL 76

RESULT 17

PCT-US02-07826-282
 ; Sequence 282, Application PC/TUS0207826
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
 ; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
 ; FILE REFERENCE: MRI-030PC
 ; CURRENT APPLICATION NUMBER: PCT/US02/07826
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/276,025
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/325,149
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: 60/276,026
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/324,967
 ; PRIOR FILING DATE: 2001/09/26
 ; PRIOR APPLICATION NUMBER: 60/311,732
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/325,102
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/323,580
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 282
 ; LENGTH: 176
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PCT-US02-07826-282

Query Match 0.6%; Score 7; DB 1; Length 176;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 122 QIDANN 128
 DB 93 QIDANN 99

RESULT 18

US-10-097-340-282
 ; Sequence 282, Application US/10097340
 ; GENERAL INFORMATION:
 ; APPLICANT: John MONAHAN
 ; APPLICANT: Manjula GANNAVAPU
 ; APPLICANT: Sebastian HOERSCH
 ; APPLICANT: Shubhangi KAMATKAR
 ; APPLICANT: Steve G. KOVATS
 ; APPLICANT: Rachel E. MEYERS
 ; APPLICANT: Michael MORRISSEY
 ; APPLICANT: Peter OLANDT
 ; APPLICANT: Ami SEN
 ; APPLICANT: Peter VEIBY
 ; APPLICANT: Gordon B. MILLS
 ; APPLICANT: Robert C. BAST, JR.
 ; APPLICANT: Karen LU
 ; APPLICANT: Rosemarie SCHMANDT
 ; APPLICANT: Xumei ZHAO
 ; APPLICANT: Karen GLATT

; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
 ; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
 ; FILE REFERENCE: MRI-030
 ; CURRENT APPLICATION NUMBER: US/10/097,340
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/276,025
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/325,149
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/276,026
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/324,967
 ; PRIOR FILING DATE: 2001/09/26
 ; PRIOR APPLICATION NUMBER: 60/311,732
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/325,102
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/323,580
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 282
 ; LENGTH: 176
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-097-340-282

Query Match 0.6%; Score 7; DB 6; Length 176;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 122 QIDANN 128
 DB 93 QIDANN 99

RESULT 19

US-10-125-540-456
 ; Sequence 456, Application US/10125540
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT214CI
 ; CURRENT APPLICATION NUMBER: US/10/125,540
 ; CURRENT FILING DATE: 2002-04-19
 ; PRIOR APPLICATION removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 646
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 456
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (183)
 ; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 ; US-10-125-540-456

Query Match 0.6%; Score 7; DB 6; Length 197;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 LLPAGLS 54
 DB 174 LLPAGLS 180

RESULT 20

US-10-106-698-6320
 ; Sequence 6320, Application US/10106698
 ; GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO: 6320
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (178)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6320

Query Match 0.6%; Score 7; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 122 QIDAMWN 128
|||||||
DB 119 QIDAMWN 125

RESULT 21
PCT-US01-46651-2
Sequence 2, Application PC/TUS0146651
GENERAL INFORMATION:
APPLICANT: Washington State University Research Foundation
APPLICANT: Druka, Arnis
APPLICANT: Von Wettstein, Dieter
TITLE OF INVENTION: Plant Promoters, and Methods of Use
FILE REFERENCE: WSUR118192
CURRENT APPLICATION NUMBER: PCT/US01/46651
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/247,161
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2
LENGTH: 229
TYPE: PRT
ORGANISM: Hordeum Vulgare
PCT-US01-46651-2

Query Match 0.6%; Score 7; DB 1; Length 229;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 851 SSSILL 857
|||||||
DB 4 SSSILL 10

RESULT 22
US-09-540-2098-8108
Sequence 8108, Application US/095402098
GENERAL INFORMATION:
APPLICANT: Gary L. Bretton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,2098

CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO: 8108
LENGTH: 259
TYPE: PRT
ORGANISM: B. fragilis
US-09-540-2098-8108

Query Match 0.6%; Score 7; DB 5; Length 259;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 LPAGLSK 55
|||||||
DB 25 LPAGLSK 31

RESULT 23
US-10-138-632-2
Sequence 2, Application US/10138632
GENERAL INFORMATION:
APPLICANT: Ozaki, Akio
Mori, Hideo
Shibasaki, Takeshi
Ando, Katsuhiko
Ochiai, Keiko
Chiba, Shigeru
Uosaki, Youichi

TITLE OF INVENTION: Process for Producing
cis-3-Hydroxy-L-Proline
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, SHOUT AND KRAUS
STREET: 1300 NORTH SEVENTEENTH STREET
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22209

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,632
FILING DATE: 06-May-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/455,406
FILING DATE: <unknown>
APPLICATION NUMBER: 08/708,856
FILING DATE: <unknown>
APPLICATION NUMBER: 08/301,654
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/474,135
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
TELEX: 248545

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Streptomyces sp.
STRAIN: TH1

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-138-632-2

Query Match 0.6%; Score 7; DB 6; Length 290;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLSDSPL 174
|||||||
DB 126 VLSDSPL 132

RESULT 24

US-10-115-123-233
; Sequence 233, Application US/10115123
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 233
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (134)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-123-233

Query Match 0.6%; Score 7; DB 6; Length 293;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NTSNSNG 62
|||||||
DB 182 NTSNSNG 188

RESULT 25

US-10-115-123-331
; Sequence 331, Application US/10115123
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 331
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-123-331

Query Match 0.6%; Score 7; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NTSNSNG 62
|||||||
DB 196 NTSNSNG 202

RESULT 26

US-10-125-540-294
; Sequence 294, Application US/10125540
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214CI
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 294
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-294

Query Match 0.6%; Score 7; DB 6; Length 358;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 LLPAGLS 54
|||||||
DB 174 LLPAGLS 180

RESULT 27

US-09-994-404-225
; Sequence 225, Application US/09994404
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: CHAN, JOHN Y.
; APPLICANT: DABROWSKI-AMARAL, CHRISTINE ELLEN
; APPLICANT: DELVECCHIO, ALFRED MICHAEL
; APPLICANT: DILLON, SUSAN B.
; APPLICANT: LEARY, JEFFREY JOSEPH
; APPLICANT: SUTTON, DAVID
; TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
; TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
; FILE REFERENCE: P50583
; CURRENT APPLICATION NUMBER: US/09/994,404

```
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/297,477
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/030,279
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/049,018
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 303
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Herpes simplex
US-09-994-404-225

Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 461;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 LLLGTL 861
    |||||
Db 222 LLLGTL 228

RESULT 28
US-09-994-404-28
; Sequence 28, Application US/09994404
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: CHAN, JOHN Y.
; APPLICANT: DABROWSKI-AMARAL, CHRISTINE ELLEN
; APPLICANT: DELVECHIO, ALFRED MICHAEL
; APPLICANT: DILLON, SUSAN B.
; APPLICANT: LEARY, JEFFREY JOSEPH
; APPLICANT: SUTTON, DAVID
; TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
; FILE REFERENCE: P50583
; CURRENT APPLICATION NUMBER: US/09/994,404
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/297,477
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/030,279
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/049,018
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 303
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Herpes simplex
US-09-994-404-28

Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 470;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 LLLGTL 861
    |||||
Db 231 LLLGTL 237

RESULT 29
US-09-994-404-158
; Sequence 158, Application US/09994404
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: CHAN, JOHN Y.
; APPLICANT: DABROWSKI-AMARAL, CHRISTINE ELLEN
; APPLICANT: DELVECHIO, ALFRED MICHAEL
```

```
; APPLICANT: DILLON, SUSAN B.
; APPLICANT: LEARY, JEFFREY JOSEPH
; APPLICANT: SUTTON, DAVID
; TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
; FILE REFERENCE: P50583
; CURRENT APPLICATION NUMBER: US/09/994,404
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/297,477
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/030,279
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/049,018
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 303
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Herpes simplex
US-09-994-404-158

Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 470;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 LLLGTL 861
    |||||
Db 231 LLLGTL 237

RESULT 30
PCT-US02-09944-442
; Sequence 442, Application PC/TUS0209944
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFEO, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Darryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHET, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.
; APPLICANT: DAM, Tam C.
; APPLICANT: LIU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLEEREID, Yael
; APPLICANT: GERSTIN, JR., Edward H.
; APPLICANT: PERALTA, Careyna H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: NARMAHA, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: IAN, Ruth Y.
; APPLICANT: URASHKA, Michael E.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1231 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09944
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/279,619; 60/280,068; 60/291,280; 60/291,8
60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-28; 2001-03-29; 2001-05-16; 2001-05-17;
```

2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 792
; SOFTWARE: PERL Program
; SEQ ID NO 442
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:208190.2.orfl:2001MAR30
PCT-US02-09944-442

Query Match 0.6%; Score 7; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 861 LISHORH 867
Db 345 LISHORH 351

RESULT 31
US-10-002-304-8
; Sequence 8, Application US/10002304
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-54 CON-S8
; CURRENT APPLICATION NUMBER: US/10/002,304
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-304-8

Query Match 0.6%; Score 7; DB 6; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 LLPAGLS 54
Db 289 LLPAGLS 295

RESULT 32
US-10-002-050-8
; Sequence 8, Application US/10002050
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Human Semaphorin-like Polypeptides
; FILE REFERENCE: 15966-554 Cura-54 CON-S14
; CURRENT APPLICATION NUMBER: US/10/002,050
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286

; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-050-8

Query Match 0.6%; Score 7; DB 6; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 LLPAGLS 54
Db 289 LLPAGLS 295

RESULT 33
US-10-003-152-8
; Sequence 8, Application US/10003152
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Novel Amino Acid Sequences for Human Semaphorin-like Polypeptides
; FILE REFERENCE: 15966-554 Cura-54 CON-S12
; CURRENT APPLICATION NUMBER: US/10/003,152
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-152-8

Query Match 0.6%; Score 7; DB 6; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 LLPAGLS 54
Db 289 LLPAGLS 295

RESULT 34
US-10-115-123-158
; Sequence 158, Application US/10115123
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509

PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 158
LENGTH: 490
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (134)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (389)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-123-158

Query Match 0.6%; Score 7; DB 6; Length 490;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 NTSNSNG 62
|||||
DB 182 NTSNSNG 188

RESULT 35
US-10-115-123-332
Sequence 332, Application US/10115123
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029630APID2
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 332
LENGTH: 504
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (403)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-123-332

Query Match 0.6%; Score 7; DB 6; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 56 NTSNSNG 62
|||||
DB 196 NTSNSNG 202

RESULT 36
US-09-573-655B-1433
Sequence 1433, Application US/09573655B
GENERAL INFORMATION:
APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
FILE REFERENCE: 2750-0876P
CURRENT APPLICATION NUMBER: US/09/573,655B
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 3281
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1433
LENGTH: 578
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-573-655B-1433

Query Match 0.6%; Score 7; DB 5; Length 578;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 CADNIEG 108
|||||
DB 71 CADNIEG 77

RESULT 37
US-09-540-209B-10008
Sequence 10008, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 10008
LENGTH: 642
TYPE: PRT
ORGANISM: B. fragilis
US-09-540-209B-10008

Query Match 0.6%; Score 7; DB 5; Length 642;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 857 LGTLLIS 863
|||||
DB 138 LGTLLIS 144

RESULT 38
PCT-US02-01339-2
Sequence 02, Application PC/TUS0201339
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LEE, Ernestine A.
APPLICANT: WALIA, Narinder K.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry

APPLICANT: THANGAVELU, Kavitha
APPLICANT: XU, Yuning
APPLICANT: ARVIZU, Chandra
APPLICANT: WARREN, Bridget A.
APPLICANT: YAO, Monique G.
APPLICANT: AU-YOUNG, Janice
APPLICANT: HAFALIA, April J.A.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: KALLICK, Deborah A.
APPLICANT: GANDHI, Ameena R.
APPLICANT: RICHARDSON, Thomas W.
APPLICANT: KHAN, Farrah A.
APPLICANT: LU, Yan
APPLICANT: SWARNKAR, Anita
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: NGUYEN, Daniel B.
APPLICANT: GRAUL, Richard
APPLICANT: LU, Dzung Aina M.
TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
FILE REFERENCE: PI-0346 PCT
CURRENT APPLICATION NUMBER: PCT/US02/01339
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/262,838; 60/265,927; 60/271,196; 60/274,549; 60/334,179
PRIOR FILING DATE: 2001-01-19; 2001-02-02; 2001-02-23; 2001-03-09; 2001-11-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 663
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 2319430CD1
PCT-US02-01339-2

Query Match 0.6%; Score 7; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 849 IISSTIL 855
DB 413 IISSTIL 419

RESULT 39
US-10-002-304-6
; Sequence 6, Application US/10002304
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meljia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
FILE REFERENCE: 15966-554 Cura-54 CON-58
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: US/10/002,304
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 788
TYPE: PRT
ORGANISM: Homo sapiens
US-10-002-304-6

Query Match 0.6%; Score 7; DB 6; Length 788;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 LLPAGLS 54
DB 604 LLPAGLS 610

RESULT 40
US-10-002-050-6
; Sequence 6, Application US/10002050
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meljia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Human Semaphorin-Like Po
FILE REFERENCE: 15966-554 Cura-54 CON-514
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: US/10/002,050
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 788
TYPE: PRT
ORGANISM: Homo sapiens
US-10-002-050-6

Query Match 0.6%; Score 7; DB 6; Length 788;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 LLPAGLS 54
DB 604 LLPAGLS 610

RESULT 41
US-10-003-152-6
; Sequence 6, Application US/10003152
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meljia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
TITLE OF INVENTION: Novel Amino Acid Sequences for Human Semaphorin-Like Polypepti
FILE REFERENCE: 15966-554 Cura-54 CON-512
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: US/10/003,152
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 788
TYPE: PRT
ORGANISM: Homo sapiens
US-10-003-152-6

Query Match 0.6%; Score 7; DB 6; Length 788;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 LLPAGLS 54
|||||||

Db 604 LLPAGLS 610

RESULT 42

US-09-540-209B-5548
; Sequence 5548, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540.209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 5548
; LENGTH: 885
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-5548

Query Match 0.6%; Score 7; DB 5; Length 885;
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1127 NINLGTS 1133
|||||||

Db 205 NINLGTS 211

RESULT 43

US-09-573-655B-2349
; Sequence 2349, Application US/09573655B
; GENERAL INFORMATION:
; APPLICANT: SOLOVIEV, Victor and TROCKMAN, Maxim
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750.0876P
; CURRENT APPLICATION NUMBER: US/09/573.655B
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 3281
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2349
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-2349

Query Match 0.6%; Score 7; DB 5; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 529 VLPDSV 535
|||||||

Db 530 VLPDSV 536

RESULT 44

US-10-128-714-3585
; Sequence 3585, Application US/10128714
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

; TITLE OF INVENTION: Methods of Use

; FILE REFERENCE: 10182-018-999

; CURRENT APPLICATION NUMBER: US/10/128.714

; CURRENT FILING DATE: 2002-04-23

; PRIOR APPLICATION NUMBER: US 60/285,697

; PRIOR FILING DATE: 2001-04-23

; PRIOR APPLICATION NUMBER: US 60/287,066

; PRIOR FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/295,890

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/303,899

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: US 60/316,362

; PRIOR FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 8603

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3585

; LENGTH: 1018

; TYPE: PRT

; ORGANISM: Aspergillus fumigatus

US-10-128-714-3585

Query Match 0.6%; Score 7; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 939 VVSLST 945
|||||||

Db 771 VVSLST 777

RESULT 45

US-10-128-714-8585
; Sequence 8585, Application US/10128714
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128.714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8585
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8585

Query Match 0.6%; Score 7; DB 6; Length 1018;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 939 VVSLST 945
|||||||

Db 771 VVSLST 777

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RESULT 46
US-09-895-913A-246
; Sequence 246, Application US/09895913A
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobacter
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 1185
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-246

Query Match          0.6%; Score 7; DB 5; Length 1185;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SATSLV 295
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Db 775 SATSLV 781

RESULT 47
PCT-US02-09809-5
; Sequence 5, Application PC/TUS0209809
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LU, DYUNG AINA M.
; APPLICANT: ARVIZU, CHANDRA S.
; APPLICANT: GANDHI, AMEENA R.
; APPLICANT: HAFALIA, APRIL J.A.
; APPLICANT: DING, LI
; APPLICANT: LU, YAN
; APPLICANT: RAMKUMAR, JAYALAXMI
; APPLICANT: SMARNAKER, ANITA
; APPLICANT: TANG, Y. TOM
; APPLICANT: YUE, HENRY
; APPLICANT: TRAN, BAO
; APPLICANT: LEE, SOO Y.
; APPLICANT: WARREN, BRIDGET A.
; APPLICANT: NGUYEN, DANNIEL B.
; APPLICANT: THANGAVELU, KAVITHA
; APPLICANT: YAO, MONIQUE G.
; APPLICANT: ELLIOTT, VICKI S.
; APPLICANT: BAUGHN, MARIAH R.
; APPLICANT: EMERLING, BROOKE M.
; APPLICANT: LAU, PREETI
; APPLICANT: GIETZEN, KIMBERLY J.
; APPLICANT: BECHA, SHANYA D.
; APPLICANT: MARQUIS, JOSEPH P.
; APPLICANT: KABLE, AMY E.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: P-0921 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09809
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/280,387; 60/282,335; 60/286,663; 60/285,484; 60/350,702;
; PRIOR FILING DATE: 2001-03-30; 2001-04-05; 2001-04-13; 2001-04-19; 2002-01-18; 2002-0
; NUMBER OF SEQ ID NOS: 46
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; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1523
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 1510943CD1
PCT-US02-09809-5

Query Match          0.6%; Score 7; DB 1; Length 1523;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 965 SEAEQTE 971
    |||||
Db 714 SEAEQTE 720

RESULT 48
US-09-423-037A-17
; Sequence 17, Application US/09423037A
; GENERAL INFORMATION:
; APPLICANT: HEERY, DAVID MICHAEL
; APPLICANT: PARKER, MALCOLM GEORGE
; TITLE OF INVENTION: INHIBITORS OF NUCLEAR PROTEIN/NUCLEAR RECEPTOR
; FILE REFERENCE: 009901/0264015
; CURRENT APPLICATION NUMBER: US/09/423,037A
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/GB98/01238
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: GB 9708676.3
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: DNA binding domain
US-09-423-037A-17

Query Match          0.5%; Score 6; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 GPULLE 914
    |||||
Db 3 GPULLE 8

RESULT 49
US-10-106-698-7746
; Sequence 7746, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
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; SEQ ID NO 7746
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (19)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7746

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Query Match          0.5%; Score 6; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 712 VTVLAI 717
DB 4 VTVLAI 9

```

```

RESULT 50
US-09-623-791A-134
; Sequence 134, Application US/09623791A
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
; FILE REFERENCE: ALBRE 11
; CURRENT APPLICATION NUMBER: US/09/623,791A
; PRIOR APPLICATION NUMBER: PCT/DE99/00721
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-791A-134

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```

Query Match          0.5%; Score 6; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 576 LSGKEY 581
DB 23 LSGKEY 28

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Job time: 258 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 06:59:21 ; Search time 18.41 Seconds
(without alignments)
1545.672 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 1165
Sequence: 1 MTCQKFCVLLHWEFIYIT.....QTCSTQTKIMENKMDLTV 1165

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Gapco 60.0, Gapext 60.0

Searched: 231628 seqs, 24425594 residues

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Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 75 summaries

Database: Issued Patents, AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1165	100.0	1165	2	US-08-599-455B-4
2	1165	100.0	1165	4	US-09-069-781B-4
3	1064	91.3	1165	4	US-09-093-814-1
4	1064	91.3	1165	4	US-08-618-957A-11
5	881	58.5	896	4	US-08-618-957A-10
6	881	58.5	898	4	US-08-693-697-36
7	881	58.5	906	4	US-08-618-957A-9
8	681	58.5	908	4	US-08-693-697-33
9	681	58.5	958	4	US-08-618-957A-8
10	681	58.5	960	1	US-08-355-888A-8
11	681	58.5	960	2	US-08-693-697-8
12	681	58.5	960	2	US-08-640-389A-3
13	681	58.5	960	3	US-08-693-696-8
14	580	49.8	960	2	US-08-588-190-3
15	580	49.8	960	4	US-08-618-957A-3
16	474	40.7	908	2	US-08-588-526-3
17	470	40.3	1165	2	US-08-640-389A-11
18	459	39.4	569	1	US-08-306-231-3
19	307	26.4	896	2	US-08-640-389A-10
20	307	26.4	906	2	US-08-640-389A-9
21	307	26.4	958	2	US-08-640-389A-8
22	77	6.6	77	4	US-08-803-346-64
23	76	6.5	76	4	US-08-803-346-61
24	42	3.6	894	2	US-08-599-455B-2
25	42	3.6	894	4	US-09-069-781B-2
26	42	3.6	894	4	US-08-618-957A-12
27	42	3.6	895	4	US-08-827-962-19

ALIGNMENTS

28	42	3.6	895	4	US-08-827-962-21	Sequence 21, Appl
29	42	3.6	896	2	US-08-640-389A-12	Sequence 12, Appl
30	42	3.6	1162	2	US-08-599-455B-4	Sequence 43, Appl
31	42	3.6	1162	4	US-08-827-962-15	Sequence 15, Appl
32	42	3.6	1162	4	US-08-827-962-20	Sequence 20, Appl
33	42	3.6	1162	4	US-08-803-346-1	Sequence 1, Appl
34	42	3.6	1162	4	US-09-069-781B-43	Sequence 43, Appl
35	34	2.1	1162	4	US-08-803-346-63	Sequence 63, Appl
36	23	2.0	23	3	US-08-701-382-6	Sequence 6, Appl
37	23	2.0	23	3	US-09-028-937-6	Sequence 6, Appl
38	23	2.0	23	4	US-08-788-820-6	Sequence 6, Appl
39	20	1.7	77	4	US-08-803-346-62	Sequence 62, Appl
40	15	1.3	15	1	US-08-306-231-14	Sequence 14, Appl
41	15	1.3	15	1	US-08-306-231-15	Sequence 15, Appl
42	15	1.3	15	1	US-08-355-888A-30	Sequence 30, Appl
43	15	1.3	15	2	US-08-355-888A-31	Sequence 31, Appl
44	15	1.3	15	2	US-08-693-697-30	Sequence 30, Appl
45	15	1.3	15	2	US-08-693-697-31	Sequence 31, Appl
46	15	1.3	15	3	US-08-693-696-30	Sequence 30, Appl
47	15	1.3	15	3	US-08-693-696-31	Sequence 31, Appl
48	13	1.1	13	1	US-08-306-231-9	Sequence 9, Appl
49	13	1.1	13	1	US-08-355-888A-25	Sequence 25, Appl
50	13	1.1	13	2	US-08-693-697-25	Sequence 25, Appl
51	13	1.1	13	3	US-08-693-696-25	Sequence 25, Appl
52	11	0.9	75	4	US-08-803-346-59	Sequence 59, Appl
53	11	0.9	75	4	US-08-803-346-60	Sequence 60, Appl
54	10	0.9	13	1	US-08-306-231-8	Sequence 8, Appl
55	10	0.9	13	1	US-08-355-888A-24	Sequence 24, Appl
56	10	0.9	13	2	US-08-693-697-24	Sequence 24, Appl
57	10	0.9	13	3	US-08-693-696-24	Sequence 24, Appl
58	10	0.9	40	4	US-08-803-346-65	Sequence 65, Appl
59	9	0.8	9	2	US-08-599-455B-31	Sequence 31, Appl
60	9	0.8	9	4	US-09-117-399-11	Sequence 11, Appl
61	9	0.8	9	4	US-09-069-781B-31	Sequence 31, Appl
62	8	0.7	8	2	US-08-599-455B-29	Sequence 29, Appl
63	8	0.7	8	2	US-08-599-455B-33	Sequence 33, Appl
64	8	0.7	8	4	US-08-803-346-75	Sequence 75, Appl
65	8	0.7	8	4	US-09-069-781B-29	Sequence 29, Appl
66	8	0.7	8	4	US-09-069-781B-33	Sequence 33, Appl
67	7	0.6	7	4	US-08-803-346-77	Sequence 77, Appl
68	7	0.6	15	1	US-08-306-231-10	Sequence 10, Appl
69	7	0.6	15	1	US-08-355-888A-26	Sequence 26, Appl
70	7	0.6	15	2	US-08-693-697-26	Sequence 26, Appl
71	7	0.6	15	3	US-08-693-696-26	Sequence 26, Appl
72	7	0.6	20	3	US-08-462-728-13	Sequence 13, Appl
73	7	0.6	101	4	US-09-199-637A-289	Sequence 289, Appl
74	7	0.6	224	1	US-08-707-793A-6	Sequence 6, Appl
75	7	0.6	224	1	US-08-707-792A-6	Sequence 6, Appl

RESULT 1
US-08-599-455B-4
Sequence 4, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

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? COMPUTER: IBM Compatible
? OPERATING SYSTEM: Windows95
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/599,455B
? FILING DATE: 22-JAN-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/563,153
? FILING DATE: 28-DEC-1995
? APPLICATION NUMBER: 08/570,142
? FILING DATE: 11-DEC-1995
? APPLICATION NUMBER: 08/569,485
? FILING DATE: 08-DEC-1995
? APPLICATION NUMBER: 08/566,622
? FILING DATE: 04-DEC-1995
? APPLICATION NUMBER: 08/562,663
? FILING DATE: 27-NOV-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Melkalejohn, Ph.D., Anita L.
? REGISTRATION NUMBER: 35,283
? REFERENCE/DOCKET NUMBER: 07334/017001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-542-5070
? TELEFAX: 617-542-8906
? TELEX: 200154
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1165 amino acids
? TYPE: amino acid
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? FRAGMENT TYPE: Internal
? US-08-599-455B-4

Query Match      100.0%; Score 1165; DB 2; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPTPMRKLSCMPNSTYDYFLLPAGLSKNTS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSTPTPMRKLSCMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVPEKFNSSGTHFSNLSKTFHCCFSEODRNCSLCNDNTEGKFTVSIVL 120
DB 61 NGHYETAVPEKFNSSGTHFSNLSKTFHCCFSEODRNCSLCNDNTEGKFTVSIVL 120
QY 121 QQIDAMNINOCWLKGLDLKLEICVESLFRNLFRNRYKVVLLVLPVLEDSPLVPQKS 180
DB 121 QQIDAMNINOCWLKGLDLKLEICVESLFRNLFRNRYKVVLLVLPVLEDSPLVPQKS 180
QY 181 FQNVHCNCSVHECCGLVPPYPAKLNDTLMLCKITSGVIFQSPIMSVQPIIMVPRDP 240
DB 181 FQNVHCNCSVHECCGLVPPYPAKLNDTLMLCKITSGVIFQSPIMSVQPIIMVPRDP 240
QY 241 LGHMETTDGNGIKISMSPPLVPFPLOYQVKSSENSTYIRADKIVASTSLVDSTLP 300
DB 241 LGHMETTDGNGIKISMSPPLVPFPLOYQVKSSENSTYIRADKIVASTSLVDSTLP 300
QY 301 GSSYEVOVRKRLDGPIMSDMSTPRVFTQDVITFPFKILTSVGSNSVPHCIYKKNKI 360
DB 301 GSSYEVOVRKRLDGPIMSDMSTPRVFTQDVITFPFKILTSVGSNSVPHCIYKKNKI 360
QY 361 VPSKEIVMMNLTAEKIPQSOYDVVSDHVSQVTFEFLNLETRPRCKFTYDAVCCNEHC 420
DB 361 VPSKEIVMMNLTAEKIPQSOYDVVSDHVSQVTFEFLNLETRPRCKFTYDAVCCNEHC 420
QY 421 RAEVLVIDVYNINISCTETGYLTKMTCRMSSTSTIOSLASTIOLRHRSSLYSDIPSIH 480
DB 421 RAEVLVIDVYNINISCTETGYLTKMTCRMSSTSTIOSLASTIOLRHRSSLYSDIPSIH 480
QY 481 PISEPKDCYLQSDGFECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVPPLP 540
DB 481 PISEPKDCYLQSDGFECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVPPLP 540

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DB 481 PISEPKDCYLQSDGFECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVPPLP 540
QY 541 SSVKAEITINIGLTKISWEKVPPENNLOFQIYVGLSGKEVOKNYEVDAKSKSVLPY 600
DB 541 SSVKAEITINIGLTKISWEKVPPENNLOFQIYVGLSGKEVOKNYEVDAKSKSVLPY 600
QY 601 PDLCAVAVQVRCRKLDDGLGYMSNMPATVYMDIKVPMGPEIWRINIGDTMKKEKNV 660
DB 601 PDLCAVAVQVRCRKLDDGLGYMSNMPATVYMDIKVPMGPEIWRINIGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTMSDVGNNHKKFFFLMFOAHYVVLAINSI 720
DB 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTMSDVGNNHKKFFFLMFOAHYVVLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIQVSLASVPLNNSCVIWSILSPDYKLMYFIEMKLNED 780
DB 721 GASVANFNLTFSWPMKSVNIQVSLASVPLNNSCVIWSILSPDYKLMYFIEMKLNED 780
QY 781 GEIKWLRISSSVAKKYYIHDFIPIEKYQFSLPIEMEGVGPRIINSTODDIEKHQSDA 840
DB 781 GEIKWLRISSSVAKKYYIHDFIPIEKYQFSLPIEMEGVGPRIINSTODDIEKHQSDA 840
QY 841 GLYVIVPVLIISSIIILGLTLLISHQMKKLFMEDVNPKNCSWAGLNFQKPEFHLPT 900
DB 841 GLYVIVPVLIISSIIILGLTLLISHQMKKLFMEDVNPKNCSWAGLNFQKPEFHLPT 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPFTVAVSLSTDLKGSVCISDQFN 960
DB 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPFTVAVSLSTDLKGSVCISDQFN 960
QY 961 SVNFSABEGTEVYTEDSQRQPVKATLISNKPSETGEQGLINSVYTKCSSLNSPL 1020
DB 961 SVNFSABEGTEVYTEDSQRQPVKATLISNKPSETGEQGLINSVYTKCSSLNSPL 1020
QY 1021 KDSFSSNWEIEQAFFIISDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKSIIYL 1080
DB 1021 KDSFSSNWEIEQAFFIISDQHPNIIISPHLTFSEGLDELKLEGNFPEENDKSIIYL 1080
QY 1081 GVTSIKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSKRTFAS 1140
DB 1081 GVTSIKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSKRTFAS 1140
QY 1141 YMPQFOTCSQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSQTHKIMENKMDLTV 1165

RESULT 2
US-09-069-781B-4
; Sequence 4, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melketojn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEPHONE: 200154
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-069-781B-4

Query Match 100.0%; Score 1165; DB 4; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVLLHMEFIYITAFNLSTPTTPWRFKLSCLPMPSTYDYLIPAGLSKNTNS 60
DB 1 MICQFCVLLHMEFIYITAFNLSTPTTPWRFKLSCLPMPSTYDYLIPAGLSKNTNS 60
QY 61 NGHETAEPRFNSSGTHFSNLSTTFHCRCRSDRNCSCADNIEKTEVSTVNSLVF 120
DB 61 NGHETAEPRFNSSGTHFSNLSTTFHCRCRSDRNCSCADNIEKTEVSTVNSLVF 120
QY 121 QOIDANNIQCWLKGDLLFCYVESLEFKNLFRNNYKVLHLYLPEVLEDSPLVPQKGS 180
DB 121 QOIDANNIQCWLKGDLLFCYVESLEFKNLFRNNYKVLHLYLPEVLEDSPLVPQKGS 180
QY 181 FQWVHCNSVHECCCECLVPVPTAKLNDTLMLCLKITSGVLFQSPILMSVOPINMWKPPDP 240
DB 181 FQWVHCNSVHECCCECLVPVPTAKLNDTLMLCLKITSGVLFQSPILMSVOPINMWKPPDP 240
QY 241 LGLHMETIDDDNLKISMSPLVPFPLOYQVKSNSSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMETIDDDNLKISMSPLVPFPLOYQVKSNSSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVGRKLDOPGLMSDMSTPRVFTTODVYFPPKILTSVGSNSVPHCIYKKNKI 360
DB 301 GSSYEVQVGRKLDOPGLMSDMSTPRVFTTODVYFPPKILTSVGSNSVPHCIYKKNKI 360
QY 361 VPSKEIYMMNLAEKIPQSDYVDVSDHVSQVTFENLNETKRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYMMNLAEKIPQSDYVDVSDHVSQVTFENLNETKRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVDVNNINISCEFDGLTKTKCWSTSTIOSLAESTLQTLAHSSSLXCSDIPSIH 480
DB 421 RYAEIYVDVNNINISCEFDGLTKTKCWSTSTIOSLAESTLQTLAHSSSLXCSDIPSIH 480

DB 421 RYAEIYVDVNNINISCEFDGLTKTKCWSTSTIOSLAESTLQTLAHSSSLXCSDIPSIH 480
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DB 481 PISEPKDCYLOSDGFECIFQPIFLLSGYTWIRINHSIGSDSPPCVLPDPSVYKPLP 540
QY 541 SSVAAETINIGLAKISEKVFPEPNNIQQFQIRGLSKREYQWKMYEYDDAKSKVSLPV 600
DB 541 SSVAAETINIGLAKISEKVFPEPNNIQQFQIRGLSKREYQWKMYEYDDAKSKVSLPV 600
QY 601 PDLCAVAVOYRCRDLGLGYWNSNPNATYVMDIKVPMKPEPWRJINCDTMRKKNV 660
DB 601 PDLCAVAVOYRCRDLGLGYWNSNPNATYVMDIKVPMKPEPWRJINCDTMRKKNV 660
QY 661 TLMKPLKNDLCSVQRYVINHTSCNGTSEEDVGNHTKFTFLWTQAHVYVLAINSI 720
DB 661 TLMKPLKNDLCSVQRYVINHTSCNGTSEEDVGNHTKFTFLWTQAHVYVLAINSI 720
QY 721 CASVANFULTSWPMKSNVIYQSLSATPLNSCVIVSILSDYKLMVFITTEKNLMD 780
DB 721 CASVANFULTSWPMKSNVIYQSLSATPLNSCVIVSILSDYKLMVFITTEKNLMD 780
QY 781 GEIKMLRISSSVKYYIHDHPIPEKYOESLYPIPEMGVGRKRIINSFTODDIEKHQSDA 840
DB 781 GEIKMLRISSSVKYYIHDHPIPEKYOESLYPIPEMGVGRKRIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSILLCTLLISHORMKLFMEDVPPNKRNSWAGLNFQRPETPEHLPFI 900
DB 841 GLYVIVPVISSILLCTLLISHORMKLFMEDVPPNKRNSWAGLNFQRPETPEHLPFI 900
QY 901 KHTASVTCGPILEPETSIEDISVDTSMKNDKEMPTTVVSLSTTDLEKGSVCISDOFN 960
DB 901 KHTASVTCGPILEPETSIEDISVDTSMKNDKEMPTTVVSLSTTDLEKGSVCISDOFN 960
QY 961 SVNFEARGTEVYEDSOROPFVYATLINSKRSSETGEEGLNNSVTCOFSSKNSPL 1020
DB 961 SVNFEARGTEVYEDSOROPFVYATLINSKRSSETGEEGLNNSVTCOFSSKNSPL 1020
QY 1021 KDSFNSSMETEAQAFLLISDHPNIIISPHLFSGLDELKLEKNFDEENNDKKSIIYL 1080
DB 1021 KDSFNSSMETEAQAFLLISDHPNIIISPHLFSGLDELKLEKNFDEENNDKKSIIYL 1080
QY 1081 GVTSTIKKRESGVLLTDKRSVSCPAPCLFTDIRVLQDSCHFVNNINLGTSSKRTAS 1140
DB 1081 GVTSTIKKRESGVLLTDKRSVSCPAPCLFTDIRVLQDSCHFVNNINLGTSSKRTAS 1140
QY 1141 YMPQFOTCSTQHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQHKIMENKMDLTV 1165

RESULT 3
US-09-093-814-1
Sequence 1, Application US/09093814
Patent No. 6270981
GENERAL INFORMATION:
APPLICANT: Carpenter et al.
TITLE OF INVENTION: ASSAY SYSTEMS FOR LEPTIN-ENHANCING AGENTS
FILE REFERENCE: REG 580-A
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/049,108
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-093-814-1

Query Match 91.3%; Score 1064; DB 4; Length 1165;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MICQRCVLLHMEFIYVITAFNLSPITPWRFKLSCMPNSTYDFLLPAGLSKNTSNS 60
DB 1 MICQRCVLLHMEFIYVITAFNLSPITPWRFKLSCMPNSTYDFLLPAGLSKNTSNS 60
QY 61 NGHYETAEPKRNSSGTHSNLSKTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
DB 61 NGHYETAEPKRNSSGTHSNLSKTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
QY 121 QOIDANMNIOQMLKGDLPICVSELEKLNFRNRYKXHLLYLVEVLEDSPLVPOKGS 180
DB 121 QOIDANMNIOQMLKGDLPICVSELEKLNFRNRYKXHLLYLVEVLEDSPLVPOKGS 180
QY 181 FQWVHCNCSVHCECELVVPTAKLNDTLMLCKITSGGVISQSPILMSVQPINMKAPEPP 240
DB 181 FQWVHCNCSVHCECELVVPTAKLNDTLMLCKITSGGVISQSPILMSVQPINMKAPEPP 240
QY 241 LGLHMEITDGNLKIWSMSPPLVPPLOQVXSENSSTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDGNLKIWSMSPPLVPPLOQVXSENSSTVIREADKIVSATSLVDSILP 300
QY 301 GGSYEVOVGRKLDGPGIWSMSTPRVFTTQDYIYFPKILTSVGSNSVFHCYKKENKI 360
DB 301 GGSYEVOVGRKLDGPGIWSMSTPRVFTTQDYIYFPKILTSVGSNSVFHCYKKENKI 360
QY 361 VPSKEIYVMMNLAERIPQSOQYDVSDHVSQVTFNNETKPRGKFTYDAVCCNEHECH 420
DB 361 VPSKEIYVMMNLAERIPQSOQYDVSDHVSQVTFNNETKPRGKFTYDAVCCNEHECH 420
QY 421 RYAEIYVIVNINISGCTDGYLTMTKRWSTSTIOSLAEIOLRYHRSLSYCSIDPSIH 480
DB 421 RYAEIYVIVNINISGCTDGYLTMTKRWSTSTIOSLAEIOLRYHRSLSYCSIDPSIH 480
QY 481 PISEPRDCYLOSGDFECPFOPIFLISGYTMMIRNHSIGSDSPCTCYLPSVYVPELP 540
DB 481 PISEPRDCYLOSGDFECPFOPIFLISGYTMMIRNHSIGSDSPCTCYLPSVYVPELP 540
QY 541 SSVKAEITINIGLKIWSKPVFPENNLOFOIRYGLSGKEVOMKMYEVDASKSVSLPV 600
DB 541 SSVKAEITINIGLKIWSKPVFPENNLOFOIRYGLSGKEVOMKMYEVDASKSVSLPV 600
QY 601 PDLCAVYAVQVRCRKLIDGIGYWSNNSPAYTYVMDIKVMPRGPERWRIINGDTMKKEKV 660
DB 601 PDLCAVYAVQVRCRKLIDGIGYWSNNSPAYTYVMDIKVMPRGPERWRIINGDTMKKEKV 660
QY 661 TLLMPLKMNDSLCSYQRYVINHHHTSCNGTSEEDVGNHRTFTLMEQAHYTVLAINSI 720
DB 661 TLLMPLKMNDSLCSYQRYVINHHHTSCNGTSEEDVGNHRTFTLMEQAHYTVLAINSI 720
QY 721 GASVANFNLTFSMPMSKVIYVOSLSAYPLNNSCVIYSWILSPSDYKLMFIEMKLNED 780
DB 721 GASVANFNLTFSMPMSKVIYVOSLSAYPLNNSCVIYSWILSPSDYKLMFIEMKLNED 780
QY 781 GEIKMLRISSSVKYYIHDFIPIEKYQSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKMLRISSSVKYYIHDFIPIEKYQSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLIYIVPVYIISILLGLTLLSHQBMKLFMEDVNPKNCSMAOGLNOKETFEHLEFI 900
DB 841 GLIYIVPVYIISILLGLTLLSHQBMKLFMEDVNPKNCSMAOGLNOKETFEHLEFI 900
QY 901 KRTASVTCGPLLEPITISEDIVDTSMKNKDEMPPTVYSLSTTDEKGSVCIISDOFN 960
DB 901 KRTASVTCGPLLEPITISEDIVDTSMKNKDEMPPTVYSLSTTDEKGSVCIISDOFN 960
QY 961 SVNFSEAEGETEYVDESGROPFVYATLISNSKPSGETGEEOGLINSVATKCFSSKNSPL 1020
DB 961 SVNFSEAEGETEYVDESGROPFVYATLISNSKPSGETGEEOGLINSVATKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAOAFILISDOHPNIIISPHLTFSGLDELLEKGNFPEENNDKKSIIYL 1080
DB 1021 KDSFNSSSWEIEAOAFILISDOHPNIIISPHLTFSGLDELLEKGNFPEENNDKKSIIYL 1080

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DB 1021 KDSFNSSSWEIEAOAFILISDOHPNIIISPHLTFSGLDELLEKGNFPEENNDKKSIIYL 1080
QY 1081 GVTSTIKKRESGVLLIDKRSVSCPEPAPCLFTDRIYLODSCSHPVENNTLGTSSKKTFS 1140
DB 1081 GVTSTIKKRESGVLLIDKRSVSCPEPAPCLFTDRIYLODSCSHPVENNTLGTSSKKTFS 1140
QY 1141 YMPQFOTCSTQTHKIMENKCDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKCDLTV 1165

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RESULT 4
US-08-618-957A-11
Sequence 11, Application US/08618957A
Patent No. 6355237

GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Clotfild, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBSE
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSED: Pennie & Edmonds LLP
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618-957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE

SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 11:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-11

Query Match 91.3%; Score 1064; DB 4; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MICQRCVLLHMEFIYVITAFNLSPITPWRFKLSCMPNSTYDFLLPAGLSKNTSNS 60
DB 1 MICQRCVLLHMEFIYVITAFNLSPITPWRFKLSCMPNSTYDFLLPAGLSKNTSNS 60
QY 61 NGHYETAEPKRNSSGTHSNLSKTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
DB 61 NGHYETAEPKRNSSGTHSNLSKTFHCCFRSEODRNCSLCADNIEGTFVSTNSLVF 120
QY 1021 KDSFNSSSWEIEAOAFILISDOHPNIIISPHLTFSGLDELLEKGNFPEENNDKKSIIYL 1080
DB 1021 KDSFNSSSWEIEAOAFILISDOHPNIIISPHLTFSGLDELLEKGNFPEENNDKKSIIYL 1080

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QY 121 QOIANNNIQCWLKGDLLKFLICYVESLFRNLFRRNNYKVVHLLYLPEVLDSPLVPQKGS 180
Db 121 QOIANNNIQCWLKGDLLKFLICYVESLFRNLFRRNNYKVVHLLYLPEVLDSPLVPQKGS 180
QY 181 FOMVHCNCSVHECCCECLVPVPAKINDTLMLCKLITSGVIFOSPLMSVOPINMKPPDP 240
Db 181 FOMVHCNCSVHECCCECLVPVPAKINDTLMLCKLITSGVIFOSPLMSVOPINMKPPDP 240
QY 241 LGLHMETDDGNLKSWSPPPLVPEPLQYQVYSENSSTTVIREADKIVASATSLDVLDP 300
Db 241 LGLHMETDDGNLKSWSPPPLVPEPLQYQVYSENSSTTVIREADKIVASATSLDVLDP 300
QY 301 GSSIEVOYGRKRLDGPGLWSMSTPRVFTTQDVYIFPPKILTSVGSNSFHCITYKENKI 360
Db 301 GSSIEVOYGRKRLDGPGLWSMSTPRVFTTQDVYIFPPKILTSVGSNSFHCITYKENKI 360
QY 361 VPSKEIYMMNLAEKIPQSOYDVSDHYSKYTFEFLNETKPRGKFTYDVAVCCNHECHH 420
Db 361 VPSKEIYMMNLAEKIPQSOYDVSDHYSKYTFEFLNETKPRGKFTYDVAVCCNHECHH 420
QY 421 RYAEIYVIDVNIINISCEIDGYLTKMTCRMSTSTIOSLAESTLQLRHRSILXCSDIPSIH 480
Db 421 RYAEIYVIDVNIINISCEIDGYLTKMTCRMSTSTIOSLAESTLQLRHRSILXCSDIPSIH 480
QY 481 PISEPKDCYLOSDFYECIFOPIFILSGYTMIRINHSLGSLDSEPTCYLPDSVYKPLPP 540
Db 481 PISEPKDCYLOSDFYECIFOPIFILSGYTMIRINHSLGSLDSEPTCYLPDSVYKPLPP 540
QY 541 SSVKKEITINIGLTKISMEKPYEPENNLOFOIRYGLSGKEVOYMKVEYVDASKSVSLPV 600
Db 541 SSVKKEITINIGLTKISMEKPYEPENNLOFOIRYGLSGKEVOYMKVEYVDASKSVSLPV 600
QY 601 PDLCAVYAVOYCKRLDLGLGYWSMNSNPATYVMDIKVPMRGPEFWRIINGDTMKRKNV 660
Db 601 PDLCAVYAVOYCKRLDLGLGYWSMNSNPATYVMDIKVPMRGPEFWRIINGDTMKRKNV 660
QY 661 TLLMKPLKKNDSLCVQRYVINHHTSCNGTASDVGNHTKFTFLTEBOHTYVLAINSI 720
Db 661 TLLMKPLKKNDSLCVQRYVINHHTSCNGTASDVGNHTKFTFLTEBOHTYVLAINSI 720
QY 721 GASVANFNLTSPMPSKNIYVOSTLAPPLNSSCVIYVMTLSLSDYKLMFIEKMLNLD 780
Db 721 GASVANFNLTSPMPSKNIYVOSTLAPPLNSSCVIYVMTLSLSDYKLMFIEKMLNLD 780
QY 781 GEIKMLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVTPIYIISSTILLSTLLSHORMKLFWEDVPRNKNCSMAOGLNOKRETEHLEFI 900
Db 841 GLYIVTPIYIISSTILLSTLLSHORMKLFWEDVPRNKNCSMAOGLNOKRETEHLEFI 900
QY 901 KHTASVTGCPILLPEPITSEDIVDTSMKNKDEMPPTVVSLLSTTDLKSGVCSIDQFN 960
Db 901 KHTASVTGCPILLPEPITSEDIVDTSMKNKDEMPPTVVSLLSTTDLKSGVCSIDQFN 960
QY 961 SVNSEAEGETEYTVDESQROPFVKYATLINSKRPSEGEQGLINSVYKCFSSKNSEPL 1020
Db 961 SVNSEAEGETEYTVDESQROPFVKYATLINSKRPSEGEQGLINSVYKCFSSKNSEPL 1020
QY 1021 KDSFNSSMELIQAOFLLISDOHPNIIISPHLTFSEGLDELLKLEGNFPRENNDKSITYYL 1080
Db 1021 KDSFNSSMELIQAOFLLISDOHPNIIISPHLTFSEGLDELLKLEGNFPRENNDKSITYYL 1080
QY 1081 GVTSIKKRESGVLIDKSKRVSCPPAPCLFTDIRVLQDSCSHFVENNIMLGTSKKTFAAS 1140
Db 1081 GVTSIKKRESGVLIDKSKRVSCPPAPCLFTDIRVLQDSCSHFVENNIMLGTSKKTFAAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKCDLYV 1165
Db 1141 YMPQFOTCSTQTHKIMENKCDLYV 1165

```

```

RESULT 5
US-08-618-957A-10
; Sequence 10, Application US/08618957A
; Patent No. 6355237
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Clotoff, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: METHODS FOR USING THE OBSE
; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618, 957A
; FILING DATE: 20-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28, 462
; REFERENCE/DOCKET NUMBER: 008907-0033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-618-957A-10

Query Match 58.5%; Score 681; DB 4; Length 896;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 110 TVSTVYNSLYFOOIDANNMIQCWLKGDLLKFLICYVESLFRNLFRRNNYKVVHLLYLPEVL 169
Db 110 TVSTVYNSLYFOOIDANNMIQCWLKGDLLKFLICYVESLFRNLFRRNNYKVVHLLYLPEVL 169
QY 170 EDSPLVPQKGSFOMVHCNCSVHECCCECLVPVPAKINDTLMLCKLITSGVIFOSPLMSV 229
Db 170 EDSPLVPQKGSFOMVHCNCSVHECCCECLVPVPAKINDTLMLCKLITSGVIFOSPLMSV 229
QY 230 QPINMWKPPPLGLHMETDDGNLKSWSPPPLVPEPLQYQVYSENSSTTVIREADKIVS 289
Db 230 QPINMWKPPPLGLHMETDDGNLKSWSPPPLVPEPLQYQVYSENSSTTVIREADKIVS 289
QY 290 ATSLVYDSTLPGSSSEYVOYGRKRLDGPGLWSMSTPRVFTTQDVYIFPPKILTSVGSNS 349
Db 290 ATSLVYDSTLPGSSSEYVOYGRKRLDGPGLWSMSTPRVFTTQDVYIFPPKILTSVGSNS 349
QY 350 FHCITYKKENKIYPSKEIYMMNLAEKIPQSOYDVSDHYSKYTFEFLNETKPRGKFTYDVA 409
Db 350 FHCITYKKENKIYPSKEIYMMNLAEKIPQSOYDVSDHYSKYTFEFLNETKPRGKFTYDVA 409

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QY 410 VYCCNHECHHRYAELIYDINININISCETDGYLTAKTCTMSTSTIOSLAESTLOLRHRS 469
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Db 410 VYCCNHECHHRYAELIYDINININISCETDGYLTAKTCTMSTSTIOSLAESTLOLRHRS 469
QY 470 SLXCSDFPSIHPISEPKDCYLOSDFYECIFOPIFLLSGYTMKIRINHSLSIDSPPTCV 529
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      |||
      |||
Db 470 SLXCSDFPSIHPISEPKDCYLOSDFYECIFOPIFLLSGYTMKIRINHSLSIDSPPTCV 529
QY 530 LPDSVVKPLPPSSVKAETITINIGLAKISWEKPYEPENNLOFOIRYGLSGKEVQMKWEY 589
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      |||
      |||
Db 530 LPDSVVKPLPPSSVKAETITINIGLAKISWEKPYEPENNLOFOIRYGLSGKEVQMKWEY 589
QY 530 LPDSVVKPLPPSSVKAETITINIGLAKISWEKPYEPENNLOFOIRYGLSGKEVQMKWEY 589
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Db 530 LPDSVVKPLPPSSVKAETITINIGLAKISWEKPYEPENNLOFOIRYGLSGKEVQMKWEY 589
QY 590 DAKSKSVSLPVPDLCAVYAVOVCRKRLDGLGYWMSNNSNPAATYVMDIKVPMGPEFWRII 649
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      |||
Db 590 DAKSKSVSLPVPDLCAVYAVOVCRKRLDGLGYWMSNNSNPAATYVMDIKVPMGPEFWRII 649
QY 650 NGDTMKKEKNVTLMLKPLKNDSLCSVQRYVINHHTSCGNTSEVGNHTKFTFLTEQA 709
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Db 650 NGDTMKKEKNVTLMLKPLKNDSLCSVQRYVINHHTSCGNTSEVGNHTKFTFLTEQA 709
QY 710 HTVTYLAINSIGASVANFNLTFSWPMKSVNIYQSLASAYPLNSSCVIVSWILSPSDYKLMY 769
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Db 710 HTVTYLAINSIGASVANFNLTFSWPMKSVNIYQSLASAYPLNSSCVIVSWILSPSDYKLMY 769
QY 770 FIEMKNLNEDEIKWLRISSSVKRYIHDHFIPIEKYQSLYPIFMEGVGKPKIINST 829
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Db 770 FIEMKNLNEDEIKWLRISSSVKRYIHDHFIPIEKYQSLYPIFMEGVGKPKIINST 829
QY 830 ODDIEKHOSDAGLYIVPIYIISSTILLGTLTISHORMKLFMEDVNPKNCSMAOGLNF 889
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      |||
Db 830 ODDIEKHOSDAGLYIVPIYIISSTILLGTLTISHORMKLFMEDVNPKNCSMAOGLNF 889
QY 890 QK 891
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      ||
Db 890 QK 891

RESULT 6
US-08-693-697-36
; Sequence 36, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Smogdans, H. R.
; APPLICANT: Clotiff, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-BL 219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556

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; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-693-697-36

Query Match 58.5%; Score 681; DB 2; Length 898;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVFOIDANNNIQCMLKGLDLFTICVYSLFKNLFRINYNVHLLYVPEVL 169
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Db 112 TFEVSTVNSLVFOIDANNNIQCMLKGLDLFTICVYSLFKNLFRINYNVHLLYVPEVL 171
QY 170 EDSPLVPQGSFQWVHCNCSVHECCCELVVPYPAKLNDTILMLCKLITSGVIFOSPMSV 229
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      |||
Db 172 EDSPLVPQGSFQWVHCNCSVHECCCELVVPYPAKLNDTILMLCKLITSGVIFOSPMSV 231
QY 230 QPIMWKPDPPLGLHMETIDGCLKISMSPLVPPLOYQVKYSENSTTVIREADKIYS 289
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Db 232 QPIMWKPDPPLGLHMETIDGCLKISMSPLVPPLOYQVKYSENSTTVIREADKIYS 291
QY 290 ATSLVDSITLPGSSYEVQYRGKRLDGLGIMSDSPFRVFTQDVYIFPKIILTVGSNVS 349
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Db 292 ATSLVDSITLPGSSYEVQYRGKRLDGLGIMSDSPFRVFTQDVYIFPKIILTVGSNVS 351
QY 350 FHCITYKKENKIYPSKEIYVMMNLAEKIPQSOYDVVSDHYSKYVFNLNKTRPKGTYYDA 409
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Db 352 FHCITYKKENKIYPSKEIYVMMNLAEKIPQSOYDVVSDHYSKYVFNLNKTRPKGTYYDA 411
QY 410 VYCCNHECHHRYAELIYDINININISCETDGYLTAKTCTMSTSTIOSLAESTLOLRHRS 469
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Db 412 VYCCNHECHHRYAELIYDINININISCETDGYLTAKTCTMSTSTIOSLAESTLOLRHRS 471
QY 470 SLXCSDFPSIHPISEPKDCYLOSDFYECIFOPIFLLSGYTMKIRINHSLSIDSPPTCV 529
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      |||
Db 472 SLXCSDFPSIHPISEPKDCYLOSDFYECIFOPIFLLSGYTMKIRINHSLSIDSPPTCV 531
QY 530 LPDSVVKPLPPSSVKAETITINIGLAKISWEKPYEPENNLOFOIRYGLSGKEVQMKWEY 589
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Db 532 LPDSVVKPLPPSSVKAETITINIGLAKISWEKPYEPENNLOFOIRYGLSGKEVQMKWEY 591
QY 590 DAKSKSVSLPVPDLCAVYAVOVCRKRLDGLGYWMSNNSNPAATYVMDIKVPMGPEFWRII 649
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Db 592 DAKSKSVSLPVPDLCAVYAVOVCRKRLDGLGYWMSNNSNPAATYVMDIKVPMGPEFWRII 651
QY 650 NGDTMKKEKNVTLMLKPLKNDSLCSVQRYVINHHTSCGNTSEVGNHTKFTFLTEQA 709
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Db 652 NGDTMKKEKNVTLMLKPLKNDSLCSVQRYVINHHTSCGNTSEVGNHTKFTFLTEQA 711
QY 710 HTVTYLAINSIGASVANFNLTFSWPMKSVNIYQSLASAYPLNSSCVIVSWILSPSDYKLMY 769
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Db 712 HTVTYLAINSIGASVANFNLTFSWPMKSVNIYQSLASAYPLNSSCVIVSWILSPSDYKLMY 771
QY 770 FIEMKNLNEDEIKWLRISSSVKRYIHDHFIPIEKYQSLYPIFMEGVGKPKIINST 829
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Db 772 FIEMKNLNEDEIKWLRISSSVKRYIHDHFIPIEKYQSLYPIFMEGVGKPKIINST 831
QY 830 ODDIEKHOSDAGLYIVPIYIISSTILLGTLTISHORMKLFMEDVNPKNCSMAOGLNF 889
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      |||
      |||
Db 832 ODDIEKHOSDAGLYIVPIYIISSTILLGTLTISHORMKLFMEDVNPKNCSMAOGLNF 891
QY 890 QK 891
      ||
      ||
Db 892 QK 891

```

RESULT 7
US-08-618-957A-9
Sequence 9, Application US/08618957A
Patent No. 6355237
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBSE
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618, 957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Polsant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-9

Query Match 58.5%; Score 681; DB 4; Length 906;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 110 TFSVTVNSLVVFOODANNICQWKLKGLKFTCYVESLEKLNFRNRYNKKVHLVYLPVL 169
Db 110 TFSVTVNSLVVFOODANNICQWKLKGLKFTCYVESLEKLNFRNRYNKKVHLVYLPVL 169
Qy 170 EDSPLVPKGSFQWVHCNCSYHECCCECLVPYPTAKLNTLMLCLKITSGVIFQSPPLMSV 229
Db 170 EDSPLVPKGSFQWVHCNCSYHECCCECLVPYPTAKLNTLMLCLKITSGVIFQSPPLMSV 229
Qy 230 QPINNVKDPPLGLHMETLTDGDKLISWSSPPLVFPLOQVQKYSSENTVIREADKIVS 289
Db 230 QPINNVKDPPLGLHMETLTDGDKLISWSSPPLVFPLOQVQKYSSENTVIREADKIVS 289
Qy 290 ATSLIVDSILVGSSEYENVRGRKRLDGPINWDMSTPRVFTTODVLYFPFKILTSVGSNVS 349
Db 290 ATSLIVDSILVGSSEYENVRGRKRLDGPINWDMSTPRVFTTODVLYFPFKILTSVGSNVS 349
Qy 350 FHCITKKNKNIYPSKEIWMNMLAEKIPQSOQYDVVSDHVSQVTFPNLNETKRGKFTYDA 409
Db 350 FHCITKKNKNIYPSKEIWMNMLAEKIPQSOQYDVVSDHVSQVTFPNLNETKRGKFTYDA 409

Qy 410 YYCCNEHECHHRVAYELVYIDVININISCETDGLTKMTCRWSTSTIQJLAESTLQLRHRS 469
Db 410 YYCCNEHECHHRVAYELVYIDVININISCETDGLTKMTCRWSTSTIQJLAESTLQLRHRS 469
Qy 470 SLYCSDDISIRHISEPKKCYQSDGFECIFOPITLLSGYTMWIALNLSGLSDSPPTCV 529
Db 470 SLYCSDDISIRHISEPKKCYQSDGFECIFOPITLLSGYTMWIALNLSGLSDSPPTCV 529
Qy 530 LPDSVVKPLPSSVVAETITINIGLKISMEKVPENNLOFIRGSGKEVQMKMEYV 589
Db 530 LPDSVVKPLPSSVVAETITINIGLKISMEKVPENNLOFIRGSGKEVQMKMEYV 589
Qy 590 DAKSKSVSLPVDDLCAYVAVOYRCRDLGLGYWMSNMPATVVDIKVPMRGPFWRII 649
Db 590 DAKSKSVSLPVDDLCAYVAVOYRCRDLGLGYWMSNMPATVVDIKVPMRGPFWRII 649
Qy 650 NGDITMKKKNVTLMLKPLMKNDLSQVQRYVYNNHTSCNGTSEVJUNHTKFTLMTQCA 709
Db 650 NGDITMKKKNVTLMLKPLMKNDLSQVQRYVYNNHTSCNGTSEVJUNHTKFTLMTQCA 709
Qy 710 HTVTVLAINSIGASVAVANFLFSPMPKSNVNIQSLSAAYPLNNSCVIYSMILSPDYKIMY 769
Db 710 HTVTVLAINSIGASVAVANFLFSPMPKSNVNIQSLSAAYPLNNSCVIYSMILSPDYKIMY 769
Qy 770 FLEKKNLNEDEIKWLRISSSVKRYVYIHDPIPLEKYQSLYPFMEGVGKPKIINSFT 829
Db 770 FLEKKNLNEDEIKWLRISSSVKRYVYIHDPIPLEKYQSLYPFMEGVGKPKIINSFT 829
Qy 830 ODDIEKHOSDAGLYIVVPIYITSSITLLGTLILSHORMKKLFWEVQPNKNSMAQGLNF 889
Db 830 ODDIEKHOSDAGLYIVVPIYITSSITLLGTLILSHORMKKLFWEVQPNKNSMAQGLNF 889
Qy 890 QK 891
Db 890 QK 891

RESULT 8
US-08-693-697-33
Sequence 33, Application US/08693697
Patent No. 5869610
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: HU-BL 219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693, 697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Polsant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 908 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-693-697-33

Query Match 58.5%; Score 681; DB 2; Length 908;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 110 TVFSTVNSLVFOQIDANNNIQCWLKGLDLKLFICYESLFKRNLFRRNYNYVHLLYLPYEV 169
DB 112 TVFSTVNSLVFOQIDANNNIQCWLKGLDLKLFICYESLFKRNLFRRNYNYVHLLYLPYEV 171
OY 170 EDSPLVPQKGSFQMVHNCNSVHECCCLVVPYPAKLNIDLMLCKITSGVIFRSPILMSV 229
DB 172 EDSPLVPQKGSFQMVHNCNSVHECCCLVVPYPAKLNIDLMLCKITSGVIFRSPILMSV 231
OY 230 QP1NNMKPPPLGLHMEITDDGNLKTISWSSPPLVPPLOQYKYSNSTTVI READKIVS 289
DB 232 QP1NNMKPPPLGLHMEITDDGNLKTISWSSPPLVPPLOQYKYSNSTTVI READKIVS 291
OY 290 ATSLAVDSILPQSSSYEVQVGRKLDGPGIWSDMSTPRVFTTODVITFPFKILITSVGSNVS 349
DB 292 ATSLAVDSILPQSSSYEVQVGRKLDGPGIWSDMSTPRVFTTODVITFPFKILITSVGSNVS 351
OY 350 FHCITYKKENKIYPSKEIVMMNLAEKIPQSQYDVVSDHYSKYTFNLNETKRGKFTYDA 409
DB 352 FHCITYKKENKIYPSKEIVMMNLAEKIPQSQYDVVSDHYSKYTFNLNETKRGKFTYDA 411
OY 410 VYCCNHECHHRAELIYDVNININISCEFDGYLTAKTCKWSTSTOSLAESTIQLYKHS 469
DB 412 VYCCNHECHHRAELIYDVNININISCEFDGYLTAKTCKWSTSTOSLAESTIQLYKHS 471
OY 470 SLVCSDFIPSIHPISPEKDCYLOSDFEFCIFOPIFLSCGYMIRINHSIGSLDSPCTCY 529
DB 472 SLVCSDFIPSIHPISPEKDCYLOSDFEFCIFOPIFLSCGYMIRINHSIGSLDSPCTCY 531
OY 530 LPDSVVKPLPPSSVKAETINIGLKTISWEKPYFPENNLQFDIRYGLSGKEVQWKMEYV 589
DB 532 LPDSVVKPLPPSSVKAETINIGLKTISWEKPYFPENNLQFDIRYGLSGKEVQWKMEYV 591
OY 590 DAKSKSVSLPVPDLCAVVAOVQRCRDLGLGYWSNNSNPAITYVMIDIKVPMRGPEFWRIT 649
DB 592 DAKSKSVSLPVPDLCAVVAOVQRCRDLGLGYWSNNSNPAITYVMIDIKVPMRGPEFWRIT 651
OY 650 NGDTMKREKNVTLMLKPLKNDKSLCSVQRYVINHTSCNGTSEIDGNTTKFTFLMTEDA 709
DB 652 NGDTMKREKNVTLMLKPLKNDKSLCSVQRYVINHTSCNGTSEIDGNTTKFTFLMTEDA 711
OY 710 HRYTVLAINSIGASVANFNULFSPMSKYNIVQSLASAYPLNSSCVIVSMILSPSDYKLMY 769
DB 712 HRYTVLAINSIGASVANFNULFSPMSKYNIVQSLASAYPLNSSCVIVSMILSPSDYKLMY 771
OY 770 FIIEEMNLNEDCEIKWLRISSSVKYYITHDHFPIEKYQPSLYPIFMEGVGRKIIINSTFT 829
DB 772 FIIEEMNLNEDCEIKWLRISSSVKYYITHDHFPIEKYQPSLYPIFMEGVGRKIIINSTFT 831
OY 830 ODDIEKHOSDAGLYIVPVYLISSSILLGLTLLISHORMKLFMEDVPNPKNSMAOGLNF 889
DB 832 ODDIEKHOSDAGLYIVPVYLISSSILLGLTLLISHORMKLFMEDVPNPKNSMAOGLNF 891
OY 890 QK 891
DB 892 QK 893

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RESULT 9
US-08-618-957A-8
Sequence 8, Application US/08618957A
Patent No. 6355237
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Clotfi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBES:
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
NUMBER OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 958 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-8

Query Match 58.5%; Score 681; DB 4; Length 958;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 110 TVFSTVNSLVFOQIDANNNIQCWLKGLDLKLFICYESLFKRNLFRRNYNYVHLLYLPYEV 169
DB 112 TVFSTVNSLVFOQIDANNNIQCWLKGLDLKLFICYESLFKRNLFRRNYNYVHLLYLPYEV 169
OY 170 EDSPLVPQKGSFQMVHNCNSVHECCCLVVPYPAKLNIDLMLCKITSGVIFRSPILMSV 229
DB 172 EDSPLVPQKGSFQMVHNCNSVHECCCLVVPYPAKLNIDLMLCKITSGVIFRSPILMSV 229
OY 230 QP1NNMKPPPLGLHMEITDDGNLKTISWSSPPLVPPLOQYKYSNSTTVI READKIVS 289
DB 232 QP1NNMKPPPLGLHMEITDDGNLKTISWSSPPLVPPLOQYKYSNSTTVI READKIVS 289
OY 290 ATSLAVDSILPQSSSYEVQVGRKLDGPGIWSDMSTPRVFTTODVITFPFKILITSVGSNVS 349
DB 292 ATSLAVDSILPQSSSYEVQVGRKLDGPGIWSDMSTPRVFTTODVITFPFKILITSVGSNVS 349
OY 350 FHCITYKKENKIYPSKEIVMMNLAEKIPQSQYDVVSDHYSKYTFNLNETKRGKFTYDA 409
DB 352 FHCITYKKENKIYPSKEIVMMNLAEKIPQSQYDVVSDHYSKYTFNLNETKRGKFTYDA 409

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: Sequence 8, Application US/08693697
: Patent No. 5869610
: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. R.
: APPLICANT: Cioffi, Joseph
: APPLICANT: Zupancic, Thomas J.
: APPLICANT: Shafer, Alan W.
: TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDICUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/693,697
: FILING DATE: 05-AUG-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 8907-0037-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-493-4935
: TELEFAX: 650-493-9556
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 960 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-693-697-8

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Query Match 58.5%; Score 681; DB 2; Length 960;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 110 TFSVTNSLVFOQIDANMNIOCLKGLDKLFCYVESLFRNLFNNYVHLTYLPEVL 169
DB 112 TFSVTNSLVFOQIDANMNIOCLKGLDKLFCYVESLFRNLFNNYVHLTYLPEVL 171
QY 170 EDSPLVPQKGFQMVHNCNVHECCCELVVPPTAKLNDTLMLCKITSGVIFQSPLMGV 229
DB 172 EDSPLVPQKGFQMVHNCNVHECCCELVVPPTAKLNDTLMLCKITSGVIFQSPLMGV 231
QY 230 QPTNWKPPPPGLIMEITDDGGLKITSMSPPPLVPPLOYQVYKSENSTTVIREAKIYS 289
DB 232 QPTNWKPPPPGLIMEITDDGGLKITSMSPPPLVPPLOYQVYKSENSTTVIREAKIYS 291
QY 290 ATSLVDSILPQSSYEVQYRGKRLDGGIMSDMSTPRVFTTDOVIYFPFKILTSVGSNS 349
DB 292 ATSLVDSILPQSSYEVQYRGKRLDGGIMSDMSTPRVFTTDOVIYFPFKILTSVGSNS 351
QY 350 FHCITYKKEKKIYPSKEIVMMNLAEKIPQSOYDVVSDHVSQVTFNLNETKPRGKFTYDA 409
DB 352 FHCITYKKEKKIYPSKEIVMMNLAEKIPQSOYDVVSDHVSQVTFNLNETKPRGKFTYDA 411
QY 410 VYCCNHECHHRYAELIYDVANINISCEFDGILTAKTCRWSSTIOSLAESTLOLRYHRS 469
DB 412 VYCCNHECHHRYAELIYDVANINISCEFDGILTAKTCRWSSTIOSLAESTLOLRYHRS 471
QY 470 SLXCSDPISIHPISEPKDCYLOSDFYECIFQPIILLSGYTMWIRINHSGLSDSPPTCV 529

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DB 472 SLXCSDPISIHPISEPKDCYLOSDFYECIFQPIILLSGYTMWIRINHSGLSDSPPTCV 531
QY 530 LPDSVYKPLPPSSVKAETITINIGLKISWEKRPVFPENNLOFOIRYGLSGKEVOMKAYEY 589
DB 532 LPDSVYKPLPPSSVKAETITINIGLKISWEKRPVFPENNLOFOIRYGLSGKEVOMKAYEY 591
QY 590 DAKSKSVSLPVPDLCAVYAVQVCRKRLDGLGYWNSNPNAYTVVMDIKVPMRGPFEFWRIT 649
DB 592 DAKSKSVSLPVPDLCAVYAVQVCRKRLDGLGYWNSNPNAYTVVMDIKVPMRGPFEFWRIT 651
QY 650 NGDTMKKERNVTLLMKPLKNDSLCSVQRYVINHHSCGNTSEIDVGNHKKFELTDEQA 709
DB 652 NGDTMKKERNVTLLMKPLKNDSLCSVQRYVINHHSCGNTSEIDVGNHKKFELTDEQA 711
QY 710 HFTVTLAINSIGASVANFNLTFSPMSKYNIVQSLSAYPLNNSCVIYSLSPSDYKLMY 769
DB 712 HFTVTLAINSIGASVANFNLTFSPMSKYNIVQSLSAYPLNNSCVIYSLSPSDYKLMY 771
QY 770 FIIEMKNLNEDEGEIKWLRISSSVKKYYIHDHFIPIEKYQSLYPIHVEGVGKPKIINSFT 829
DB 772 FIIEMKNLNEDEGEIKWLRISSSVKKYYIHDHFIPIEKYQSLYPIHVEGVGKPKIINSFT 831
QY 830 QDDIEKHQSDAGLYVPIYISSLTGLTLISHORMKLFWEVDPNPKNCSMAOGLNF 889
DB 832 QDDIEKHQSDAGLYVPIYISSLTGLTLISHORMKLFWEVDPNPKNCSMAOGLNF 891
QY 890 QK 891
DB 892 QK 893

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RESULT 12
 US-08-640-389A-3
 : Sequence 3, Application US/08640389A
 : Patent No. 5912123
 : GENERAL INFORMATION:
 : APPLICANT: Snodgrass, H. R.
 : APPLICANT: Cioffi, Joseph
 : APPLICANT: Zupancic, Thomas J.
 : APPLICANT: Shafer, Alan W.
 : TITLE OF INVENTION: DETECTION OF THE LEPTIN
 : TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
 : NUMBER OF SEQUENCES: 16
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pennie & Edmonds LLP
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10036-2711
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/640,389A
 : FILING DATE: 29-APR-1996
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Poissant, Brian M.
 : REGISTRATION NUMBER: 28,462
 : REFERENCE/DOCKET NUMBER: 8907-0032
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 869-9741/8864
 : TELEFAX: (212) 869-9741/8864
 : TELEX: 66141 PENNIE
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 960 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-640-389A-3

Query Match 58.5%; Score 681; DB 2; Length 960;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 110 TFSVNSLVFQOQIDANNIQCMLKGLDKLFLICYVESLFKNLFERNYKRVHLLYLPEVL 169
DB 112 TFSVNSLVFQOQIDANNIQCMLKGLDKLFLICYVESLFKNLFERNYKRVHLLYLPEVL 171
QY 170 EDSPLVPQKGSQVMHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVIFRSPKMSV 229
DB 172 EDSPLVPQKGSQVMHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVIFRSPKMSV 231
QY 230 QPINNVKPPPLGLHMETIDGDLKISMSPPPLVPPLOVYKYSNSTVIREADKIVS 289
DB 232 QPINNVKPPPLGLHMETIDGDLKISMSPPPLVPPLOVYKYSNSTVIREADKIVS 291
QY 290 ATSLVDSILPGSSVEYQVRGKRLDGPGLMSDMSPPRVFTTQDVLYFPFKILTSVGSNVS 349
DB 292 ATSLVDSILPGSSVEYQVRGKRLDGPGLMSDMSPPRVFTTQDVLYFPFKILTSVGSNVS 351
QY 350 FHCITKKNKIYPSKEIYVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDA 409
DB 352 FHCITKKNKIYPSKEIYVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDA 411
QY 410 VYCCNEHCHHRYAEIYDVNINISCEFDGYLTMTCTCRWSTIQLAESLTLQRLYHRS 469
DB 412 VYCCNEHCHHRYAEIYDVNINISCEFDGYLTMTCTCRWSTIQLAESLTLQRLYHRS 471
QY 470 SLVCSDFPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTMKIRINHSIGSLDSPPTCV 529
DB 472 SLVCSDFPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTMKIRINHSIGSLDSPPTCV 531
QY 530 LPDSVVKPLPPSSVKAETIINIGLLKISWEKVPFPENNLOFOIRGLSKEVQMKMYEY 589
DB 532 LPDSVVKPLPPSSVKAETIINIGLLKISWEKVPFPENNLOFOIRGLSKEVQMKMYEY 591
QY 590 DAKSVSLPVPDCAVYAVOYRCKRLDGLGYKMSNMPAYVVDIKVPMGPEFWRTI 649
DB 592 DAKSVSLPVPDCAVYAVOYRCKRLDGLGYKMSNMPAYVVDIKVPMGPEFWRTI 651
QY 650 NGDTMKKKNVTLLMKPLKKNDSLCSVORYVINHTSCNGTSEDVGNHTKFTFLMTEQA 709
DB 652 NGDTMKKKNVTLLMKPLKKNDSLCSVORYVINHTSCNGTSEDVGNHTKFTFLMTEQA 711
QY 710 HTVTYLAINSIGASVANRLFTFSWPMKSVNIYQSLSAVPLNSCVIYVNLSPSDYKLMY 769
DB 712 HTVTYLAINSIGASVANRLFTFSWPMKSVNIYQSLSAVPLNSCVIYVNLSPSDYKLMY 771
QY 770 FFIEMKNLNEDEIKMLRISSSVKKYIHDHFIPIEKYOFSLPIPFMEVGVGPKIINSFT 829
DB 772 FFIEMKNLNEDEIKMLRISSSVKKYIHDHFIPIEKYOFSLPIPFMEVGVGPKIINSFT 831
QY 830 ODDIEKHOSDAGLYIVPYIISSSILLGLTLLISHQRMKLEFMEDEVNPNKNCSSWAGLNF 889
DB 832 ODDIEKHOSDAGLYIVPYIISSSILLGLTLLISHQRMKLEFMEDEVNPNKNCSSWAGLNF 891
QY 890 OK 891
DB 892 OK 893

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RESULT 13
US-08-693-696-8
Sequence 8, Application US/08693696
Patent No. 6005080
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.

```

APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,888
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-693-696-8

Query Match 58.5%; Score 681; DB 3; Length 960;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFSVNSLVFQOQIDANNIQCMLKGLDKLFLICYVESLFKNLFERNYKRVHLLYLPEVL 169
DB 112 TFSVNSLVFQOQIDANNIQCMLKGLDKLFLICYVESLFKNLFERNYKRVHLLYLPEVL 171
QY 170 EDSPLVPQKGSQVMHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVIFRSPKMSV 229
DB 172 EDSPLVPQKGSQVMHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVIFRSPKMSV 231
QY 230 QPINNVKPPPLGLHMETIDGDLKISMSPPPLVPPLOVYKYSNSTVIREADKIVS 289
DB 232 QPINNVKPPPLGLHMETIDGDLKISMSPPPLVPPLOVYKYSNSTVIREADKIVS 291
QY 290 ATSLVDSILPGSSVEYQVRGKRLDGPGLMSDMSPPRVFTTQDVLYFPFKILTSVGSNVS 349
DB 292 ATSLVDSILPGSSVEYQVRGKRLDGPGLMSDMSPPRVFTTQDVLYFPFKILTSVGSNVS 351
QY 350 FHCITKKNKIYPSKEIYVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDA 409
DB 352 FHCITKKNKIYPSKEIYVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDA 411
QY 410 VYCCNEHCHHRYAEIYDVNINISCEFDGYLTMTCTCRWSTIQLAESLTLQRLYHRS 469
DB 412 VYCCNEHCHHRYAEIYDVNINISCEFDGYLTMTCTCRWSTIQLAESLTLQRLYHRS 471
QY 470 SLVCSDFPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTMKIRINHSIGSLDSPPTCV 529
DB 472 SLVCSDFPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTMKIRINHSIGSLDSPPTCV 531
QY 530 LPDSVVKPLPPSSVKAETIINIGLLKISWEKVPFPENNLOFOIRGLSKEVQMKMYEY 589

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Db 532 LPDSVVKPLPPSSVKAETITINIGLKIEMKVPFENNLOFOIRGLSGKEVQWKMEYV 591
QY 590 DAKSKSVSLPVPDLCAYVAVQVRCKRLDGLGYWMSNMSNPAYTVVMDIKPMPGPEFRRII 649
Db 592 DAKSKSVSLPVPDLCAYVAVQVRCKRLDGLGYWMSNMSNPAYTVVMDIKPMPGPEFRRII 651
QY 650 NGDTMKKEKNVTLMLKPLMKNDLSVQRYVINHTSCNGTWSSEVGNHTKFTFLMTEQA 709
Db 652 NGDTMKKEKNVTLMLKPLMKNDLSVQRYVINHTSCNGTWSSEVGNHTKFTFLMTEQA 711
QY 710 HTVTYLAISIGASVANFNLTFSWPMKSVNIOSLSAYPLNSCVIVSILSPSDYKLMY 769
Db 712 HTVTYLAISIGASVANFNLTFSWPMKSVNIOSLSAYPLNSCVIVSILSPSDYKLMY 771
QY 770 FIEMKLNLEDGEIKMLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFT 829
Db 772 FIEMKLNLEDGEIKMLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFT 831
QY 830 QDDIEKHOSDAGLYIVPYIITSSILLGTLLISHQRMKKLWEVDPNPKNCWMAOGLNF 889
Db 832 QDDIEKHOSDAGLYIVPYIITSSILLGTLLISHQRMKKLWEVDPNPKNCWMAOGLNF 891
QY 890 OK 891
Db 892 OK 893

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RESULT 14
US-08-588-190-3
; Sequence 3, Application US/08588190
; Patent No. 5856098
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
; TITLE OF INVENTION: VARIANT AND METHODS FOR REGULATING OBESITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,190
; FILING DATE: 18-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 008907-0029-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-5556
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; US-08-588-190-3
Query Match 49.8%; Score 580; DB 2; Length 960;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 760; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 110 TEVSTVNSLVFQOIDANMNIQCLKGLDLKFLICYSESLFRNLFRNYNRVHLLYVLEVL 169
Db 112 TEVSTVNSLVFQOIDANMNIQCLKGLDLKFLICYSESLFRNLFRNYNRVHLLYVLEVL 171
QY 170 EDSPLVPQKGSQPMWCHNCNCSYHECCCLVPPYPAKANDTLMLCKLTGSGVIFQSPLMAY 229
Db 172 EDSPLVPQKGSQPMWCHNCNCSYHECCCLVPPYPAKANDTLMLCKLTGSGVIFQSPLMAY 231
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Db 232 OPTNMYKPPPLGLHMEITDDGNLKISWSSPPLVPEPLQYQVYKSSNSTTVIREADKIYS 291
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QY 350 FHCITYKKNKIYPSKRIYMMNLAERIKPOSQYDVSDHYSKYTFINLNETKPRGKFTYA 409
Db 352 FHCITYKKNKIYPSKRIYMMNLAERIKPOSQYDVSDHYSKYTFINLNETKPRGKFTYA 411
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Db 412 VYCCNEHECHHRYAELIYDVNINISCEFDGYLTWKTCWSTSIQSLAESTQLRHRHS 471
QY 470 SLVCSDFPSIHPISEPKDCYLOSDFEYECIPDIFLLSGYTMKIRINHSLSIDSEPTCV 529
Db 472 SLVCSDFPSIHPISEPKDCYLOSDFEYECIPDIFLLSGYTMKIRINHSLSIDSEPTCV 531
QY 530 LPDSVVKPLPPSSVKAETITINIGLKIEMKVPFENNLOFOIRGLSGKEVQWKMEYV 589
Db 532 LPDSVVKPLPPSSVKAETITINIGLKIEMKVPFENNLOFOIRGLSGKEVQWKMEYV 591
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Db 592 DAKSKSVSLPVPDLCAYVAVQVRCKRLDGLGYWMSNMSNPAYTVVMDIKPMPGPEFRRII 651
QY 650 NGDTMKKEKNVTLMLKPLMKNDLSVQRYVINHTSCNGTWSSEVGNHTKFTFLMTEQA 709
Db 652 NGDTMKKEKNVTLMLKPLMKNDLSVQRYVINHTSCNGTWSSEVGNHTKFTFLMTEQA 711
QY 710 HTVTYLAISIGASVANFNLTFSWPMKSVNIOSLSAYPLNSCVIVSILSPSDYKLMY 769
Db 712 HTVTYLAISIGASVANFNLTFSWPMKSVNIOSLSAYPLNSCVIVSILSPSDYKLMY 771
QY 770 FIEMKLNLEDGEIKMLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFT 829
Db 772 FIEMKLNLEDGEIKMLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFT 831
QY 830 QDDIEKHOSDAGLYIVPYIITSSILLGTLLISHQRMKKLWEVDPNPKNCWMAOGLNF 889
Db 832 QDDIEKHOSDAGLYIVPYIITSSILLGTLLISHQRMKKLWEVDPNPKNCWMAOGLNF 891
QY 890 OK 891
Db 892 OK 893

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RESULT 15
US-08-618-957A-3
; Sequence 3, Application US/08618957A
; Patent No. 6355237
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas Joel

```


APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBSE
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-3

Query Match 49.8%; Score 580; DB 4; Length 960;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 110 TFSVSTNSLVFQOQIDANNIOCMKGLDKLFICYESLFFKNLFNNYKVVHLLVLEVL 169
DB 112 TFSVSTNSLVFQOQIDANNIOCMKGLDKLFICYESLFFKNLFNNYKVVHLLVLEVL 171
QY 170 EDSPLVPKGSFQWVHCNCVHECCCECLVPVPTAKLNDTLMLCKITSGVIFQSPMSV 229
DB 172 EDSPLVPKGSFQWVHCNCVHECCCECLVPVPTAKLNDTLMLCKITSGVIFQSPMSV 231
QY 230 QPINNVKRPDLGLHMETTDGONLKSMSPPVLPFLOQYKYSNSTTVIREDKIVS 289
DB 232 QPINNVKRPDLGLHMETTDGONLKSMSPPVLPFLOQYKYSNSTTVIREDKIVS 291
QY 290 ATSLVDSILPGSSYEYVGRKRLDGPGLWSDMSTPRVFTTODVLYFPFKILTSVGSNVS 349
DB 292 ATSLVDSILPGSSYEYVGRKRLDGPGLWSDMSTPRVFTTODVLYFPFKILTSVGSNVS 351
QY 350 FHCYIKKKNKLVPSKEIYVMMNLAKIPOSQYDVVSDHVSQVTFNNLNETKRGKFTYDA 409
DB 352 FHCYIKKKNKLVPSKEIYVMMNLAKIPOSQYDVVSDHVSQVTFNNLNETKRGKFTYDA 411
QY 410 VYCCNEHCCHRYALVLYDVNINISCEFDGLTKMTCRWSTSTOSIAESTLOLRHNS 469
DB 412 VYCCNEHCCHRYALVLYDVNINISCEFDGLTKMTCRWSTSTOSIAESTLOLRHNS 471
QY 470 SLVCSDFISHPISRPKCYLQSDGFYECIFQPIFLSLGYTMMIRINISLGLSDSPPTCV 529
DB 472 SLVCSDFISHPISRPKCYLQSDGFYECIFQPIFLSLGYTMMIRINISLGLSDSPPTCV 531

QY 530 LPDSVYKPLPSSVKAETITINIGLLKISWEKVPENNLOFOIRVGLSGKEVOMKMEYV 589
DB 532 LPDSVYKPLPSSVKAETITINIGLLKISWEKVPENNLOFOIRVGLSGKEVOMKMEYV 591
QY 590 DAKRSVSLPVPDLCAYAVOYRCKRDLGCLGYNWMSNPATVVDIVPMGPEFWRII 649
DB 592 DAKRSVSLPVPDLCAYAVOYRCKRDLGCLGYNWMSNPATVVDIVPMGPEFWRII 651
QY 650 NGDTMKKEKNVTLMLKPLMKNDLCSVQRYVNIHTSCNGTSEVGNHTKTFPLMTBOA 709
DB 652 NGDTMKKEKNVTLMLKPLMKNDLCSVQRYVNIHTSCNGTSEVGNHTKTFPLMTBOA 711
QY 710 HTVTVLAINSIGAVANFLFSPMPSKVNIVQSLAAYPLNCSVIVSWILSPSDYKLMY 769
DB 712 HTVTVLAINSIGAVANFLFSPMPSKVNIVQSLAAYPLNCSVIVSWILSPSDYKLMY 771
QY 770 FIEKKNLNEDEIWMRLSSSVKRYIHDHPIEKKYQSLYF-FMEGVGPKIINSET 829
DB 772 FIEKKNLNEDEIWMRLSSSVKRYIHDHPIEKKYQSLYF-FMEGVGPKIINSET 831
QY 830 ODDIEKHOSDAGLYIVPYIISSTILLGTLISHQMKKLFWEIVPNNPKNSMAQGLNF 889
DB 832 ODDIEKHOSDAGLYIVPYIISSTILLGTLISHQMKKLFWEIVPNNPKNSMAQGLNF 891
QY 890 OK 891
DB 892 OK 893

RESULT 16
US-08-568-526-3
Sequence 3, Application US/08588526
Patent No. 5882860
GENERAL INFORMATION:
APPLICANT: Snodgrass, H.
APPLICANT: Clotfll, Joseph
APPLICANT: Zupancic, Thomas
TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
TITLE OF INVENTION: VARIANT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,526
FILING DATE: 18-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-588-526-3

Query Match	40.7%;	Score 474;	DB 2;	Length 908;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 774;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0;

QY	110	TFEVSFVSLVFOQIDAMNNIOCMFKGDLKJFICVESFEPNLPFNPNYKHLHLYVBEVL	169
Db	112	TFEVSFVSLVFOQIDAMNNIOCMFKGDLKJFICVESFEPNLPFNPNYKHLHLYVBEVL	171
QY	170	EDSPLVPOKGSFOMVHCNCSVHECCBCLVPPYPAKLNDTLMLCKLINSGVIFQSPLMV	229
Db	172	EDSPLVPOKGSFOMVHCNCSVHECCBCLVPPYPAKLNDTLMLCKLINSGVIFRSPLMV	221
QY	230	QPIWVVPDPLGLHMETDIDGNLKITWSSPPLVPFLOYOVKSENSTVIREADKIVS	289
Db	232	QPIWVVPDPLGLHMETDIDGNLKITWSSPPLVPFLOYOVKSENSTVIREADKIVS	291
QY	290	ATSLVDSILPFGSSYEVOVRKRLDGGINSMDSTPNTFOTDITYPPKILUSGVNS	349
Db	292	ATSLVDSILPFGSSYEVOVRKRLDGGINSMDSTPNTFOTDITYPPKILUSGVNS	351
QY	350	FHCITYKKNKIVPSKETIVMMNIAEKIPQSOYDVSDHVSXVTFEFNINETKPRCKFTYDA	409
Db	352	FHCITYKKNKIVPSKETIVMMNIAEKIPQSOYDVSDHVSXVTFEFNINETKPRCKFTYDA	411
QY	410	YVCCNEHECHHRYAELVYIDVNIINSETDGYLTKMKCNSTSTQSLASTIOLRHS	469
Db	412	YVCCNEHECHHRYAELVYIDVNIINSETDGYLTKMKCNSTSTQSLASTIOLRHS	471
QY	470	SLYCSDDPSIHPISPEPKDCYOSGFECEJFOPFTLLSGTMMIRIHSIGSDSPTCV	529
Db	472	SLYCSDDPSIHPISPEPKDCYOSGFECEJFOPFTLLSGTMMIRIHSIGSDSPTCV	531
QY	530	LPDSVAPPLPSSVYKAEITTINGLKLISWEKVPFENNLOFOIRYGLSGREVOMKMEYV	589
Db	532	LPDSVAPPLPSSVYKAEITTINGLKLISWEKVPFENNLOFOIRYGLSGREVOMKMEYV	591
QY	590	DAKKSYSPLPBDLCANYAAYOVRCRKLDDGAGYMSNMSNPATVYMDIKVPMGPEWRIT	649
Db	592	DAKKSYSPLPBDLCANYAAYOVRCRKLDDGAGYMSNMSNPATVYMDIKVPMGPEWRIT	651
QY	650	NGDPMKKEKNVTLMLKPLMKNDKSLCSQVORYVINHTHSCNCTWSESDVGNHKKFFLMEQA	709
Db	652	NGDPMKKEKNVTLMLKPLMKNDKSLCSQVORYVINHTHSCNCTWSESDVGNHKKFFLMEQA	711
QY	710	HTVAVLAINSIGASVANFNLTFSWPMKRVINVOISLAPPLNSSCQVYSWLTSDDYKLMY	769
Db	712	HTVAVLAINSIGASVANFNLTFSWPMKRVINVOISLAPPLNSSCQVYSWLTSDDYKLMY	771
QY	770	FIEMKULNEDGELIKWLRISSSVYKYYIHDFPIPIEKYQFSLVPIEMEGVAKRIINSFT	829
Db	772	FIEMKULNEDGELIKWLRISSSVYKYYIHDFPIPIEKYQFSLVPIEMEGVAKRIINSFT	831
QY	830	QDDLEKHOSQAGLVIVPVIISSILLGLTLLSHQMKMLFMEDEVNPNKNCMAQ	886
Db	832	QDDLEKHOSQAGLVIVPVIISSILLGLTLLSHQMKMLFMEDEVNPNKNCMAQ	888

RESULT 17
US-08-640-389A-11

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/88864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
OS-08-640-389A-11

Query Match	40.3%	Score 470;	DB 2;	Length 1165;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 970;	Conservative	0;	Mismatches 5;	Indels 0;
				Gaps 0;

QY	1	MICKFCVLLHMFIVITAFNLSTYITPMRFSLSCMPNNTYIVFELPAGLSKNTNS	60
Db	1	MICKFCVLLHMFIVITAFNLSTYITPMRFSLSCMPNNTYIVFELPAGLSKNTNS	60
QY	61	NGHYETAVEBKFNSSGTHFNSLSKTTPEHCCFRSEBDRNCSLCADNIEGKTFVTSVLVF	120
Db	61	NGHYETAVEBKFNSSGTHFNSLSKTTPEHCCFRSEBDRNCSLCADNIEGKTFVTSVLVF	120
QY	121	QOIDANNICOMLKGDLKLFICYVESIEFKULFRYNYKVALLV,PEVLDEDSLVPQOKS	180
Db	121	QOIDANNICOMLKGDLKLFICYVESIEFKULFRYNYKVALLV,PEVLDEDSLVPQOKS	180
QY	181	FQWVHCNCVHECECECLVPPPAKLNDTLMLCKLTISGVIYFOSPLNSVQPIIMVKRPDP	240
Db	181	FQWVHCNCVHECECECLVPPPAKLNDTLMLCKLTISGVIYFOSPLNSVQPIIMVKRPDP	240
QY	241	LGJHMETTDGONLKIWSMSPPLVPEPLQYOVKYSENSTYIRADKIVASTSLLYDSILP	300
Db	241	LGJHMETTDGONLKIWSMSPPLVPEPLQYOVKYSENSTYIRADKIVASTSLLYDSILP	300
QY	301	GSSYEVOVRCKRLDGPIMSDMSTPRVFTQDVIYEPFKILTSVGSNVSFHCYKREKNI	360
Db	301	GSSYEVOVRCKRLDGPIMSDMSTPRVFTQDVIYEPFKILTSVGSNVSFHCYKREKNI	360
QY	361	VPSKEIYVMMNMLAEKTIQOSQYDVVSDHVSXVTFEFLNLETKPRCKFTYDAYCCNEHECHH	420
Db	361	VPSKEIYVMMNMLAEKTIQOSQYDVVSDHVSXVTFEFLNLETKPRCKFTYDAYCCNEHECHH	420
QY	421	RYAELVYIDVNNISCTEDGYLTKMTCRMWSTIQSLAESTIOLRYHRSSLYCSDIPSIH	480
Db	421	RYAELVYIDVNNISCTEDGYLTKMTCRMWSTIQSLAESTIOLRYHRSSLYCSDIPSIH	480
QY	481	PISPRKCTCIQSDGFCYTCIQPIFLLSGTYMMIRINHSGLSDSPPCVLPDSVVKPLPP	540
Db	481	PISPRKCTCIQSDGFCYTCIQPIFLLSGTYMMIRINHSGLSDSPPCVLPDSVVKPLPP	540

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QY 541 SSVKAEITINIGLKTISMEKPYFENNLOFOIRYGLSGREYOMKYEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKTISMEKPYFENNLOFOIRYGLSGREYOMKYEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVCRKLDGLGYWNSNRPAYTVYVMDIKVPMRCPERRLINGDTMKKEKRV 660
Db 601 PDLCAVYAVQVCRKLDGLGYWNSNRPAYTVYVMDIKVPMRCPERRLINGDTMKKEKRV 660
QY 661 TLLMKPLMKNDLSGVORVIVNHHTSCNCTWAGEDVGNHRTKFFLMTQEAHTVLAINSI 720
Db 661 TLLMKPLMKNDLSGVORVIVNHHTSCNCTWAGEDVGNHRTKFFLMTQEAHTVLAINSI 720
QY 721 GASVANFNLTFSPMPSKVNIVOSLSAYPLNSSCVIYVSWILSPDYKLMVFTEEMKLNED 780
Db 721 GASVANFNLTFSPMPSKVNIVOSLSAYPLNSSCVIYVSWILSPDYKLMVFTEEMKLNED 780
QY 781 GEIKMLRISSSVKYKYIHDFPIPEIKYQSLYPIFMEGVGAKRLINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRISSSVKYKYIHDFPIPEIKYQSLYPIFMEGVGAKRLINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSILLGLTGLISHORMKLFMEDVNPKNCSMAOGLNFOKPEFPHLFI 900
Db 841 GLYVIVPVISSILLGLTGLISHORMKLFMEDVNPKNCSMAOGLNFOKPEFPHLFI 900
QY 901 KHTASVTCGPLEPPTISEDIVDTSMKNKDEMMPTTVVSLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLEPPTISEDIVDTSMKNKDEMMPTTVVSLSTTDLEKGSVCISDQFN 960
QY 961 SYNFSAEGETEYVE 975
Db 961 SYNFSAEGETEYVE 975

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RESULT 18

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US-08-306-231-3
; Sequence 3, Application US/08306231
; Patent No. 5643748
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,231
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-076
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 569 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-306-231-3

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Query Match 39.4%; Score 459; DB 1: Length 569;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 224 SPLMSVQPIINMVKPPPLDLHMEITDDGNLKTISWSSPPLVPPLOQVYVSESTVIRE 283
Db 111 SPLMSVQPIINMVKPPPLDLHMEITDDGNLKTISWSSPPLVPPLOQVYVSESTVIRE 170
QY 284 ADKIVATSILVDSILPGSSVEYQVGRKRLDGGIWSDMSTPRVTTQDVYIFPPKILTS 343
Db 171 ADKIVATSILVDSILPGSSVEYQVGRKRLDGGIWSDMSTPRVTTQDVYIFPPKILTS 230
QY 344 VGSNVSFHCITKKENKIVPSKEIYMMNLAEKIPQSOYDVVSDHVSKVTFPNLNETKPRG 403
Db 231 VGSNVSFHCITKKENKIVPSKEIYMMNLAEKIPQSOYDVVSDHVSKVTFPNLNETKPRG 290
QY 404 KFTYDAVYCCNEHECHRRYAEIYVDVNNINISCTDGYLTMCNWSSTIOSIAESTIQ 463
Db 291 KFTYDAVYCCNEHECHRRYAEIYVDVNNINISCTDGYLTMCNWSSTIOSIAESTIQ 350
QY 464 LRYHRSLSYCSPIPSIHPISSEPCDYLOSDFEFCIFQPIFLLSGYTMIRINHSLSGSD 523
Db 351 LRYHRSLSYCSPIPSIHPISSEPCDYLOSDFEFCIFQPIFLLSGYTMIRINHSLSGSD 410
QY 524 SPPTCVLPDSVYKPLPPSSVKAETINIGLKTISMEKPYFENNLOFOIRYGLSGREYOM 583
Db 411 SPPTCVLPDSVYKPLPPSSVKAETINIGLKTISMEKPYFENNLOFOIRYGLSGREYOM 470
QY 584 KMEYVDAKSKSVSLPVPDLCAYVAVQVCRKLDGLGYWNSNRPAYTVYVMDIKVPMRGP 643
Db 471 KMEYVDAKSKSVSLPVPDLCAYVAVQVCRKLDGLGYWNSNRPAYTVYVMDIKVPMRGP 530
QY 644 EFWRLINGDTMKKEKNVTLLMKPLMKNDLSGVORVIN 682
Db 531 EFWRLINGDTMKKEKNVTLLMKPLMKNDLSGVORVIN 569

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RESULT 19

```

US-08-640-389A-10
; Sequence 10, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEFTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

NAME: Poissant, Brian M.
 REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 8907-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 896 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-640-389A-10

Query Match 26.4%; Score 307; DB 2: Length 896;
 Best Local Similarity 99.5%; Pred. No. 3.7e-301;
 Matches 607; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 282 READKIVSATSLVDSILPGSSYEVQVGRKRLDGPIMSDMSTPRVFTQDVYIFPPKIL 341
 DB 282 READKIVSATSLVDSILPGSSYEVQVGRKRLDGPIMSDMSTPRVFTQDVYIFPPKIL 341
 QY 342 TSVGSNVSFHCICYKKENKIYPSKEIYMMNLAEKIPQSOYDVSDHVSQVTFENLNETRP 401
 DB 342 TSVGSNVSFHCICYKKENKIYPSKEIYMMNLAEKIPQSOYDVSDHVSQVTFENLNETRP 401
 QY 402 RGFETTDAYCCNEHCHECHRYAELIYIDVNIINISCTEDGYLTRMTCRWSTIQSIAEST 461
 DB 402 RGFETTDAYCCNEHCHECHRYAELIYIDVNIINISCTEDGYLTRMTCRWSTIQSIAEST 461
 QY 462 LQLRHRSLSYCSIDIPSIHPISPEKDCYLOSDFEYCFIQPIFLLSGYTMMIRINHSLS 521
 DB 462 LQLRHRSLSYCSIDIPSIHPISPEKDCYLOSDFEYCFIQPIFLLSGYTMMIRINHSLS 521
 QY 522 LQSPPTCVLPDSVVKPLPPSSVKAETITNGILKISMEKRVPEENNLOQIRYGLSGKEY 581
 DB 522 LQSPPTCVLPDSVVKPLPPSSVKAETITNGILKISMEKRVPEENNLOQIRYGLSGKEY 581
 QY 582 QMKMYEYDAKSKSVSLPVDLCAYAVOVRCKRLDGLGYSWMSNPATVVDIVPMR 641
 DB 582 QMKMYEYDAKSKSVSLPVDLCAYAVOVRCKRLDGLGYSWMSNPATVVDIVPMR 641
 QY 642 GPEFRINGDTMKKKNVTLMLKPLMKNDLSLCSVQRYVINHHTSCNGTMSDEVGNHTRF 701
 DB 642 GPEFRINGDTMKKKNVTLMLKPLMKNDLSLCSVQRYVINHHTSCNGTMSDEVGNHTRF 701
 QY 702 TFLMTEQAHVTYVLAISIGASVAFNLTFSWPMKVNIVOSLSAYPLNSSCVIYSWILS 761
 DB 702 TFLMTEQAHVTYVLAISIGASVAFNLTFSWPMKVNIVOSLSAYPLNSSCVIYSWILS 761
 QY 762 PSYKIMAFYIEEMKNLNEGEIKWLRISSSVKKYTHDHPRIPEKOFSLYIFEMGVGR 821
 DB 762 PSYKIMAFYIEEMKNLNEGEIKWLRISSSVKKYTHDHPRIPEKOFSLYIFEMGVGR 821
 QY 822 PKIINSFTODDIEKHOSDAGLYIVPEVLISSSILGLTLLISHQRMKLFWEDEVPPKNC 881
 DB 822 PKIINSFTODDIEKHOSDAGLYIVPEVLISSSILGLTLLISHQRMKLFWEDEVPPKNC 881
 QY 882 SMAOGLNFOR 891
 DB 882 SMAOGLNFOR 891

RESULT 20
 US-08-640-389A-9
 Sequence 9, Application US/08640389A
 Patent No. 5912123
 GENERAL INFORMATION:
 APPLICANT: Snodgrass, H. R.
 APPLICANT: Ciofili, Joseph

APPLICANT: Zupancic, Thomas J.
 APPLICANT: Shafer, Alan W.
 TITLE OF INVENTION: DETECTION OF THE LEPTIN
 TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
 TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/640,389A
 FILING DATE: 29-APR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Poissant, Brian M.
 REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 8907-032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 906 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-640-389A-9

Query Match 26.4%; Score 307; DB 2: Length 906;
 Best Local Similarity 99.5%; Pred. No. 3.8e-301;
 Matches 607; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 282 READKIVSATSLVDSILPGSSYEVQVGRKRLDGPIMSDMSTPRVFTQDVYIFPPKIL 341
 DB 282 READKIVSATSLVDSILPGSSYEVQVGRKRLDGPIMSDMSTPRVFTQDVYIFPPKIL 341
 QY 342 TSVGSNVSFHCICYKKENKIYPSKEIYMMNLAEKIPQSOYDVSDHVSQVTFENLNETRP 401
 DB 342 TSVGSNVSFHCICYKKENKIYPSKEIYMMNLAEKIPQSOYDVSDHVSQVTFENLNETRP 401
 QY 402 RGFETTDAYCCNEHCHECHRYAELIYIDVNIINISCTEDGYLTRMTCRWSTIQSIAEST 461
 DB 402 RGFETTDAYCCNEHCHECHRYAELIYIDVNIINISCTEDGYLTRMTCRWSTIQSIAEST 461
 QY 462 LQLRHRSLSYCSIDIPSIHPISPEKDCYLOSDFEYCFIQPIFLLSGYTMMIRINHSLS 521
 DB 462 LQLRHRSLSYCSIDIPSIHPISPEKDCYLOSDFEYCFIQPIFLLSGYTMMIRINHSLS 521
 QY 522 LQSPPTCVLPDSVVKPLPPSSVKAETITNGILKISMEKRVPEENNLOQIRYGLSGKEY 581
 DB 522 LQSPPTCVLPDSVVKPLPPSSVKAETITNGILKISMEKRVPEENNLOQIRYGLSGKEY 581
 QY 582 QMKMYEYDAKSKSVSLPVDLCAYAVOVRCKRLDGLGYSWMSNPATVVDIVPMR 641
 DB 582 QMKMYEYDAKSKSVSLPVDLCAYAVOVRCKRLDGLGYSWMSNPATVVDIVPMR 641
 QY 642 GPEFRINGDTMKKKNVTLMLKPLMKNDLSLCSVQRYVINHHTSCNGTMSDEVGNHTRF 701
 DB 642 GPEFRINGDTMKKKNVTLMLKPLMKNDLSLCSVQRYVINHHTSCNGTMSDEVGNHTRF 701
 QY 702 TFLMTEQAHVTYVLAISIGASVAFNLTFSWPMKVNIVOSLSAYPLNSSCVIYSWILS 761

|||||
Db 702 TPLMTEQAHTVTVLAINSIGASVANFNLFSPMSKVNIVOSLSAVPLNSSCVIYSWILS 761
Qy 762 PSDYKLMFIIEMKMLNEDGEIKMLRISSSVKYYIHDFIPIEKYQSLYIFMEGVK 821
Db 762 PSDYKLMFIIEMKMLNEDGEIKMLRISSSVKYYIHDFIPIEKYQSLYIFMEGVK 821
Qy 822 PKINSFTODDIEKHOSDAGLYVIVPVISSSILGLTLLISHQRKMLFMEVDPNPKNC 881
Db 822 PKINSFTODDIEKHOSDAGLYVIVPVISSSILGLTLLISHQRKMLFMEVDPNPKNC 881
Qy 882 SWAOGINFOK 891
Db 882 SWAOGINFOK 891

RESULT 21
US-08-640-389A-8
: Sequence 8, Application US/08640389A
: Patent No. 5912123
: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. R.
: APPLICANT: Cioffi, Joseph
: APPLICANT: Zupancic, Thomas J.
: APPLICANT: Shafer, Alan W.
: TITLE OF INVENTION: DETECTION OF THE LEPTIN
: TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/640.389A
: FILING DATE: 29-APR-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28, 462
: REFERENCE/DOCKET NUMBER: 8907-032
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELE: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 958 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
US-08-640-389A-8

Query Match 26.4%; Score 307; DB 2; Length 958;
Best Local Similarity 99.5%; Pred. No. 4e-301;
Matches 607; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 342 TSVGSNVSPHCYIKKENKIVPSKETVMMNLAKEIPQSOYDVVSDHVKVTFENLNETKP 401
Qy 402 RKGFTYDAVYCCNEHECHRRVAELVYDVNINI SCETDGLTKMTCRMSTSTYIOSLAEST 461
Db 402 RKGFTYDAVYCCNEHECHRRVAELVYDVNINI SCETDGLTKMTCRMSTSTYIOSLAEST 461
Qy 462 LQRYHRSSLVCSDIPTSHPISEPKDCYIOSDGFEECFQFPFLLSGYTMWRIRNHSLS 521
Db 462 LQRYHRSSLVCSDIPTSHPISEPKDCYIOSDGFEECFQFPFLLSGYTMWRIRNHSLS 521
Qy 522 LPSPTCVLPDSVVKPLPPSSVKAETITNTGLKISMEKVPENNLQFOIRYGLSGKEY 581
Db 522 LPSPTCVLPDSVVKPLPPSSVKAETITNTGLKISMEKVPENNLQFOIRYGLSGKEY 581
Qy 582 QMKMTEYVDKSKSVSLPVPDLCAYAVOVRCKRLDGLGYSWMSNPATVYMDIKVPMR 641
Db 582 QMKMTEYVDKSKSVSLPVPDLCAYAVOVRCKRLDGLGYSWMSNPATVYMDIKVPMR 641
Qy 642 GPEFRIINGDTMKKEKNVTLMLKPLMKNDSLCSQORYYINHTSCNGTWSDEDGNHTKF 701
Db 642 GPEFRIINGDTMKKEKNVTLMLKPLMKNDSLCSQORYYINHTSCNGTWSDEDGNHTKF 701
Qy 702 TPLMTEQAHTVTVLAINSIGASVANFNLFSPMSKVNIVOSLSAVPLNSSCVIYSWILS 761
Db 702 TPLMTEQAHTVTVLAINSIGASVANFNLFSPMSKVNIVOSLSAVPLNSSCVIYSWILS 761
Qy 762 PSDYKLMFIIEMKMLNEDGEIKMLRISSSVKYYIHDFIPIEKYQSLYIFMEGVK 821
Db 762 PSDYKLMFIIEMKMLNEDGEIKMLRISSSVKYYIHDFIPIEKYQSLYIFMEGVK 821
Qy 822 PKINSFTODDIEKHOSDAGLYVIVPVISSSILGLTLLISHQRKMLFMEVDPNPKNC 881
Db 822 PKINSFTODDIEKHOSDAGLYVIVPVISSSILGLTLLISHQRKMLFMEVDPNPKNC 881
Qy 882 SWAOGINFOK 891
Db 882 SWAOGINFOK 891

RESULT 22
US-08-803-346-64
: Sequence 64, Application US/08803346
: Patent No. 6281346
: GENERAL INFORMATION:
: APPLICANT: HESS, JOHN W.
: APPLICANT: CASKEY, C. THOMAS
: APPLICANT: LIU, QINGYUN
: APPLICANT: PHILLIPS, MICHAEL SEAN
: TITLE OF INVENTION: RAT OR RECEPTORS AND NUCLEOTIDES
: NUMBER OF SEQUENCES: 77
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
: STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
: CITY: RAHWAY
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/803.346
: FILING DATE: 20-FEB-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: GIESSEY, JOANNE M
: REGISTRATION NUMBER: 32,838

REFERENCE/DOCKET NUMBER: 19642Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-803-346-64

Query Match 6.6%; Score 77; DB 4; length 77;
Best Local Similarity 100.0%; Pred. No. 6.6e-70;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 553 LKISWEKFPENNLOFQIRYGLSGKEVQMKNEYVDKSKSVSLPVDLCVAVAYQVR 612
|||||
DB 1 LKISWEKFPENNLOFQIRYGLSGKEVQMKNEYVDKSKSVSLPVDLCVAVAYQVR 60
|||||

QY 613 CKRLDGLGYWSMNSPA 629
|||||
DB 61 CKRLDGLGYWSMNSPA 77
|||||

RESULT 23
US-08-803-346-61
Sequence 61, Application US/08803346
Patent No. 6281346
GENERAL INFORMATION:
APPLICANT: HESS, JOHN W.
APPLICANT: CASKEY, C. THOMAS
APPLICANT: LIU, QINGYUN
APPLICANT: PHILLIPS, MICHAEL SEAN
TITLE OF INVENTION: RAT OR RECEPTORS AND NUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSER: JOANNE M. GIESSEY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000,
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSEY, JOANNE M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19642Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-803-346-61

Query Match 6.5%; Score 76; DB 4; length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-69;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 NLKISWSPPLVPFLOVQKXSENSITVIRADKIVATSILVNSILPGSSYEVQVRCK 311
|||||
DB 1 NLKISWSPPLVPFLOVQKXSENSITVIRADKIVATSILVNSILPGSSYEVQVRCK 60
|||||

QY 312 RLDGPGIWSMDSTPRV 327
|||||
DB 61 RLDGPGIWSMDSTPRV 76
|||||

RESULT 24
US-08-599-455B-2
Sequence 2, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkijohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-2

Query Match 3.6%; Score 42; DB 2; length 894;

Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKRLPPS 541
Db 498 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKRLPPS 539

RESULT 25

US-09-069-781B-2

Sequence 2, Application US/09069781B

Patent No. 6287782

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069, 781B

FILING DATE: 29-APRIL-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/864,564

FILING DATE: 28-MAY-1997

APPLICATION NUMBER: US 08/708,123

FILING DATE: 03-SEP-1996

APPLICATION NUMBER: US 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: US 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: US 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: US 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: US 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: US 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: US 08/562,663

FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Melkielejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/082001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 894 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-069-781B-2

Query Match 3.6%; Score 42; DB 4; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKRLPPS 541
Db 498 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKRLPPS 539

RESULT 26

US-08-618-957A-12

Sequence 12, Application US/08618957A

Patent No. 6355237

GENERAL INFORMATION:

APPLICANT: Snodgrass, H. Ralph

APPLICANT: Cioffi, Joseph

APPLICANT: Zupancic, Thomas Joel

APPLICANT: Shafer, Alan Wayne

TITLE OF INVENTION: METHODS FOR USING THE OBES

TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC

TITLE OF INVENTION: DEVELOPMENT

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue Of The Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/618,957A

FILING DATE: 20-MAR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 008907-0033-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 894 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-618-957A-12

Query Match 3.6%; Score 42; DB 4; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKRLPPS 541
Db 498 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKRLPPS 539

RESULT 27

US-08-827-962-19

Sequence 19, Application US/08827962A

Patent No. 6258944

GENERAL INFORMATION:

APPLICANT: MERCK & CO., INC.
TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS
FILE REFERENCE: 19693
CURRENT APPLICATION NUMBER: US/08/827,962A
CURRENT FILING DATE: 1997-05-06
PRIOR APPLICATION NUMBER: 60/016,899
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 895
TYPE: PRF
ORGANISM: Rattus No. 6258944vegicus
US-08-827-962-19

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 28
US-08-827-962-21
Sequence 21, Application US/08827962A
Patent No. 6258944
GENERAL INFORMATION:
APPLICANT: MERCK & CO., INC.
TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS
FILE REFERENCE: 19693
CURRENT APPLICATION NUMBER: US/08/827,962A
CURRENT FILING DATE: 1997-05-06
PRIOR APPLICATION NUMBER: 60/016,899
PRIOR FILING DATE: 1996-05-06
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 895
TYPE: PRF
ORGANISM: Rattus No. 6258944vegicus
US-08-827-962-21

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541
Db 498 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 539

RESULT 29
US-08-640-389A-12
Sequence 12, Application US/08640389A
Patent No. 5912123
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cloutier, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTION OF THE LEFTIN
TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-640-389A-12

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541
Db 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541

RESULT 30
US-08-599-455B-43
Sequence 43, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkiesohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-43

Query Match 3.6%; Score 42; DB 2; Length 1162;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSLSLSDSPPTCVLPDVSVKPLPPS 541
DB 498 FQPIFLSGYTMWIRINHSLSLSDSPPTCVLPDVSVKPLPPS 539

RESULT 31
US-08-827-962-15
Sequence 15, Application US/08827962A
Patent No. 6258944
GENERAL INFORMATION:
APPLICANT: MERCK & CO., INC.
TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS
FILE REFERENCE: 19693
CURRENT APPLICATION NUMBER: US/08/827,962A
CURRENT FILING DATE: 1997-05-06
PRIOR APPLICATION NUMBER: 60/016,899
PRIOR FILING DATE: 1996-05-06
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1162
TYPE: PRT
ORGANISM: Rattus No. 6258944vegicus
US-08-827-962-15

Query Match 3.6%; Score 42; DB 4; Length 1162;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSLSLSDSPPTCVLPDVSVKPLPPS 541
DB 498 FQPIFLSGYTMWIRINHSLSLSDSPPTCVLPDVSVKPLPPS 539

RESULT 32
US-08-827-962-20
Sequence 20, Application US/08827962A
Patent No. 6258944
GENERAL INFORMATION:
APPLICANT: MERCK & CO., INC.
TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS
FILE REFERENCE: 19693
CURRENT APPLICATION NUMBER: US/08/827,962A
CURRENT FILING DATE: 1997-05-06

PRIOR APPLICATION NUMBER: 60/016,899
PRIOR FILING DATE: 1996-05-06
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 1162
TYPE: PRT
ORGANISM: Rattus No. 6258944vegicus
US-08-827-962-20

Query Match 3.6%; Score 42; DB 4; Length 1162;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSLSLSDSPPTCVLPDVSVKPLPPS 541
DB 498 FQPIFLSGYTMWIRINHSLSLSDSPPTCVLPDVSVKPLPPS 539

RESULT 33
US-08-803-346-1
Sequence 1, Application US/08803346
Patent No. 6281346
GENERAL INFORMATION:
APPLICANT: HESS, JOHN W.
APPLICANT: CASKEY, C. THOMAS
APPLICANT: LIU, QINGYUN
APPLICANT: PHILLIPS, MICHAEL SEAN
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSEY, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19642Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-803-346-1

Query Match 3.6%; Score 42; DB 4; Length 1162;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINSLGSLDSEPTCVLPDSVVKPLPPS 541
DB 498 FQPIFLSGYTMWIRINSLGSLDSEPTCVLPDSVVKPLPPS 539

RESULT 34

US-09-069-781B-43
Sequence 43, Application US/09069781B
Patent No. 6287782
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/069,781B
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-09-069-781B-43

Query Match 3.6%; Score 42; DB 4; Length 1162;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINSLGSLDSEPTCVLPDSVVKPLPPS 541
DB 498 FQPIFLSGYTMWIRINSLGSLDSEPTCVLPDSVVKPLPPS 539

RESULT 35

US-08-803-346-63
Sequence 63, Application US/08803346
Patent No. 6281346
GENERAL INFORMATION:
APPLICANT: HESS, JOHN W.
APPLICANT: CASKEY, C. THOMAS
APPLICANT: LIU, QINGYUN
APPLICANT: PHILLIPS, MICHAEL SEAN
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/803,346
APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19642Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-803-346-63

Query Match 2.1%; Score 24; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 557 SWEKPVFPENNLOFQIRYGLSGKE 580
DB 5 SWEKPVFPENNLOFQIRYGLSGKE 28

RESULT 36
US-08-701-382-6
Sequence 6, Application US/08701382
Patent No. 6004758
GENERAL INFORMATION:
APPLICANT: OLSSON, Lennart
APPLICANT: NAVREND, Tatjana
TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES INVOLVED IN
TITLE OF INVENTION: MODULATION OF RESPONSE TO LIGAND BINDING

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,382
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SHERWOOD, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A63139-1/PJS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-8700
TELEFAX: 415-494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-701-382-6

Query Match 2.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.3e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 KKENKIVPSKEIVMMNLAERIP 377
|||||
DB 1 KKENKIVPSKEIVMMNLAERIP 23

RESULT 37
US-09-028-937-6
Sequence 6, Application US/09028937
Patent No. 6333031
GENERAL INFORMATION:
APPLICANT: Olsson, Lennart
APPLICANT: Naranda, Tatjana
TITLE OF INVENTION: Receptor Derived Peptides As Modulators
TITLE OF INVENTION: Of Receptor Activity
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,937
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/788,820
FILING DATE: 23-JAN-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/701,382
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,995
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-028-937-6

Query Match 2.0%; Score 23; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.3e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 KKENKIVPSKEIVMMNLAERIP 377
|||||
DB 1 KKENKIVPSKEIVMMNLAERIP 23

RESULT 38
US-08-788-820-6
Sequence 6, Application US/08788820
Patent No. 6346390
GENERAL INFORMATION:
APPLICANT: Olsson, Lennart
APPLICANT: Naranda, Tatjana
TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES INVOLVED IN
TITLE OF INVENTION: MODULATION OF RESPONSE TO LIGAND BINDING
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,820
FILING DATE: 23-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,999
FILING DATE: 08-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/701,382
FILING DATE: 22-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Treccarlin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-63139-2/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 50..1030
US-08-788-820-6

Query Match 2.0%; Score 23; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.3e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 KKENKIVPSKEIYMMNLAEKIP 377
DB 1 KKENKIVPSKEIYMMNLAEKIP 23

RESULT 39
US-08-803-346-62
Sequence 62, Application US/08803346
Patent No. 6281346
GENERAL INFORMATION:
APPLICANT: HESS, JOHN W.
APPLICANT: CASKEY, C. THOMAS
APPLICANT: LIU, QINGYUN
APPLICANT: PHILLIPS, MICHAEL SEAN
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803.346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19642Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-803-346-62

Query Match 1.7%; Score 20; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 SWEKPVFPENNLOFOIRYGL 576
DB 5 SWEKPVFPENNLOFOIRYGL 24

RESULT 40
US-08-306-231-14
Sequence 14, Application US/08306231
Patent No. 5643748
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Clotfi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306.231
FILING DATE: 14-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-306-231-14

Query Match 1.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GGSYEYQVGRKRLDG 315
DB 1 GGSYEYQVGRKRLDG 15

RESULT 41
US-08-306-231-15
Sequence 15, Application US/08306231
Patent No. 5643748
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Clotfi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 15

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036-2711
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/306,231
;; FILING DATE: 14-SEP-1994
;;
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poissant, Brian M.
;; REGISTRATION NUMBER: 7225-076
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;;
;; TELEX: 66141 PENNIE
;;
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;;
;; MOLECULE TYPE: peptide
;;
;; US-08-306-231-15

Query Match 1.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 CAVYAVQVCKRLDG 618
|||||

Db 1 CAVYAVQVCKRLDG 15

RESULT 42
US-08-355-888A-30
; Sequence 30, Application US/08355888A
; Patent No. 5763211
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,888A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.

;; REGISTRATION NUMBER: 28,462
;; REFERENCE/DOCKET NUMBER: 7225-078
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;;
;; TELEX: 66141 PENNIE
;;
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;;
;; MOLECULE TYPE: peptide
;;
;; US-08-355-888A-30

Query Match 1.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GSSYEYQVGRKRLDG 315
|||||

Db 1 GSSYEYQVGRKRLDG 15

RESULT 43
US-08-355-888A-31
; Sequence 31, Application US/08355888A
; Patent No. 5763211
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,888A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
;
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-355-888A-31

Query Match 1.3%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 CAVYAVQVCKRLDG 618
|||||
DB 1 CAVYAVQVCKRLDG 15

RESULT 44
US-08-693-697-30
; Sequence 30, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693.697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-693-697-30

Query Match 1.3%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GSSYEYQVGRKRLDG 315
|||||
DB 1 GSSYEYQVGRKRLDG 15

RESULT 45
US-08-693-697-31
; Sequence 31, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR

NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693.697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-693-697-31

Query Match 1.3%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 CAVYAVQVCKRLDG 618
|||||
DB 1 CAVYAVQVCKRLDG 15

RESULT 46
US-08-693-696-30
; Sequence 30, Application US/08693696
; Patent No. 6005080
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693.696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/355,888
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-693-696-30

Query Match 1.3%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GSSYEVQYRKRLDG 315
|||||
DB 1 GSSYEVQYRKRLDG 15

RESULT 47
US-08-693-696-31
Sequence 31, Application US/08693696
Patent No. 6005080
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,888
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-693-696-31

Query Match 1.3%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 CAVYAVQYRKRLDG 618
|||||
DB 1 CAVYAVQYRKRLDG 15

RESULT 48
US-08-306-231-9
Sequence 9, Application US/08306231
Patent No. 5643748
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,231
FILING DATE: 14-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-306-231-9

Query Match 1.1%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 569 QFOIRYGLSGKEV 581
|||||
DB 1 QFOIRYGLSGKEV 13

RESULT 49
US-08-355-888A-25
Sequence 25, Application US/08355888A
Patent No. 5763211

GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: HU-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,888A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-355-888A-25

Query Match 1.1%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 OFOIRYGLSGKEY 581
DB 1 QFOIRYGLSGKEY 13

RESULT 50
US-08-693-697-25
Sequence 25, Application US/08693697
Patent No. 5869610
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: HU-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-693-697-25

Query Match 1.1%; Score 13; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 OFOIRYGLSGKEY 581
DB 1 QFOIRYGLSGKEY 13

Search completed: May 18, 2002, 07:04:11
Job time: 290 sec

Sun May 19 08:38:55 2002

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